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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:15:31 ; Search time 87.4 Seconds
(without alignments)
3712.721 Million cell updates/sec

Title: US-09-396-985B-2
Perfect score: 4355
Sequence: 1.MMSASRLAGTLIPAMAFISC.....SMNPEGTGTCNNQCATSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4355	100.0	839	6	ABU04773 Human exp
2	4355	100.0	839	6	ABU04774 Human exp
3	4355	100.0	839	6	ABU04775 Human exp
4	4355	100.0	839	7	ADC78785 Human PRO
5	4355	100.0	839	7	ADD48826 Human PRO
6	4335.5	99.6	837	5	AAW86361 Human DNA
7	4335.5	99.6	837	5	AAE16102 Human DNA
8	4335.5	99.6	837	5	ABU04776 Human exp
9	4328.5	99.4	837	5	AAE16116 Human DNA
10	4178	95.9	808	8	ADOS7782 Chimpanze
11	4167	95.7	808	8	ADOS7785 Gorilla t
12	4164	95.6	808	8	ADOS7803 Chimpanze
13	4141	95.1	799	5	AAW86352 Human DNA
14	4141	95.1	799	5	AAE16093 Human DNA
15	4141	95.1	799	5	ABH83162 Human Tol
16	4141	95.1	799	6	ABR42863 Human Tol
17	4141	95.1	799	7	ADB39121 Human Tol
18	4141	95.1	799	7	ADP56656 Human Tol
19	4141	95.1	799	8	ADP48597 Human Tol
20	4040	92.8	801	8	ADOS7788 Gibbon to
21	3918	90.0	795	8	ADOS7791 Rhesus mo
22	3892	89.4	795	8	ADOS7800 Hamadryas
23	3819	87.7	801	8	ADOS7797 Squirrel
24	3681.5	84.6	738	8	ADP29455 Human sec
25	3501	80.4	745	8	ADOS7794 White-fac

26	1090	25.0	208	3	AAV88059 Human Tol
27	919	21.1	178	8	ADN12270 IL-1R/TLR
28	785	18.0	179	7	ADC42707 Murine To
29	629.5	14.5	661	2	AAW28510 Product o
30	629.5	14.5	661	2	AAW87556 B cell su
31	629.5	14.5	661	7	ADC38652 Human sec
32	629.5	14.5	661	7	ADP69098 Human MP5
33	628.5	14.4	650	3	AAV82527 Human RP1
34	615.5	14.1	661	2	AAW47274 Human B-C
35	603.5	13.9	784	2	AAW86350 Human DNA
36	603.5	13.9	784	5	AAE16091 Human DNA
37	603.5	13.9	784	5	ABH83161 Human Tol
38	603.5	13.9	784	8	ADN02005 Human Inf
39	602.5	13.8	784	2	AAV05869 Human Tol
40	602.5	13.8	784	6	ABU61956 Human Tol
41	602.5	13.8	784	7	ADL15005 Human Tol
42	602.5	13.8	784	8	ADP56652 Human Tol
43	602.5	13.8	784	8	ADP48593 Human Tol
44	602.5	13.8	784	8	ADP23787 PRO polyP
45	602.5	13.8	784	8	ADQ39727 Human myo

ALIGNMENTS

RESULT 1	ABU04773	standard; protein; 839 AA.
ID	ABU04773	
XX	ABU04773;	
AC	ABU04773;	
XX	29-JAN-2003	(first entry)
DT	29-JAN-2003	(first entry)
XX	Human expressed protein tag (EPT) #1439.	
DE	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;	
XX	protease; protease inhibitor; transporter; cytoskeletal protein;	
KW	receptor; transcription factor; cancer; MHC;	
KW	major histocompatibility complex; myeloma; lymphoma; leukemia;	
KW	adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.	
OS	Homo sapiens.	
XX	WO200278524-A2.	
PN	10-OCT-2002.	
XX	28-MAR-2002; 2002WO-US009671.	
PF	28-MAR-2001; 2001US-0279495P.	
XX	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326370P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358985P.	
XX	(ZYCO-) ZYCO INC.	
XX	Chicz RM, Tomlinson AJ, Urban RG;	
PI	WPI; 2003-040607/03.	
DR	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,	
PT	cytoskeletal proteins, receptors or transcription factors), useful for	
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or	
PT	leukemia.	
PS	Example 2; SEQ ID NO 1439; 134dp; English.	
XX	The invention describes a purified polypeptide, which comprises a	
CC	fragment of a kinase, phosphatase, protease, protease inhibitor,	
CC	transporter, cytoskeletal protein, receptor or transcription factor. The	
CC	polypeptide is useful as an immunogenic composition for eliciting in a	

Query Match	100.0%	Score 4355	DB 6	Length 839
Best Local Similarity	100.0%	Pred. No. 0		
Matches 839	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MMSASRLAGTLLPAMAFISCVRPESMEPCVEVVPNTTYQCMELNPKYKIDNLPFSTKNDL	60	
Db	1	MMSASRLAGTLLPAMAFISCVRPESMEPCVEVVPNTTYQCMELNPKYKIDNLPFSTKNDL	60	
QY	61	LSFNRLRHSGSFFSPFPELQVLDLSRCICITIBGAYOSLSHLSLTLITGNPIQSLAG	120	
Db	61	LSFNRLRHSGSFFSPFPELQVLDLSRCICITIBGAYOSLSHLSLTLITGNPIQSLAG	120	
QY	121	AFSGSLSLQKLVAVETNLTASLENPFIGHKLTKELVANHLIQSFGLPEYFSNLTNLBHL	180	
Db	121	AFSGSLSLQKLVAVETNLTASLENPFIGHKLTKELVANHLIQSFGLPEYFSNLTNLBHL	180	
QY	181	DLSSNKIOSIYCTDLRVLHOMPLNLSIDLINPMNFIOPGAFKELRLHKLTLRNNPDSL	240	
Db	181	DLSSNKIOSIYCTDLRVLHOMPLNLSIDLINPMNFIOPGAFKELRLHKLTLRNNPDSL	240	
QY	241	NVMKTCIOGLAGLEVHRLVYGFRRNEGNIKEKDKALBGLCNLTITBEPRLAYLDYLDI	300	
Db	241	NVMKTCIOGLAGLEVHRLVYGFRRNEGNIKEKDKALBGLCNLTITBEPRLAYLDYLDI	300	
QY	301	IDLFNCLINWSSFSLSVATIERVKDPSVNFQGMHLELVNCKRGOPPTLKLSIKRLTPTS	360	
Db	301	IDLFNCLINWSSFSLSVATIERVKDPSVNFQGMHLELVNCKRGOPPTLKLSIKRLTPTS	360	
QY	361	NKGNAFSEVLDPSLEFLDLSRNGHSFKGCSQSDPGTTSLSKYLDLSFNGVITMSNPLG	420	
Db	361	NKGNAFSEVLDPSLEFLDLSRNGHSFKGCSQSDPGTTSLSKYLDLSFNGVITMSNPLG	420	
QY	421	LEQLHLDLPOHSNLTQOMSEFSYFSLRLNLIYLDISHTRVAFNGIFNGLSLEVLKXAG	480	
Db	421	LEQLHLDLPOHSNLTQOMSEFSYFSLRLNLIYLDISHTRVAFNGIFNGLSLEVLKXAG	480	
QY	481	NSFOENFLPDLFTELRNLTLPLDLSGCOLBOLSPFANSLISLYLVNMSNNNPFSLDTPPY	540	
Db	481	NSFOENFLPDLFTELRNLTLPLDLSGCOLBOLSPFANSLISLYLVNMSNNNPFSLDTPPY	540	
QY	541	KCLNSLYLDVSLNHNIMTSSKKQELCHFPSSSLAFMLITONDFACTCEHOSFLQWIDQROL	600	
Db	541	KCLNSLYLDVSLNHNIMTSSKKQELCHFPSSSLAFMLITONDFACTCEHOSFLQWIDQROL	600	
QY	601	LVEVERMECAPSPSDKQMPVLSLNTTCOMNKTIIIGVSVLSVLVSVVAVLVYKFYFHLML	660	
Db	601	LVEVERMECAPSPSDKQMPVLSLNTTCOMNKTIIIGVSVLSVLVSVVAVLVYKFYFHLML	660	
QY	661	LAGCTKYRGENTIYDAFIYSSQDDDWARNELVKNLEGGVPPQCLHYRDTIPEVALAA	720	
Db	661	LAGCTKYRGENTIYDAFIYSSQDDDWARNELVKNLEGGVPPQCLHYRDTIPEVALAA	720	
QY	721	NIIEHGFSKRSKVIYVVSQHFIOSEWCIFEYEIAOTWQFLSSRAGIIFVLOKVEKTLIR	780	
Db	721	NIIEHGFSKRSKVIYVVSQHFIOSEWCIFEYEIAOTWQFLSSRAGIIFVLOKVEKTLIR	780	
QY	781	QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDGSNNBEGTVGTCMMQDEATSI	839	

Db 761 QCVELXRLSRITYLEMEDSVGRHIFWRRLKALLDGSKNPEIGTIGTCNMQBEATSI 839

RESULT 2
ID ABU04774
XX ABU04774 standard; protein; 839 AA.
XX AC ABU04774;
XX DT
XX 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1440.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX OS
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX PS Example 2; SEQ ID NO 1440; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp://ipo.int/pub/published_pct_sequences

Sequence 839 AA;
SQ

Query Match 100.0%; Score 4355; DB 6; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 MMASASRLAGTILPAAFLSCVAPESMECEVEVPNITVQCMELNFKIKIPDNLPTSTKND 60

Db 301 IDLFCNLTVSSFSLSVSTIERVKDPSYNFGQHLVNCCKFGQPTLKLSKLRLTTS 360
Qy 361 NKGNAPSEVDLPSEFLDLNRNGLSFRGCCSQSDPGTSTLKYLDLSFNGVITMSSNPLG 420
Db 361 NKGNAPSEVDLPSEFLDLNRNGLSFRGCCSQSDPGTSTLKYLDLSFNGVITMSSNPLG 420
Qy 421 LEQLEHLDPQHSNKLQKQSEFSVFLSLRNLIYLDISHTTRVAFNGIFNGLSLEVLKXAG 480
Db 421 LEQLEHLDPQHSNKLQKQSEFSVFLSLRNLIYLDISHTTRVAFNGIFNGLSLEVLKXAG 480
Qy 481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLMNSHNNFSLDTPPY 540
Db 481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLMNSHNNFSLDTPPY 540
Qy 541 KCLNSLOVLDVSLNHNMTSKQELQHPSSSLAFNLTONDPACTCEHOSFLQWIKDQRL 600
Db 541 KCLNSLOVLDVSLNHNMTSKQELQHPSSSLAFNLTONDPACTCEHOSFLQWIKDQRL 600
Qy 601 LVEVERMECATPPSDQKQMPVLSLNTTCOMNKTIIIGVSVLSVLSVVAVLVYKFFHML 660
Db 601 LVEVERMECATPPSDQKQMPVLSLNTTCOMNKTIIIGVSVLSVLSVVAVLVYKFFHML 660
Qy 661 LAGCIKYGRENIDAFVIYSSODEDWVRNELVKRLKEGVPFPOLCLHYRDFIPGVAIAA 720
Db 661 LAGCIKYGRENIDAFVIYSSODEDWVRNELVKRLKEGVPFPOLCLHYRDFIPGVAIAA 720
Qy 721 NIHEGFHKSRRVIVVVSQHPFIOHRKCIPEYELAQTMQFLSSRAGIIFIVLQKVEKTLIR 780
Db 721 NIHEGFHKSRRVIVVVSQHPFIOHRKCIPEYELAQTMQFLSSRAGIIFIVLQKVEKTLIR 780
Qy 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNMPEGTGTGCMQEAISI 839
Db 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNMPEGTGTGCMQEAISI 839

RESULT 4
ADC78785
ID ADC78785 standard; procein; 839 AA.
XX
AC ADC78785;
XX
DT 01-JAN-2004 (first entry)
XX
DB Human PRO protein #7.
XX
KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX
OS Homo sapiens.
XX
PN M02003034984-A2.
XX
PD 01-MAY-2003.
XX
PF 15-OCT-2002; 2002MO-US033070.
XX
PR 19-OCT-2001; 2001US-0340083P.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL;
XX
DR WPI; 2003-481990/45.
XX
DR N-PSDB; ADC78784.
XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
PT disorder e.g., ulcerative colitis or Crohn's disease.
PS Claim 12; SEQ ID NO 14; 327BP; English.
XX
XX The invention comprises the amino acid and coding sequences of human PRO
CC proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
CC sequence represents a human PRO protein of the invention.
XX
SQ Sequence 839 AA:
Query Match 100.0%; Score 4355; DB 7; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMSASRLAGTILPMAFLSCVRPESWPCVAVNINITYQCMELPYKIPDNLPESTKXLD 60
Db 1 MMSASRLAGTILPMAFLSCVRPESWPCVAVNINITYQCMELPYKIPDNLPESTKXLD 60
Qy 61 LSPFPLRLHLSYSPFSPELQVLDLSRCEIQTIEDGAVQSSLSHTLITGNPIQSLALG 120
Db 61 LSPFPLRLHLSYSPFSPELQVLDLSRCEIQTIEDGAVQSSLSHTLITGNPIQSLALG 120
Qy 121 AFSGLSLQKLVAVETNLASLENPPIGHLTKLELVANHLIQSPKLPYFSSNLTNLEHL 180
Db 121 AFSGLSLQKLVAVETNLASLENPPIGHLTKLELVANHLIQSPKLPYFSSNLTNLEHL 180
Qy 181 DLSGNKIOSITCTDRLVLRHQLNLSDLSLNMNFIQPAFKEIRLKLTLRNNPSTL 240
Db 181 DLSGNKIOSITCTDRLVLRHQLNLSDLSLNMNFIQPAFKEIRLKLTLRNNPSTL 240
Qy 241 NVMTKCIQGLAGLVHRLVLGEFNEGNLEKFDKSALEGLCNLTIEEPRLAYLDYLDLI 300
Db 241 NVMTKCIQGLAGLVHRLVLGEFNEGNLEKFDKSALEGLCNLTIEEPRLAYLDYLDLI 300
Qy 301 IDLFCNLTVSSFSLSVSTIERVKDPSYNFGQHLVNCCKFGQPTLKLSKLRLTTS 360
Db 301 IDLFCNLTVSSFSLSVSTIERVKDPSYNFGQHLVNCCKFGQPTLKLSKLRLTTS 360
Qy 361 NKGNAPSEVDLPSEFLDLNRNGLSFRGCCSQSDPGTSTLKYLDLSFNGVITMSSNPLG 420
Db 361 NKGNAPSEVDLPSEFLDLNRNGLSFRGCCSQSDPGTSTLKYLDLSFNGVITMSSNPLG 420
Qy 421 LEQLEHLDPQHSNKLQKQSEFSVFLSLRNLIYLDISHTTRVAFNGIFNGLSLEVLKXAG 480
Db 421 LEQLEHLDPQHSNKLQKQSEFSVFLSLRNLIYLDISHTTRVAFNGIFNGLSLEVLKXAG 480
Qy 481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLMNSHNNFSLDTPPY 540
Db 481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLMNSHNNFSLDTPPY 540
Qy 541 KCLNSLOVLDVSLNHNMTSKQELQHPSSSLAFNLTONDPACTCEHOSFLQWIKDQRL 600
Db 541 KCLNSLOVLDVSLNHNMTSKQELQHPSSSLAFNLTONDPACTCEHOSFLQWIKDQRL 600
Qy 601 LVEVERMECATPPSDQKQMPVLSLNTTCOMNKTIIIGVSVLSVLSVVAVLVYKFFHML 660
Db 601 LVEVERMECATPPSDQKQMPVLSLNTTCOMNKTIIIGVSVLSVLSVVAVLVYKFFHML 660
Qy 661 LAGCIKYGRENIDAFVIYSSODEDWVRNELVKRLKEGVPFPOLCLHYRDFIPGVAIAA 720
Db 661 LAGCIKYGRENIDAFVIYSSODEDWVRNELVKRLKEGVPFPOLCLHYRDFIPGVAIAA 720
Qy 721 NIHEGFHKSRRVIVVVSQHPFIOHRKCIPEYELAQTMQFLSSRAGIIFIVLQKVEKTLIR 780
Db 721 NIHEGFHKSRRVIVVVSQHPFIOHRKCIPEYELAQTMQFLSSRAGIIFIVLQKVEKTLIR 780
Qy 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNMPEGTGTGCMQEAISI 839
Db 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNMPEGTGTGCMQEAISI 839

RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
XX
AC ADD48826;
XX

DT 02-DEC-2004 (revised)
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein AAF05316, SEQ ID NO 14536.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 OS Unidentified.
 XX
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (PARB) BAYER AG.
 PI Woolf C, D'Urso D, Refort K, Costigan M;
 PI WPI; 2003-268312/26.
 DR GENBANK; AAF05316.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Example 1; Page: 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (described in Table 3
 CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WPI at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 839 AA;

Query Match 100.0%; Score 4355; DB 7; Length 839;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMSASRLAGTILIPMAFLSCVRPSWPCVEVPVITQCMELNFKYKIPDNLPSTKMLD 60
 DB 1 MMSASRLAGTILIPMAFLSCVRPSWPCVEVPVITQCMELNFKYKIPDNLPSTKMLD 60

OY 61 LSFNPLHLGSSYSPFPPELQVLDLSRCCEIQTEDAGYQSLSHSTLILNGNPIQSLALG 120
 DB 61 LSFNPLHLGSSYSPFPPELQVLDLSRCCEIQTEDAGYQSLSHSTLILNGNPIQSLALG 120
 OY 121 AFGSLSLQKLVAVETNLASLBNPPIGHLTKLKELANAHNLIOGFKPEVPSNLTNLEHL 180
 DB 121 AFGSLSLQKLVAVETNLASLBNPPIGHLTKLKELANAHNLIOGFKPEVPSNLTNLEHL 180
 OY 181 DLSNNKIOSIYCTDLRLVLAHQMPPLNLISLISLNPMPNFIQGAPEKIRLKLTLNNPDSL 240
 DB 181 DLSNNKIOSIYCTDLRLVLAHQMPPLNLISLISLNPMPNFIQGAPEKIRLKLTLNNPDSL 240
 OY 241 NVMKTCIQGLAGLEVHRLVIGEPFNNBGNLEKFDKSALEGLCNLTIEEFRLAYLDYDDI 300
 DB 241 NVMKTCIQGLAGLEVHRLVIGEPFNNBGNLEKFDKSALEGLCNLTIEEFRLAYLDYDDI 300
 OY 301 IDLFNCLTNVSSPSLVSVTLERVKDFSYNFGMOHLELVNCKFGQFPTLKLSLRLEPFS 360
 DB 301 IDLFNCLTNVSSPSLVSVTLERVKDFSYNFGMOHLELVNCKFGQFPTLKLSLRLEPFS 360
 OY 361 NKGNAFSEYDLSLEFLDLSRNLSPKGCOSQDFGTTSLKYDLSPNGVITWSSNPLG 420
 DB 361 NKGNAFSEYDLSLEFLDLSRNLSPKGCOSQDFGTTSLKYDLSPNGVITWSSNPLG 420
 OY 421 LEQLEHLDFOHSNKKQMSFVPLSLRNLIYLDISHTHTVAENGIRNGLSLELVKAG 480
 DB 421 LEQLEHLDFOHSNKKQMSFVPLSLRNLIYLDISHTHTVAENGIRNGLSLELVKAG 480
 OY 481 NSFOENFLPIFTELRLNLTFLDLSOCOLBOLSPFAPNSLSIOVLANSHNNFSLDTPPY 540
 DB 481 NSFOENFLPIFTELRLNLTFLDLSOCOLBOLSPFAPNSLSIOVLANSHNNFSLDTPPY 540
 OY 541 KCLNSLOVLDYSLNHIMTSKKOBLQHPSSLAFLNLTQNDFACTCEHQSFLOWTKDQRL 600
 DB 541 KCLNSLOVLDYSLNHIMTSKKOBLQHPSSLAFLNLTQNDFACTCEHQSFLOWTKDQRL 600
 OY 601 LVEYERMECATPSDKQGMPLVSLNTQNMKTIIIGVSVLVVSVVAVLVYKRYFHLML 660
 DB 601 LVEYERMECATPSDKQGMPLVSLNTQNMKTIIIGVSVLVVSVVAVLVYKRYFHLML 660
 OY 661 LAGCIRKGRBNITVDAVIVSSODEMVRNLELVNLEEGVPPOLCLHYHDFITGVALLA 720
 DB 661 LAGCIRKGRBNITVDAVIVSSODEMVRNLELVNLEEGVPPOLCLHYHDFITGVALLA 720
 OY 721 NIIEGHFKSRKVIIVVVSQHFIOGRWCIFEYELAQTWQPLSSRAGIIFIVLQKYEKTLRL 780
 DB 721 NIIEGHFKSRKVIIVVVSQHFIOGRWCIFEYELAQTWQPLSSRAGIIFIVLQKYEKTLRL 780
 OY 781 QQVELVRLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPBGVGTGCMQGEATSI 839
 DB 781 QQVELVRLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPBGVGTGCMQGEATSI 839

RESULT 6

AAW86361
 ID AAW86361 standard; protein; 837 AA.

AAW86361;

15-MAR-1999 (first entry)

Human DNAX toll-1-like receptor DTLR4.

KW DNAX toll-1-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
 KW interleukin 1 receptor; phosphate metabolism; innate immunity response;
 KW modulate inflammatory function; morphological effect;
 KW immunological disorder.

OS Homo sapiens.

PN WO9805047-A2.

PD 12-NOV-1998.

CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTR or cells that express it. The present sequence is
 CC human DTR4 protein. The DTR4 gene is located on chromosome 9q32-33.
 CC Note: The present sequence SEQ ID NO 26 is stated to be similar to the
 CC sequence shown in page 240-243 (AAB1616). However these sequences differ
 CC at several locations
 CC
 XX

XX Sequence 837 AA;

Query March 99.6%; Score 4335.5; DB 5; Length 837;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 MSASRLAGTLIPAAAFSCVAPESMEPCVEVVPNTTYQCMELNFKYKIPDNLPSTKNL 61
 Db 1 MSASRLAGTLIPAAAFSCVAPESMEPCVE-VPNITTYQCMELNFKYKIPDNLPSTKNL 59
 QY 62 SFNPLRHIGSYSPSPPELQVLDLSRCEIQITIEDGAYQSLSHSLTLITGNPIQSLALGA 121
 Db 60 SFNPLRHIGSYSPSPPELQVLDLSRCEIQITIEDGAYQSLSHSLTLITGNPIQSLALGA 119
 QY 122 FSGSLSLQKLVAVENNLASLENPFGHKTKELVANNLIQSPCLPEYFENLTLEHLD 181
 Db 120 FSGSLSLQKLVAVENNLASLENPFGHKTKELVANNLIQSPCLPEYFENLTLEHLD 179
 QY 182 LSNKTIQSYCTDRLVHQPMLNLSLDPNPMNFIOGAFKELRLKLTLRNPFDSLN 241
 Db 180 LSNKTIQSYCTDRLVHQPMLNLSLDPNPMNFIOGAFKELRLKLTLRNPFDSLN 239
 QY 242 VMKTCIQGLAEVRLVGEFRNEGNLEKFDKSLBGLCNLTIEBFLAVLDYDII 301
 Db 240 VMKTCIQGLAEVRLVGEFRNEGNLEKFDKSLBGLCNLTIEBFLAVLDYDII 299
 QY 302 DLFNCLTVSSFSLSVTVTERKQDSYVNGQHELVNCKRGQPTTLKSLKLTFTSN 361
 Db 300 DLFNCLTVSSFSLSVTVTERKQDSYVNGQHELVNCKRGQPTTLKSLKLTFTSN 359
 QY 362 KGNNAFSEVDLPSEFLFLSRNGLSFKGCCSOSDGTTLKYLDSFNGVITMSNFG 421
 Db 360 KGNNAFSEVDLPSEFLFLSRNGLSFKGCCSOSDGTTLKYLDSFNGVITMSNFG 419
 QY 422 EQLHLDFOHNSNLKOMSEFVFLSLRNLIYLDISHTHTVAFNGIENGLSLEVLKMA 481
 Db 420 EQLHLDFOHNSNLKOMSEFVFLSLRNLIYLDISHTHTVAFNGIENGLSLEVLKMA 479
 QY 482 SFQENFLPDITELRNLTFLDLSQCLHQLSPFANSLSLQVLMNSHNNPFLDTPPYK 541
 Db 480 SFQENFLPDITELRNLTFLDLSQCLHQLSPFANSLSLQVLMNSHNNPFLDTPPYK 539
 QY 542 CLNSIQVLDYSLNHNMTSKKOLHFPSSLAFLNLTNDPACTCHQSFLQWIKQOR 601
 Db 540 CLNSIQVLDYSLNHNMTSKKOLHFPSSLAFLNLTNDPACTCHQSFLQWIKQOR 599
 QY 602 VEVERMECATSDKQGMFVLNLTITCQANKITIIIGSVLSVAVVAVLVYKFEYHML 661
 Db 600 VEVERMECATSDKQGMFVLNLTITCQANKITIIIGSVLSVAVVAVLVYKFEYHML 659
 QY 662 AGCTYGGENIYDAFVIYSSODEDVENELVKNLEGGVPOLCLAYRDPIDVAAIAN 721
 Db 660 AGCTYGGENIYDAFVIYSSODEDVENELVKNLEGGVPOLCLAYRDPIDVAAIAN 719
 QY 722 IHHGFHRSRVIVVVOHFIOSRWCIFEYEIAQWQFLSSAGIIFVLQKVEKTLTRO 781
 Db 720 IHHGFHRSRVIVVVOHFIOSRWCIFEYEIAQWQFLSSAGIIFVLQKVEKTLTRO 779
 QY 782 QVELYRLLSRNTYLEMEDSVLGRHIFWRRLRKALLDGKSNPEGTVGTCMWOEATSI 839
 Db 780 QVELYRLLSRNTYLEMEDSVLGRHIFWRRLRKALLDGKSNPEGTVGTCMWOEATSI 837

RESULT 8
 ABU04776

ID ABU04776 standard; protein; 837 AA.

XX ABU04776;

XX 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1442.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW cytochrome; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX Example 2; SEQ ID NO 1442; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, or transcription factor.
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_ptc_sequences
 XX

XX Sequence 837 AA;

Query March 99.6%; Score 4335.5; DB 6; Length 837;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 MSASRLAGTLIPAAAFSCVAPESMEPCVEVVPNTTYQCMELNFKYKIPDNLPSTKNL 61
 Db 1 MSASRLAGTLIPAAAFSCVAPESMEPCVE-VPNITTYQCMELNFKYKIPDNLPSTKNL 59
 QY 62 SFNPLRHIGSYSPSPPELQVLDLSRCEIQITIEDGAYQSLSHSLTLITGNPIQSLALGA 121
 Db 60 SFNPLRHIGSYSPSPPELQVLDLSRCEIQITIEDGAYQSLSHSLTLITGNPIQSLALGA 119

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QY 122 FSGLSSTLQKVAVETNLASLENPPIGHLKTLKEINVAHNLIOQFKLPEYFSNLTNLEHLD 181
XX |||
XX 120 FSGLSSTLQKVAVETNLASLENPPIGHLKTLKEINVAHNLIOQFKLPEYFSNLTNLEHLD 179
XX |||
QY 182 LSSNKIOSICTDRLRVLHQWPLNLSLDLSLNPNPFIOGPAFKRIHLAKTLRNPFSLN 241
XX |||
XX 180 LSSNKIOSICTDRLRVLHQWPLNLSLDLSLNPNPFIOGPAFKRIHLAKTLRNPFSLN 239
XX |||
QY 242 VMKTCIOGLAGLEVHRLVGEFRNEGNLEKFDKSALEGLCNLTIEEPRLAYLDYLDII 301
XX |||
XX 240 VMKTCIOGLAGLEVHRLVGEFRNEGNLEKFDKSALEGLCNLTIEEPRLAYLDYLDII 299
XX |||
QY 302 DLFNCLTNVSSFSIVSVTIERVKDFSYNFGMOHLELVNCKFGQPPTLKLSKRLTFTSN 361
XX |||
XX 300 DLFNCLTNVSSFSIVSVTIERVKDFSYNFGMOHLELVNCKFGQPPTLKLSKRLTFTSN 359
XX |||
QY 362 KGGNAFSEVDLPSELEFLDLSRNGLSFKGCCSQSDPGTTSLKYLDLSFNGVITMSSNPLGL 421
XX |||
XX 360 KGGNAFSEVDLPSELEFLDLSRNGLSFKGCCSQSDPGTTSLKYLDLSFNGVITMSSNPLGL 419
XX |||
QY 422 EQLBHLDFOHSNLSKQMSFVFLSLRNLTYLDISHTHTRVAFNGIFNGLSLEVLKMAGN 481
XX |||
XX 420 EQLBHLDFOHSNLSKQMSFVFLSLRNLTYLDISHTHTRVAFNGIFNGLSLEVLKMAGN 479
XX |||
QY 482 SFQENFLPDIPTTELRLNLTFLDLSQCCLEQLSPFAFNSISLQVIMSHNPFSLDTPPYK 541
XX |||
XX 480 SFQENFLPDIPTTELRLNLTFLDLSQCCLEQLSPFAFNSISLQVIMSHNPFSLDTPPYK 539
XX |||
QY 542 CLNLSLOYLDVSLNIMTSSKQELQHPBSLAFNLNTQDFACTGHEOSFLQWIDQOQL 601
XX |||
XX 540 CLNLSLOYLDVSLNIMTSSKQELQHPBSLAFNLNTQDFACTGHEOSFLQWIDQOQL 599
XX |||
QY 602 VEVRMCAFPSPDQGMFVSLNITCQNKTIIGSVSLVSVVAVLVYKFEFHLML 661
XX |||
XX 600 VEVRMCAFPSPDQGMFVSLNITCQNKTIIGSVSLVSVVAVLVYKFEFHLML 659
XX |||
QY 662 AGCIKYGGENIYDAFYIYSSQDEDMWNELVKNLEBGPFPOLCLHYRDFIPGVAIAAN 721
XX |||
XX 660 AGCIKYGGENIYDAFYIYSSQDEDMWNELVKNLEBGPFPOLCLHYRDFIPGVAIAAN 719
XX |||
QY 722 IIHGFHSKRKYTVVSGHFIQSRWCTFEYEAIAQTWQPLSRAGIIFVLQKREKTLRLQ 781
XX |||
XX 720 IIHGFHSKRKYTVVSGHFIQSRWCTFEYEAIAQTWQPLSRAGIIFVLQKREKTLRLQ 779
XX |||
QY 782 QVELYRLLSRNTYLEMEDSVLGRHIFWRRLRKALLDGKSNPEGTGNCWQOATS1 839
XX |||
XX 780 QVELYRLLSRNTYLEMEDSVLGRHIFWRRLRKALLDGKSNPEGTGNCWQOATS1 837
XX |||

RESULT 9
AAE16116
ID AAE16116 standard; protein; 837 AA.
XX
XX AAE16116;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human DNAX Toll like receptor (DTRLR) 4 #2, alternative version.
XX
XX Human DNAX Toll like receptor; DTRLR; therapy; immunological disorder;
XX Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX MISC-difference 211
XX FT /label= Unknown
XX FT /note= "Encoded by AAY"
XX
XX PN MO200190151-A2.
XX
XX 29-NOV-2001.

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XX XX
XX PF 23-MAY-2001; 2001WO-US016766.
XX XX
XX PR 25-MAY-2000; 2000US-0207558P.
XX XX
XX PA (SCHE) SCHERING CORP.
XX PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX DR WPI; 2002-083085/11.
XX XX
XX N-PSDB; AAD26306.
XX
XX PT New DNAX Toll like receptor (DTRLR) proteins, useful for treating
XX conditions exhibiting abnormal expression of the receptors of their
XX ligands, particularly abnormalities manifested by immunological
XX disorders.
XX
XX PS Claim 3; Page 240-243; 297pp; English.
XX
XX CC The invention relates to mammalian receptor proteins, e.g., primate,
XX human DNAX Toll like receptor (DTRLR) protein and their corresponding
XX nucleic acids. The DTRLR is useful for treating conditions exhibiting
XX abnormal expression of the receptors of their ligands. Such abnormality
XX is manifested by immunological disorders. In particular, the DTRLR is
XX useful for treating various disease or disorders associated with abnormal
XX expression or abnormal triggering of response to a ligand. The DTRLR is
XX also useful as an immunogen for the production of antisera or antibodies
XX specific, e.g., capable of distinguishing between other interleukin (IL)-1
XX receptor family members, for the DTRLR or its various fragments. The
XX purified DTRLR can be used to screen monoclonal antibodies or antigen-
XX binding fragments. The antibodies are useful for screening expression
XX libraries for particular expression products. These are useful for
XX detecting or diagnosing various immunological conditions related to
XX expression of DTRLR or cells that express it. The present sequence is
XX human DTRLR4 protein, alternative version. The DTRLR4 gene is located on
XX chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
XX be similar to the sequence shown in page 41 (AAE16102). However these
XX sequences differ at several locations
XX
XX SQ Sequence 837 AA;
XX
XX Query Match 99.4%; Score 4328.5; DB 5; Length 837;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 836; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX
XX QY 2 MSASRLAGTLIPMAAFSCVRPSPWPCVENVNITYQCELNFPYKIPDNLPESTKQDL 61
XX 1 MSASRLAGTLIPMAAFSCVRPSPWPCVENVNITYQCELNFPYKIPDNLPESTKQDL 59
XX |||
QY 62 SFNPLRHLSGSYSPFPELQVLDLSRCEIQTIEDGAYOSLSHLSTLITGNPIQSLALGA 121
XX |||
XX 60 SFNPLRHLSGSYSPFPELQVLDLSRCEIQTIEDGAYOSLSHLSTLITGNPIQSLALGA 119
XX |||
QY 122 FSGLSSTLQKVAVETNLASLENPPIGHLKTLKEINVAHNLIOQFKLPEYFSNLTNLEHLD 181
XX |||
XX 120 FSGLSSTLQKVAVETNLASLENPPIGHLKTLKEINVAHNLIOQFKLPEYFSNLTNLEHLD 179
XX |||
QY 182 LSSNKIOSICTDRLRVLHQWPLNLSLDLSLNPNPFIOGPAFKRIHLAKTLRNPFSLN 241
XX |||
XX 180 LSSNKIOSICTDRLRVLHQWPLNLSLDLSLNPNPFIOGPAFKRIHLAKTLRNPFSLN 239
XX |||
QY 242 VMKTCIOGLAGLEVHRLVGEFRNEGNLEKFDKSALEGLCNLTIEEPRLAYLDYLDII 301
XX |||
XX 240 VMKTCIOGLAGLEVHRLVGEFRNEGNLEKFDKSALEGLCNLTIEEPRLAYLDYLDII 299
XX |||
QY 302 DLFNCLTNVSSFSIVSVTIERVKDFSYNFGMOHLELVNCKFGQPPTLKLSKRLTFTSN 361
XX |||
XX 300 DLFNCLTNVSSFSIVSVTIERVKDFSYNFGMOHLELVNCKFGQPPTLKLSKRLTFTSN 359
XX |||
QY 362 KGGNAFSEVDLPSELEFLDLSRNGLSFKGCCSQSDPGTTSLKYLDLSFNGVITMSSNPLGL 421
XX |||
XX 360 KGGNAFSEVDLPSELEFLDLSRNGLSFKGCCSQSDPGTTSLKYLDLSFNGVITMSSNPLGL 419
XX |||

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QY 422 EOLEHLDPROHSLKQMSSESVFLSLRNLIYLDISHTRVAFNGIFNGLSLEVLKMAGN 481
 Db 420 EOLEHLDPROHSLKQMSSESVFLSLRNLIYLDISHTRVAFNGIFNGLSLEVLKMAGN 479
 QY 482 SFOENFLPDIFTELNLTFPLDLSQCOLOLSPATANSLSLQVLMNSHNPFLDTPPK 541
 Db 480 SFOENFLPDIFTELNLTFPLDLSQCOLOLSPATANSLSLQVLMNSHNPFLDTPPK 539
 QY 542 CLNSLQVLDYSLNHIMTSKQELQHPSSLAFLNTQNDFACTCHOSFLQWIKDQRL 601
 Db 540 CLNSLQVLDYSLNHIMTSKQELQHPSSLAFLNTQNDFACTCHOSFLQWIKDQRL 599
 QY 602 VEVERMECATPSDQKQMPVLSLNTTCQNMKTIIGVSVLSVAVLVVYKFFHMLL 661
 Db 600 VEVERMECATPSDQKQMPVLSLNTTCQNMKTIIGVSVLSVAVLVVYKFFHMLL 659
 QY 662 AGCIKYGGENTYDAFVYSSODEDMVKNELVKNLEEGVPPQLCLHYRDFIPGVAIAAN 721
 Db 660 AGCIKYGGENTYDAFVYSSODEDMVKNELVKNLEEGVPPQLCLHYRDFIPGVAIAAN 719
 QY 722 IIHGFFHKSRYIVVSOHFIQSRWCIFEYELAQTMQFLSPRAGIIFIVLOKVEKTLRQ 781
 Db 720 IIHGFFHKSRYIVVSOHFIQSRWCIFEYELAQTMQFLSPRAGIIFIVLOKVEKTLRQ 779
 QY 782 QVELYRLISRYTYLEWEDSVLGRHIFWRRLRKLALDQKSNPEGTGTCNMQEATSI 839
 Db 780 QVELYRLISRYTYLEWEDSVLGRHIFWRRLRKLALDQKSNPEGTGTCNMQEATSI 837

RESULT 10

ID ADO57782 standard; protein; 808 AA.
 AC ADO57782;
 XX

DT 12-AUG-2004 (first entry)
 XX

DE Chimpanzee toll-like receptor 4 SEQ ID NO:3.
 XX

KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
 immunosuppressive; asthmatic; Gram-negative bacterial infection;
 sepsis; severe sepsis; septic shock; asthma; chimpanzee.
 XX

OS Pan troglodytes.
 XX

PN MO2004042365-A2.
 XX

PD 21-MAY-2004.
 XX

PF 03-NOV-2003; 2003WO-US036247.
 XX

PR 01-NOV-2002; 2002US-0423113P.
 XX

PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
 XX

P1 Messier W;
 XX

XX WPI; 2004-400726/37.
 DR

DR N-PSDB; ADO57780, ADO57781.
 XX

PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 sequence of the Old World monkey with that of a human.
 XX

PS Example 1; SEQ ID NO 3; 11pp; English.
 XX

CC The invention relates to a novel method for identifying a nucleotide
 change in a TLR4 polynucleotide sequence of an old world monkey
 comprising comparing the TLR4 polynucleotide sequence of the Old World
 monkey with corresponding TLR4 polynucleotide sequence of a human. The
 method of the invention has antibacterial, immunosuppressive, and
 antiasthmatic activity. The method is useful in identifying a nucleotide
 change in a TLR4 polynucleotide sequence of an Old World monkey where the

CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents chimpanzee TLR4.
 XX

SO Sequence 808 AA;

Query Match 95.9%; Score 4178; DB 8; Length 808;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 805; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 32 VVPIITTCQMEINLRYKIPDNLPSTKNLDSFNPRLHIGSYSPSPPELQVLDLSRCEIQ 91
 Db 1 VVPIITTCQMEINLRYKIPDNLPSTKNLDSFNPRLHIGSYSPSPPELQVLDLSRCEIQ 60
 QY 92 TIEDGAYOSLSHSLTILITGNPISLALGASGSLQKLVAVETNLASLNPPIGHKXT 151
 Db 61 TIEDGAYOSLSHSLTILITGNPISLALGASGSLQKLVAVETNLASLNPPIGHKXT 120
 QY 152 LKEINLVANHLIQSEPLPEYFENLNLNLEHLDLSNKKIOSIYCTDRLVHQMPLNLSDLS 211
 Db 121 LKEINLVANHLIQSEPLPEYFENLNLNLEHLDLSNKKIOSIYCTDRLVHQMPLNLSDLS 180
 QY 212 LNPANFIOPGAFKEIRLHKLTLRNPPSLNVMKTCIOGLAGLEVHRLVLSFRRNEGLEK 271
 Db 181 LNPANFIOPGAFKEIRLHKLTLRNPPSLNVMKTCIOGLAGLEVHRLVLSFRRNEGLEK 240
 QY 272 FDKSALBGLCNLTIEBFLAYLDYLDIIDLFNCLTNVSSFSLSVLTIEVKPSTVNG 331
 Db 241 FDKSALBGLCNLTIEBFLAYLDYLDIIDLFNCLTNVSSFSLSVLTIEVKPSTVNG 300
 QY 332 WQHELVNCKEFGQPEPTLKLKSLKRLTFTSNKGNAFSEVDLPSEFLDLSHNGLSFKGCC 391
 Db 301 WQHELVNCKEFGQPEPTLKLKSLKRLTFTSNKGNAFSEVDLPSEFLDLSHNGLSFKGCC 360
 QY 392 SOSDFGTTSLKYLDLSRNGVITMSSNPLGLEQLEHLDPOHSLKQMSSESVFLSLRNLIY 451
 Db 361 SOSDFGTTSLKYLDLSRNGVITMSSNPLGLEQLEHLDPOHSLKQMSSESVFLSLRNLIY 420
 QY 452 LDISHTRVAFNGIFNGLSLEVLKMAGNSFOENPDPITELRNLTFLDLSQCOLEQL 511
 Db 421 LDISHTRVAFNGIFNGLSLEVLKMAGNSFOENPDPITELRNLTFLDLSQCOLEQL 480
 QY 512 SPTAFNSLSLQVLMNSHNPFFSLDTPPYKCLNSLQVLDYSLNHIMTSKQELQHPSSL 571
 Db 481 SPTAFNSLSLQVLMNSHNPFFSLDTPPYKCLNSLQVLDYSLNHIMTSKQELQHPSSL 540
 QY 572 AFLNLTONDFACTCHOSFLQWIKDQRLVEVERMECATPSDQKQMPVLSLNTTCQMK 631
 Db 541 AFLNLTONDFACTCHOSFLQWIKDQRLVEVERMECATPSDQKQMPVLSLNTTCQMK 600
 QY 632 TIIGSVLSVLSVAVLVVYKFFHMLLAGCTKYRGENTYDAFYSSODDQWANE 691
 Db 601 TIIGSVLSVLSVAVLVVYKFFHMLLAGCTKYRGENTYDAFYSSODDQWANE 660
 QY 692 LVKNLEEGVPPQLCLHYRDFIPGVAIAANIIEHGFHKSRYIVVSOHFIQSRWCIFEY 751
 Db 661 LVKNLEEGVPPQLCLHYRDFIPGVAIAANIIEHGFHKSRYIVVSOHFIQSRWCIFEY 720
 QY 752 EIAQTMQFLSPRAGIIFIVLOKVEKTLRQVELYRLISRYTYLEWEDSVLGRHIFWRRL 811
 Db 721 EIAQTMQFLSPRAGIIFIVLOKVEKTLRQVELYRLISRYTYLEWEDSVLGRHIFWRRL 780
 QY 812 RKALLDGKSNPPEGTGTCNMQEATSI 839
 Db 781 RKALLDGKSNPPEGTGTCNMQEATSI 808

RESULT 11

ID ADO57785 standard; protein; 808 AA.
 AC ADO57785;

XX 12-AUG-2004 (first entry)
DT Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; gorilla.
XX
OS Gorilla gorilla.
XX
XX WO2004042365-A2.
XX
XX 21-MAY-2004.
XX
XX 03-NOV-2003; 2003WO-US036247.
XX
XX 01-NOV-2002; 2002US-0423113P.
XX
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
XX Messier W;
XX
XX WPI; 2004-400726/37.
XX
XX N-PSDB; ADO57783, ADO57784.
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
XX Example 1; SEQ ID NO 6, 111pp; English.
XX
XX The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents gorilla TLR4.
XX
XX Sequence 808 AA;
SQ
Query Match 95.7%; Score 4167; DB 8; Length 808;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 803; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 32 VVNNITVQCMELNFKYKIPDNLPFSTKNLDSFNPLRHLGYSFSPFELQVLDLSRCEIQ 91
DB 1 VVNNITVQCMELNFKYKIPDNLPFSTKNLDSFNPLRHLGYSFSPFELQVLDLSRCEIQ 60
QY 92 TIEBGAYOSLSHSLTLLITGNPIOSLALGAFSGLSLOKLVAVETNLASLENPIGHLKT 151
DB 61 TIEBGAYOSLSHSLTLLITGNPIOSLALGAFSGLSLOKLVAVETNLASLENPIGHLKT 120
QY 152 LKEILNVAHNLIQSFLPEYFSNLTNLEHLDSNKKIOSYCTDRLVHQWMLNLSLDLS 211
DB 121 LKEILNVAHNLIQSFLPEYFSNLTNLEHLDSNKKIOSYCTDRLVHQWMLNLSLDLS 180
QY 212 LNPNNFTOPGAFKEIRLHKLTLRNNPDSLNMKTCIOGLAGLEVHRLVLSGFRNENLEK 271
DB 181 LNPNNFTOPGAFKEIRLHKLTLRNNPDSLNMKTCIOGLAGLEVHRLVLSGFRNENLEK 240
QY 272 FDKSALBGLCNLTIEBRLAYLDYLDIDLFNCLTNVSSFSLSVVTIERVKDPSYNG 331
DB 241 FDKSALBGLCNLTIEBRLAYLDYLDIDLFNCLTNVSSFSLSVVTIERVKDPSYNG 300
QY 332 MOHELVNCKRGOPPTLTKLSIKLTPTSNKGNAFSEVDLPSEFLDLSNGLSFGGCC 391
DB 301 MOHELVNCKRGOPPTLTKLSIKLTPTSNKGNAFSEVDLPSEFLDLSNGLSFGGCC 360

QY 392 SOSDFGTTSLKYLDLSFNGVITMSSNFLAGLEQLHLPQHSNLRKQSEFSVFLSLRNLIY 451
DB 361 SOSDFGTTSLKYLDLSFNGVITMSSNFLAGLEQLHLPQHSNLRKQSEFSVFLSLRNLIY 420
QY 452 LDISHTHTRAVFNGIFNGLSLEVLKMAGNSFOENFLPDIFTELRLNLTFLDLSQCOLEQL 511
DB 421 LDISHTHTRAVFNGIFNGLSLEVLKMAGNSFOENFLPDIFTELRLNLTFLDLSQCOLEQL 480
QY 512 SPTAFNSLSLQVLMNSHNPFSLDTPPYKCLNSLRVLDVSLNIMTSKQELQHPSSL 571
DB 481 SPTAFNSLSLQVLMNSHNPFSLDTPPYKCLNSLRVLDVSLNIMTSKQELQHPSSL 540
QY 572 AFLNLTQNDFACTCEHOSFLOMIDKORQLLVEVERMECATPSPDQGNPVLSTNTQCMNK 631
DB 541 AFLNLTQNDFACTCEHOSFLOMIDKORQLLVEVERMECATPSPDQGNPVLSTNTQCMNK 600
QY 632 TIIGSVLSVLVSVAVLVYKFFHMLLAGCIKYGREGENIYDAFVIYSSQDEDDWRNE 691
DB 601 TIIGSVLSVLVSVAVLVYKFFHMLLAGCIKYGREGENIYDAFVIYSSQDEDDWRNE 660
QY 692 LVKNLEEGVPPFQCLHYRDPFPGVALAANIHEGFHRSKRVLYVVSQHPISQWCIFEX 751
DB 661 LVKNLEEGVPPFQCLHYRDPFPGVALAANIHEGFHRSKRVLYVVSQHPISQWCIFEX 720
QY 752 EIAQTWQFLSSRAGIIFIVLOKVEKTLRQOVELYRLSNRTYLEMDSVLAGRIIPWRL 811
DB 721 EIAQTWQFLSSRAGIIFIVLOKVEKTLRQOVELYRLSNRTYLEMDSVLAGRIIPWRL 780
QY 812 RKALLDGKSNMPEGTVGTGCNMQEATSI 839
DB 781 RKALLDGKSNMPEGTVGTGCNMQEATSI 808
RESULT 12
ID ADO57803 standard; protein; 808 AA.
XX
XX ADO57803;
AC
XX 12-AUG-2004 (first entry)
DT
XX Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
XX Pan troglodytes.
OS
XX WO2004042365-A2.
XX
XX 21-MAY-2004.
XX
XX 03-NOV-2003; 2003WO-US036247.
XX
XX 01-NOV-2002; 2002US-0423113P.
XX
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
XX Messier W;
XX
XX WPI; 2004-400726/37.
XX
XX N-PSDB; ADO57801, ADO57802.
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
XX Disclosure; SEQ ID NO 24; 111pp; English.
XX
XX The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey

comparing comparing the TLR4 polynucleotide sequence of the Old World monkey with corresponding TLR4 polynucleotide sequence of a human. The method of the invention has antibacterial, immunosuppressive, and antiasthmatic activity. The method is useful in identifying a nucleotide change in a TLR4 polynucleotide sequence of an Old World monkey where the change may be associated with reduced sensitivity to Gram-negative bacterial infection. The methods, agents and composition are useful in treating sepsis, severe sepsis or septic shock and asthma. The present sequence represents chimpanzee TLR4.

Sequence 808 AA;

Query Match 95.6%; Score 4164; DB 8; Length 808;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 803; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

QY 32 VVPNTYOCMEINPKIPDNLPSTKNDLSFNPRLHSGVSFFSPPELVLDLSRCEIQ 91
DB 1 VVPNTYOCMEINPKIPDNLPSTKNDLSFNPRLHSGVSFFSPPELVLDLSRCEIQ 60
QY 92 TIEBGAYOSLSHSLTLITGNPIQSIALGAFSGLSLOKLVAVETNLASLENFPIGHKT 151
DB 61 TIEBGAYOSLSHSLTLITGNPIQSIALGAFSGLSLOKLVAVETNLASLENFPIGHKT 120
QY 152 LKELVANHLIQSEKLPYFSNLTNLEHLDSSNKIQSIYCTDLRVLHQPMLNLSLDS 211
DB 121 LKELVANHLIQSEKLPYFSNLTNLEHLDSSNKIQSIYCTDLRVLHQPMLNLSLDS 180
QY 212 LNPMPFLOPGAFKEIRLHKLTLRNNPDSLNMKTCIOGLAGLEVHRLVGEFRNGNLEK 271
DB 181 LNPMPFLOPGAFKEIRLHKLTLRNNPDSLNMKTCIOGLAGLEVHRLVGEFRNGNLEK 240
QY 272 FDKSALLEGJLNLTEEFRLAYLDYLDIIDLFCNLTVNSFSYVTERKQDSYNGF 331
DB 241 FDKSALLEGJLNLTEEFRLAYLDYLDIIDLFCNLTVNSFSYVTERKQDSYNGF 300
QY 332 WOHELVNCKFGQFPFLTKLSKRLTFTSNKGNASEVDLPSEFLDLSRNGLSFKGCC 391
DB 301 WOHELVNCKFGQFPFLTKLSKRLTFTSNKGNASEVDLPSEFLDLSRNGLSFKGCC 360
QY 392 SOSDGTSLKTYLDSFNGVITMSNFIQLEHLDLQHSNLSKMSFSVFLSRNLTLY 451
DB 361 SOSDGTSLKTYLDSFNGVITMSNFIQLEHLDLQHSNLSKMSFSVFLSRNLTLY 420
QY 452 LDISHTHRAVFNGLSLEVLKMGANSFOENFLPDIETELRNLTFLDLSOQQLBOL 511
DB 421 LDISHTHRAVFNGLSLEVLKMGANSFOENFLPDIETELRNLTFLDLSOQQLBOL 480
QY 512 SPFAENSLSLQVLNMSHNNFSLDTFPYKCLNSLOVLDSLNHIMTSKQELQHPSSL 571
DB 481 SPFAENSLSLQVLNMSHNNFSLDTFPYKCLNSLOVLDSLNHIMTSKQELQHPSSL 540
QY 572 AFLNLTQNDPACTCHOSFLOMIKQROLVVEVMECATPSDKGMVLSINTCCQNNK 631
DB 541 AFLNLTQNDPACTCHOSFLOMIKQROLVVEVMECATPSDKGMVLSINTCCQNNK 600
QY 632 TIIGSVSVSVVAVAVLVYKFFHMLLAGCIKYGGENYDYAFVLYSSODEBWMVNE 691
DB 601 TIIGSVSVSVVAVAVLVYKFFHMLLAGCIKYGGENYDYAFVLYSSODEBWMVNE 660
QY 692 LVKNLEBVPFQOLCIHYRDFIPGVALANIIHGBFHSRKVIVVSOHFIOSRWCIFEY 751
DB 661 LVKNLEBVPFQOLCIHYRDFIPGVALANIIHGBFHSRKVIVVSOHFIOSRWCIFEY 720
QY 752 EIAQTWQSLSRAGIIFIVLOKVEKTLRQVVELYRLSRNTYLEWESVJGRHIFWRRL 811
DB 721 EIAQTWQSLSRAGIIFIVLOKVEKTLRQVVELYRLSRNTYLEWESVJGRHIFWRRL 780
QY 812 RKALLDGKSNPEGTVTGCMQOATS 839
DB 781 RKALLDGKSNPEGTVTGCMQOATS 808

```

RESULT 13

AAW86352

ID AAW86352 standard; protein; 799 AA.

XX AAW86352;

AC 15-MAR-1999 (first entry)

DT Human DNAX toll-like receptor DTLR4.

DE Human DNAX toll-like receptor DTLR4.

XX DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;

XX interleukin 1 receptor; phosphate metabolism; innate immunity response;

KM modulate inflammatory function; morphological effect;

KM immunological disorder.

OS Homo sapiens.

PN WO9850547-A2.

PD 12-NOV-1998.

PF 07-MAY-1998; 98WO-US008979.

PR 07-MAY-1997; 97US-0044293P.

PR 22-JAN-1998; 98US-0072212P.

PR 05-MAR-1998; 98US-0076947P.

PA (SCHE) SCHERING CORP.

FI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;

DR WPI; 1999-059670/05.

DR N-PSDB; AAV80666.

PT Human DNAX toll-like receptor, DTLR 2-10 - used to, e.g. alter phosphate

PT metabolism, modulate inflammatory function or innate immunity responses.

XX Example; Page 115-117; 171pp; English.

XX The present invention specifically describes human DNAX toll-like

XX receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given

CC in the present invention. Also described are: (1) a fusion protein

CC comprising a DTLR protein or peptide; (2) a binding compound, preferably

CC an antibody or antibody fragment which specifically binds to a DTLR

CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide

CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a

CC host cell comprising the vector of (4). The host cell of (5) can be used

CC to produce the DTLR proteins. The DTLR proteins can be used to alter

CC phosphate metabolism, to modulate inflammatory function, innate immunity

CC responses or morphological effects. The DTLR proteins can be used in the

CC treatment of conditions exhibiting abnormal expression of the receptors

CC of their ligands. These abnormalities are typically manifested by

CC immunological disorders

XX Sequence 799 AA;

Query Match 95.1%; Score 4141; DB 2; Length 799;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 41 MELNFKYKIPDNLPSTKNDLSFNPRLHSGVSFFSPPELVLDLSRCEIQTIEBGAYOS 100
DB 1 MELNFKYKIPDNLPSTKNDLSFNPRLHSGVSFFSPPELVLDLSRCEIQTIEBGAYOS 60
QY 101 LSHSLTLITGNPIQSIALGAFSGLSLOKLVAVETNLASLENFPIGHKTLELVAN 160
DB 61 LSHSLTLITGNPIQSIALGAFSGLSLOKLVAVETNLASLENFPIGHKTLELVAN 120
QY 161 LIQSEKLPYFSNLTNLEHLDSSNKIQSIYCTDLRVLHQPMLNLSLDSLNPNPFIOP 220
DB 121 LIQSEKLPYFSNLTNLEHLDSSNKIQSIYCTDLRVLHQPMLNLSLDSLNPNPFIOP 180
QY 221 GAFFKIRLHKLTLRNNPDSLNMKTCIOGLAGLEVHRLVGEFRNGNLEKFDKSALEGL 280

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Db 181 GAFKEIRLHKLTIRNNFDSINVMKTCIOGLAGLEVHRLVIGEFNREGNLEKFDKSALEGL 240
Qy 281 CNLTIEEFLAYLDYLDIIDLFCNCLTNVSSFSLVSTIERKDFSYNFGWOHLELVNC 340
Db 241 CNLTIEEFLAYLDYLDIIDLFCNCLTNVSSFSLVSTIERKDFSYNFGWOHLELVNC 300
Qy 341 KFGQFPTLKLKSLKRLTFTSNKGNASEVDLPSELFTDLDSRNGLSFKGCCSQSDFGTTS 400
Db 301 KFGQFPTLKLKSLKRLTFTSNKGNASEVDLPSELFTDLDSRNGLSFKGCCSQSDFGTTS 360
Qy 401 LKYLDLSPNGVITMSSNFLGJEOLHLDFOHSLNKQMSSEFVLSLRNLTYLIDISHHTTR 460
Db 361 LKYLDLSPNGVITMSSNFLGJEOLHLDFOHSLNKQMSSEFVLSLRNLTYLIDISHHTTR 420
Qy 461 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCEQLSPTAFNLS 520
Db 421 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCEQLSPTAFNLS 480
Qy 521 SLOVLNMSHNNFSLDTPPYKCLNSLOVLDSLNHMTSKQELQHPSSLAFLNLQND 580
Db 540 SLOVLNMSHNNFSLDTPPYKCLNSLOVLDSLNHMTSKQELQHPSSLAFLNLQND 540
Qy 581 FACTCEHOSFLOWKIDORQLLVEVERMECATPSDKQMPVLSLNTTCOMNKTIIIGSVLS 640
Db 541 FACTCEHOSFLOWKIDORQLLVEVERMECATPSDKQMPVLSLNTTCOMNKTIIIGSVLS 600
Qy 641 VLVSVVAVLVYKFFHMLLAGCIKYRGENIYDAFVIYSSODEDWVRNELVYNLEEGV 700
Db 601 VLVSVVAVLVYKFFHMLLAGCIKYRGENIYDAFVIYSSODEDWVRNELVYNLEEGV 660
Qy 701 PPOLCLAHYRPIFGVAIAANIIEHGFKSKRVIVVSOHTIOSRWCIFYEIQAQWQFL 760
Db 720 PPOLCLAHYRPIFGVAIAANIIEHGFKSKRVIVVSOHTIOSRWCIFYEIQAQWQFL 720
Qy 761 SSRAGIIFIVQKEKTLRQOVELYRLSRNTYLEMEDSVLGRHIFMRRLKALDQKS 820
Db 721 SSRAGIIFIVQKEKTLRQOVELYRLSRNTYLEMEDSVLGRHIFMRRLKALDQKS 780
Qy 821 WNPBGTVGTGCNMOEATSI 839
Db 781 WNPBGTVGTGCNMOEATSI 799

RESULT 14
AAE16093
ID AAE16093 standard; protein; 799 AA.
XX
AC AAE16093;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX Toll like receptor (DTLR) 4 #1.
XX
KW Human: DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS Homo sapiens.
XX
PN WO200190151-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016766.
XX
PR 25-MAY-2000; 2000US-0207558P.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX
DR WPI; 2002-083085/11.
DR N-PSDB; AAD26283.
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XX New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
PS Claim 1; Page 35; 297pp; English.
XX
XX The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33
XX
SQ Sequence 799 AA;
Query Match 95.1%; Score 4141; DB 5; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 41 MELNFKYKIPDNLPSTNYKNDLSFNPLRHLSYSFSPPELOVLDLSRCEIQTIEDGAYQS 100
Db 1 MELNFKYKIPDNLPSTNYKNDLSFNPLRHLSYSFSPPELOVLDLSRCEIQTIEDGAYQS 60
Qy 101 LSHLSTLILGNPILQSLALGAFSGLSLOKLVANETMLASLENPIGHLKTLKELNVAHN 160
Db 61 LSHLSTLILGNPILQSLALGAFSGLSLOKLVANETMLASLENPIGHLKTLKELNVAHN 120
Qy 161 LIQSFKLPEYFNSNLTNLEHLDLSNKKIQSIYCTDLRYLHQWPLNLSLDSLPMNFLOP 220
Db 121 LIQSFKLPEYFNSNLTNLEHLDLSNKKIQSIYCTDLRYLHQWPLNLSLDSLPMNFLOP 180
Qy 221 GAFKEIRLHKLTIRNNFDSINVMKTCIOGLAGLEVHRLVIGEFNREGNLEKFDKSALEGL 280
Db 181 GAFKEIRLHKLTIRNNFDSINVMKTCIOGLAGLEVHRLVIGEFNREGNLEKFDKSALEGL 240
Qy 281 CNLTIEEFLAYLDYLDIIDLFCNCLTNVSSFSLVSTIERKDFSYNFGWOHLELVNC 340
Db 241 CNLTIEEFLAYLDYLDIIDLFCNCLTNVSSFSLVSTIERKDFSYNFGWOHLELVNC 300
Qy 341 KFGQFPTLKLKSLKRLTFTSNKGNASEVDLPSELFTDLDSRNGLSFKGCCSQSDFGTTS 400
Db 301 KFGQFPTLKLKSLKRLTFTSNKGNASEVDLPSELFTDLDSRNGLSFKGCCSQSDFGTTS 360
Qy 401 LKYLDLSPNGVITMSSNFLGJEOLHLDFOHSLNKQMSSEFVLSLRNLTYLIDISHHTTR 460
Db 361 LKYLDLSPNGVITMSSNFLGJEOLHLDFOHSLNKQMSSEFVLSLRNLTYLIDISHHTTR 420
Qy 461 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCEQLSPTAFNLS 520
Db 421 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCEQLSPTAFNLS 480
Qy 521 SLOVLNMSHNNFSLDTPPYKCLNSLOVLDSLNHMTSKQELQHPSSLAFLNLQND 580
Db 540 SLOVLNMSHNNFSLDTPPYKCLNSLOVLDSLNHMTSKQELQHPSSLAFLNLQND 540
Qy 581 FACTCEHOSFLOWKIDORQLLVEVERMECATPSDKQMPVLSLNTTCOMNKTIIIGSVLS 640
Db 541 FACTCEHOSFLOWKIDORQLLVEVERMECATPSDKQMPVLSLNTTCOMNKTIIIGSVLS 600
Qy 641 VLVSVVAVLVYKFFHMLLAGCIKYRGENIYDAFVIYSSODEDWVRNELVYNLEEGV 700
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Db 601 VLVVSVAVLVYKFFHMLLAGCIKYRGENTYDAFYISSQDEWDWRNELVKNLEBGV 660

Qy 701 PPFOLCHYRDFIPGVAIAANIHEGFKSRKVIYVVSQHFIOQRWCIFEEYIAQTWQFL 760

Db 661 PPFOLCHYRDFIPGVAIAANIHEGFKSRKVIYVVSQHFIOQRWCIFEEYIAQTWQFL 720

Qy 761 SSRAGIIFIVLOKVEKTLRQOVELYRLLSRNTYLEMDSVLRGRIIFRRRLKALLDGS 820

Db 721 SSRAGIIFIVLOKVEKTLRQOVELYRLLSRNTYLEMDSVLRGRIIFRRRLKALLDGS 780

Qy 821 WNPBGTVGTGCMQOEATSI 839

Db 781 WNPBGTVGTGCMQOEATSI 799

RESULT 15

ABB83162

ID ABB83162 standard; protein; 799 AA.

XX ABB83162;

AC ABB83162;

XX 09-AUG-2002 (first entry)

DT 09-AUG-2002 (first entry)

XX Human Toll-like receptor-4, Tlr4.

DE Human; virucide; antibacterial; fungicide; parasiticide; receptor;

XX cytosolic; immunostimulatory; scavenger receptor; Toll receptor;

KM respiratory tract infection; Toll-like receptor; Tlr4.

XX Homo sapiens.

OS WO200235236-A1.

PN 02-MAY-2002.

PD 26-OCT-2001; 2001WO-FR003352.

XX 27-OCT-2000; 2000FR-00013883.

PR (FABRE MEDICAMENT SA PIERRE.

PA Jeanm P, Magistrelli G, Herbault N, Bonnefoy J;

PI WPI; 2002-383586/41.

DR N-PSDB; AEN83318.

XX Identifying agent that binds to scavenger receptors and signals through a

PT Toll receptor, useful as carrier or adjuvant in vaccines, promotes a

PT cytotoxic T cell response.

XX Disclosure; Page 58-60; 71pp; French.

PS The present invention relates to a method for identifying new therapeutic

CC compounds (I) by selecting molecules that bind to scavenger receptors and

CC signal through a Toll receptor. The present sequence is the protein

CC sequence for human Toll-like receptor-4, Tlr4, which was used to

CC illustrate the method of the invention. (I) are useful as carriers and/or

CC adjuvants in prophylactic or therapeutic vaccines, particularly where the

CC antigen is derived from a virus, bacterium, yeast, fungus, parasite or

CC tumour cell, especially a pathogen that causes respiratory tract

CC infection, also more generally for inducing an immune response. (I) can

CC also be used for specific targeting of active agents (antigens etc.) to

CC antigen-presenting cells (especially immature dendritic cells), for

CC subsequent internalisation by these cells

XX Sequence 799 AA;

SO

Query Match 95.1%; Score 4141; DB 5; Length 799;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 MELNFKYKPDNLPESTKULDSFNPRLHLSGYSFFSPPELOYLDLSRCEIQTIEDGAYQS 100

Db 1 MELNFKYKPDNLPESTKULDSFNPRLHLSGYSFFSPPELOYLDLSRCEIQTIEDGAYQS 60

Qy 101 LSHLSTLILTNPIQSIALGAFSGISLQKLVAVETNLASLENPIGHLTKTLKEILNAVN 160

Db 61 LSHLSTLILTNPIQSIALGAFSGISLQKLVAVETNLASLENPIGHLTKTLKEILNAVN 120

Qy 161 LIQSPKLPREYSNLTNLEHDLSSNKTQSITCTDLRYLHOMPLNLSTLSDLSINPNFTOP 220

Db 121 LIQSPKLPREYSNLTNLEHDLSSNKTQSITCTDLRYLHOMPLNLSTLSDLSINPNFTOP 180

Qy 221 GAFKEIRLHKLTLLNNPDSLNVMTKCIQGLAGLEVHRLVLGEFNEGNLEKFDKSALEGL 280

Db 181 GAFKEIRLHKLTLLNNPDSLNVMTKCIQGLAGLEVHRLVLGEFNEGNLEKFDKSALEGL 240

Qy 281 CNLTIIEERLAVLDYLDIIDLFNCLTNVSSFSLSVSTIERVDFSNFGMOHLELVNC 340

Db 241 CNLTIIEERLAVLDYLDIIDLFNCLTNVSSFSLSVSTIERVDFSNFGMOHLELVNC 300

Qy 341 KFGQPTLKLSLRRLFTSNKGNAPSEVDLPSELFLDLSRNLSPFKCCSQSDFGTTS 400

Db 301 KFGQPTLKLSLRRLFTSNKGNAPSEVDLPSELFLDLSRNLSPFKCCSQSDFGTTS 360

Qy 401 LKYLDLSFNGVITMSSNPLGLEOLEHLDPOHSNLSKOMSESVPLSLRLIYLDLSHTTTR 460

Db 361 LKYLDLSFNGVITMSSNPLGLEOLEHLDPOHSNLSKOMSESVPLSLRLIYLDLSHTTTR 420

Qy 461 VAFNGIFNGLSLSEVLKMAGNSFOENPLPDIFTELRLNLTFLDLSQCLQSLPTAFNSLS 520

Db 421 VAFNGIFNGLSLSEVLKMAGNSFOENPLPDIFTELRLNLTFLDLSQCLQSLPTAFNSLS 480

Qy 521 SLOVLNMSHNNPFSLDTPPYKCLNSLOYLDYSLNHIKTSKQOELOHPSSLAFLNLTOND 580

Db 481 SLOVLNMSHNNPFSLDTPPYKCLNSLOYLDYSLNHIKTSKQOELOHPSSLAFLNLTOND 540

Qy 581 FACTCEHOSFLOWKDORQLVEYERMECAPSPDKQGPVLSLNTCOMNKTIIIGSVYLS 640

Db 541 FACTCEHOSFLOWKDORQLVEYERMECAPSPDKQGPVLSLNTCOMNKTIIIGSVYLS 600

Qy 641 VLVVSVAVLVYKFFHMLLAGCIKYRGENTYDAFYISSQDEWDWRNELVKNLEBGV 700

Db 601 VLVVSVAVLVYKFFHMLLAGCIKYRGENTYDAFYISSQDEWDWRNELVKNLEBGV 660

Qy 701 PPFOLCHYRDFIPGVAIAANIHEGFKSRKVIYVVSQHFIOQRWCIFEEYIAQTWQFL 760

Db 661 PPFOLCHYRDFIPGVAIAANIHEGFKSRKVIYVVSQHFIOQRWCIFEEYIAQTWQFL 720

Qy 761 SSRAGIIFIVLOKVEKTLRQOVELYRLLSRNTYLEMDSVLRGRIIFRRRLKALLDGS 820

Db 721 SSRAGIIFIVLOKVEKTLRQOVELYRLLSRNTYLEMDSVLRGRIIFRRRLKALLDGS 780

Qy 821 WNPBGTVGTGCMQOEATSI 839

Db 781 WNPBGTVGTGCMQOEATSI 799

Search completed: March 12, 2005, 19:54:56

Job time : 97.4 secs

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OM protein - protein search, using SW model

Run on: March 12, 2005, 19:34:46 ; Search time 23.0639 Seconds
(without alignments)
2715.523 Million cell updates/sec

Title: US-09-396-985B-2

Perfect score: 4355

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Database :

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 - 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
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 - 5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep:*
 - 6: /cgn2_6/ptodata/1/iaa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	629.5	14.5	661	1	US-08-833-823-4
4	599.5	13.8	784	4	US-09-982-308B-23
5	539	12.4	775	4	US-09-949-016-8799
6	316	7.3	605	3	US-09-063-950-5
7	305	7.0	623	4	US-09-949-016-10995
8	303	7.0	605	1	US-08-190-802A-49
9	303	7.0	605	3	US-08-477-346-49
10	303	7.0	605	3	US-08-473-089-49
11	303	7.0	605	4	US-08-487-072A-49
12	303	7.0	605	4	US-09-538-092-1087
13	299.5	6.9	662	4	US-09-538-092-1325
14	299.5	6.9	662	4	US-09-949-016-6619
15	299.5	6.9	662	4	US-09-949-016-10710
16	299	6.9	1525	3	US-09-191-647-2
17	299	6.9	1525	3	US-09-540-245A-2
18	299	6.9	1525	3	US-09-540-153-2
19	296	6.8	603	1	US-08-190-802A-50
20	296	6.8	603	3	US-08-477-346-50
21	296	6.8	603	3	US-08-473-089-50
22	296	6.8	603	4	US-08-487-072A-50
23	292.5	6.7	907	4	US-09-170-496D-264
24	292.5	6.7	907	4	US-09-170-496D-264
25	289.5	6.6	1112	3	US-09-353-585-3
26	289	6.6	1112	3	US-09-312-283C-396
27	286	6.6	1112	3	US-09-353-585-2

28	285	6.5	1523	3	US-09-182-024A-2	Sequence 2, Appli
29	283.5	6.5	1166	4	US-10-101-464A-900	Sequence 900, App
30	281	6.5	1101	3	US-08-986-485-2	Sequence 2, Appli
31	278	6.4	1091	3	US-08-986-485-5	Sequence 5, Appli
32	275	6.3	620	4	US-09-907-794A-73	Sequence 73, Appli
33	275	6.3	620	4	US-09-905-125A-73	Sequence 73, Appli
34	275	6.3	620	4	US-09-902-775A-73	Sequence 73, Appli
35	275	6.3	620	4	US-09-906-700-73	Sequence 73, Appli
36	275	6.3	620	4	US-09-903-603A-73	Sequence 73, Appli
37	275	6.3	620	4	US-09-904-920A-73	Sequence 73, Appli
38	275	6.3	620	4	US-09-905-064-73	Sequence 73, Appli
39	275	6.3	620	4	US-09-905-381A-73	Sequence 73, Appli
40	275	6.3	620	4	US-09-906-618-73	Sequence 73, Appli
41	272	6.2	1480	3	US-09-191-647-7	Sequence 7, Appli
42	272	6.2	1480	3	US-09-540-245A-7	Sequence 7, Appli
43	272	6.2	1480	3	US-09-540-153-7	Sequence 7, Appli
44	272	6.2	1480	5	PCT-US91-09055-2	Sequence 2, Appli
45	271	6.2	1139	4	US-09-513-505-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9438

Query Match 96.4%; Score 4197; DB 4; Length 844;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 EVVNNITVQCEMLNFYKIPDNLPRSTKNLDSFPLPHLHSGYSFSPPELOVLSRCEI 90
DB 36 EVVNNITVQCEMLNFYKIPDNLPRSTKNLDSFPLPHLHSGYSFSPPELOVLSRCEI 95
QY 91 QTIEDGAYOSLSHSLTILITGNPISQIALGAFSGLSLQKVAETNLALENPIGHK 150
DB 96 QTIEDGAYOSLSHSLTILITGNPISQIALGAFSGLSLQKVAETNLALENPIGHK 155
QY 151 TKELVNVAHNLIOGFKLPEYFSNLTNLEHLDSSNKIOSITYCTDLRVYHQMPLNLSIDL 210
DB 156 TKELVNVAHNLIOGFKLPEYFSNLTNLEHLDSSNKIOSITYCTDLRVYHQMPLNLSIDL 215
QY 211 SLNPMNFIQGAPEIRLHLKTLTPNPDLSLNWKTCTQGLAGLEVHVLVGEFNEGNLE 270
DB 216 SLNPMNFIQGAPEIRLHLKTLTPNPDLSLNWKTCTQGLAGLEVHVLVGEFNEGNLE 275
QY 271 KFDKSALEGCNLTIEEFRLAYLDYDDIIDLFPNCLTNVSSFSVLVETTERVDFSYNF 330
DB 276 KFDKSALEGCNLTIEEFRLAYLDYDDIIDLFPNCLTNVSSFSVLVETTERVDFSYNF 335
QY 331 GWOHLIELVNCKFGQFPTLKLSLKRLLTFTSNKGNAPSEVDLPSEFLDLSRNGLSFKGC 390

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Db 336 GMDHLELVNCKRGQPPYLKLSKRLTTSNKGNAFSEVDLPSEFLDLSNGLSFGKC 395
Qy 391 CSQSDFGTTSKYLDLSFNGVITWSSNFGLEQLEHLDFOHNLKOMSEFVSFLSLRMLI 450
Db 396 CSQSDFGTTSKYLDLSFNGVITWSSNFGLEQLEHLDFOHNLKOMSEFVSFLSLRMLI 455
Qy 451 YLDSHTHTRYAFNGIFNGLSLEVLKXAGNSFOENFLPDIFTELRLNLTPLDLSQCLEQ 510
Db 456 YLDSHTHTRYAFNGIFNGLSLEVLKXAGNSFOENFLPDIFTELRLNLTPLDLSQCLEQ 515
Qy 511 LSPFAFNSLSLYVNMHNNPFLDTPPYKCLNSLYLDVSLNIMTSKQELQHPSS 570
Db 516 LSPFAFNSLSLYVNMHNNPFLDTPPYKCLNSLYLDVSLNIMTSKQELQHPSS 575
Qy 571 LAFNLTONDPACTCEHOSFLQWIKDQRLVVEVERMECATPSPDKQMPVLSLNTTCOMN 630
Db 576 LAFNLTONDPACTCEHOSFLQWIKDQRLVVEVERMECATPSPDKQMPVLSLNTTCOMN 635
Qy 631 KTIIGVSVLSVSVAVLVYKFFHMLLAGCIKRGGENIYDAFVIYSSODEDVRN 690
Db 636 KTIIGVSVLSVSVAVLVYKFFHMLLAGCIKRGGENIYDAFVIYSSODEDVRN 695
Qy 691 ELVKNLEBGPVPCCLHYRDPFPGVAITANIIHGFHRSKRVIVVSOHPTQSRWCTFE 750
Db 696 ELVKNLEBGPVPCCLHYRDPFPGVAITANIIHGFHRSKRVIVVSOHPTQSRWCTFE 755
Qy 751 YEIAQTWQFLSSRAGIIFIVLQKYEKTLRLQOVELYRLSNRYLEWEDSVLGRHIFWR 810
Db 756 YEIAQTWQFLSSRAGIIFIVLQKYEKTLRLQOVELYRLSNRYLEWEDSVLGRHIFWR 815
Qy 811 LRKALLDGKSNPBGCTVGTGCMQEAISI 839
Db 816 LRKALLDGKSNPBGCTVGTGCMQEAISI 844

RESULT 2
US-08-514-014-4
/ Sequence 4, Application US/08514014
/ Patent No. 5707829
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: McCoy, John
/ APPLICANT: Kelleher, Kerry
/ APPLICANT: Carlin, McKeough
/ TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
/ STREET: 87 Cambridgepark Drive
/ CITY: Cambridge
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02140
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/514,014
/ FILING DATE:
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Brown, Scott A.
/ REGISTRATION NUMBER: 32,724
/ REFERENCE/DOCKET NUMBER: G16000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 876-8224
/ TELEFAX: (617) 876-5851
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:

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; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-514-014-4

Query Match 14.5%; Score 629.5; DB 1; Length 661;
Best Local Similarity 29.7%; Pred. No. 5:36-49;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

Qy 25 SWEP-CYEVVPIITVOCMEINFYKIPDNLPESTKNLDSFPLPHLSYSFSPPELQVL 83
Db 23 SWDMCKIEKANKTYNCENGLSLIPDLPTTELEFSFPLTINRKFSLMANLTF 82
Qy 84 DLSRCEIQTIEDGAYQSLSHSLTLITGNPFIQSLALGAFSGLSLQKLVAVETIASLEN 143
Db 83 DLTRCQINWTHIEDPQSHHQSLTVLGNPLIFMAEISLNGPKSLKHLFLIGTISNDEF 142
Qy 144 PFIHLKTLKELVANHNLQSFKLPEYPSNLTNLEHLDLSNKKIQSIYCTDLRYLHQMPL 203
Db 143 IPVHNLNLLESLYLSGNHISISIKPPDPP-ARNIKVLDPQNNAIHYISREDMRLEQ--A 199
Qy 204 LNLSDLSLNPMPNFIQGAPEIRLHLKTLRNPDSLNWKTCTQGLAGLEVHNLVGEF 263
Db 200 LNLSDLSLNPMPNFIQGAPEIRLHLKTLRNPDSLNWKTCTQGLAGLEVHNLVGEF 255
Qy 264 RNEGULEKFDKSALEGLCNLTIEBFRLAYLDYLDIID-LFNCLTVVSSFSVSVTIER 322
Db 256 EDIDD-EDISSAMLKGCMSVBSLNQ--EHRSDLSSTTFQCFQLOGLDLTRATHLKG 312
Qy 323 VKDPSYFNGMOHLELVN-----CKF--GQFPTL-----KLKSLKRLTTSN 361
Db 313 LPS-----GKGLNLTLKLVLSVNHFPQLQISANPSPSLTHLYIRGNVKKLHLGVCL 367
Qy 362 KGNAPFSEVDLPSEFLDLSRNGLSFKGCCSQSDFGTTSKYLDLSFNGVITWSSN-FLG 420
Db 368 KLGN-----LQTLDSHNDIEASDCCSLQKNLSHQLTNLSNEBPGLOSQAFKE 418
Qy 421 LEQLEHLDFO-----HSNLKOMSEFS--VFLSLRLIY--LDISHTHTRYAFNGIFNGLS 472
Db 419 CPQLEHLDLAFTRHIAAPQ-SPPQNHLFQVLYNTLCPFDTSNQ-----LLAALPV 470
Qy 473 LEVIXMAGNSFOENFL--PPIFTELRLNLTPLDLSQCLEQLEBOLSPFAFNSLSLYVLSV 530
Db 471 LRHLNKGNHFOGTITKTMLOTVGSLVLISSCGILSIDQAFHSLGKMSHVDLSHN 530
Qy 531 NFF--SLDTPPY-----KCLNSLYLDVSLNIMTSKQELQHPSSLAFLNLTONDF 581
Db 531 SLTCDSTDSLHLKGIYLNLAANSINITSPRLPIL-----SQOSTNLSHNPL 579
Qy 582 ACTCEHOSFLQWIKDQRLVVEVERMECATPSPDKQMPVLSLNTTCOMNKTIIIGSVLSV 641
Db 580 DCTCSNHFLLTWYKENHLKLGSEETTCANPSPILRGVKLSDVLSGCI--TAIGIFPLIV 637
Qy 642 LVYSVAVLVY 652
Db 638 FLI-LTALILF 647

RESULT 3
US-08-833-823-4
/ Sequence 4, Application US/08833823
/ Patent No. 5969093
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: McCoy, John
/ APPLICANT: Kelleher, Kerry
/ APPLICANT: Carlin, McKeough
/ TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs

```

STREET: 87 Cambridge Park Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,823
FILING DATE: 10-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-823-4

Query Match 14.5%; Score 629.5; DB 2; Length 661;
Best Local Similarity 29.7%; Pred. No. 5,3e-49;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

25 SWEP-CVEVENVITYQCWELNFKIPDNLPSTKNLDSFNDLRHLSYSPSPPELOVL 83
23 SWDQCIKKEANKYCNCEMLGSEIPDLPTLPTTEFLSEFNLPTIHRFTSRLNMLFL 82
84 DLSRCEIQTEIDGAQOSLSHSTLITGNPIOSLALGAFSGLSLOKLVAVETNLSLEN 143
83 DLRQIWMIHEDTQSHHQSTLVLTGNPLIFMAETSLNGKSLKHLFIQTGINSLEP 142
144 PPIGHLTKELKELVAMNLIQSFKLPEYFSNLTNLHLDLSNKSISYCTDLRVLHOMPL 203
143 IPVNLLENLESLYLSGNNHISIKFKDPP-ANLKVLDPPONNAIYISREDKRSLEQ--A 199
204 LNLSDLSINPMNFIQPGAFKEIRLKLTLRNPNFSLNVMKTCIOGLAGLEVRHLVLEGF 263
200 INLSINFGNNVKGIEGAFDSTVFSQ--NFGATPMLSVIFNGLQNSTTQSLMLGTF 255
264 RNEGLLEFDSALGECNLTIEEFLRLAYLDYLDIID-LPNCITNWSRSLVVTIER 322
256 EDIID-EDISSAMLGCEMSVESLNLQ--EHRFSDISSTTFQCTOLOELDLTATHKG 312
323 VKDFSYNGFQWHLIELVN-----CKP--GQPTL-----KLKSLKRLTPTSN 361
313 LPS-----GMKGLNLKLVLSVNHFDQLQISANFSLTHTLYRGNVKKLHLCVGLCE 367
362 KGNNAFSEVDLPSEFLDLSRNGLSFKGCCSOSDGTSTLKYLDLSFNGVITMSN-FLG 420
368 KLGN-----LQTLDSHNDIEASDCSLQKNLSHLQTLNLSHNBPLGLSQAKKE 418
421 LEQLEHLDPQ--HSNLKQMSERS--VFLSLRNLIY--LDISHTHTVAENGAINGLSS 472
419 CPQLELDLAFTRLIHNAPO--SPFQNHFLQVNLTYCFLDLSNQH-----LLAGLPV 470
473 LEVLMAAGNSFOENFL--PDIFTELRLNLTFLDLSQCOLQOLSPPTAFNSLSLQVNMGSN 530
471 LRHLNLKGNHPODGTITKTNLQTYGSLFVLISLSCGLISIQQAFLSGKMSHVDLSHN 530
531 NFF--SLDTFPY-----KCLNSLQVLDYLSLNHIMTISKQELQHPSSLAFLNLTQNDP 581

531 SLTCDISLSHLKGIYLNLANSSINIISPLPL-----SQOSTINLSHNP. 579
582 ACTCEHSEFLOWIKDQROLVVERMECATPSDKQMPVLSLNTCKNNKTIIGSVLSV 641
580 DCTCSNHFILTYKXENLHKLRSGETTCANPSPSLRGVLSVDKSLCGI--TAIGLFLIV 637
642 LVSVVAVLVY 652
638 FLI-LIATILF 647

RESULT 4
US-09-982-308B-23
Sequence 23, Application US/09982308B
Patent No. 6531290
GENERAL INFORMATION:
APPLICANT: Dalie, Barbara
APPLICANT: Fan, Xuedong
APPLICANT: Lundell, Daniel
APPLICANT: Lunn, Charles A.
APPLICANT: Tan, Jimmy C.
APPLICANT: Zavodny, Paul J.
TITLE OF INVENTION: Mammalian TNF-alpha Convertases
FILE REFERENCE: JBO601QC
CURRENT APPLICATION NUMBER: US/09/982,308B
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/156,163
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 08/889,909
PRIOR FILING DATE: 1997-07-10
PRIOR APPLICATION NUMBER: 60/021,710
PRIOR FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent In version 3.1
SEQ ID NO 23
LENGTH: 784
TYPE: PRT
ORGANISM: Homo sapiens
US-09-982-308B-23

Query Match 13.8%; Score 599.5; DB 4; Length 784;
Best Local Similarity 27.0%; Pred. No. 4.1e-46;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

48 IPDNLPTSTKNLDSFNDLRHLSYSPSPPELOVLDSRCEIQTEIDGAQOSLSHSTL 107
46 IPSGLTERVXKSLDSNNRITYISNSDLQRCVNLQALVLTNGINTIEEDSFSSLSLEHL 105
108 ILTGNPIOSLALGAFSGLSLOKLVAVETNLSLENPPIGHLKT----- 151
106 DLSYNSLSSNLSMFKPLSSITFLNLGNPKYKTIGETSLFSLHKLQTLRGNMDTFYKI 165
152 -----LKELVAMNLIQSFKLPEYFSNLTNLHLDLSNKN-----IOSI 190
166 QKDFAGLTFLEBELEIDASDLQSYE-PKSLKSIGNVSHLILHMKOHILILEIPVDVTSV 224
191 YCTDLRVLHOMPLNLSLDSINPMNFIQPGAFKEIRLKLTLRN--NFDLS-NVMK 244
225 ECLER-----DPTDLDTFHSSELSGTGTNSL-IKKTFRNVKTYIDESLFQVMK 271
245 TC--IOGLAGLEVRHLVY--GEFRNNGNLEKFPKSLALGECNLTIEEFLRLA--YLDVYL 297
272 LNLQISGLLEBEFDDCTLNGVGNFRASDNDRAVIDPGKVE--YTLIRLHLPFYLFY-- 326
298 DDIDLFNCLTNVSSFSLSVYTIERYVDPSYNGFQWHLIELVNCCKFGQFPPLKLSLRLT 357
327 -DLSTLYSLTERVK-----RITVENSKV-----LVPCLLSQ----- 357
358 FTSKNGNAFSEVDLPSEFLDLSRNGLSFKGCCSOSDGTSTLKYLDLSFNGV 412
358 -----HKSLELYDLSENLMVEBYLNKNSAC-----EDAMPBLOTLILRN--- 397

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OY 413 TMSNPLGLEBQLEHLDPOHSNLSKOMSEPSVLSLRNLIYDLSHTHTVAENGIPNGLSS 472
DB 398 -----HL-----ASLEKTEG--TLTTLKNTLNIDISK----- 422
OY 473 LEVLKMGNSFOENFLPDIFTELRLNLTFLDLSQCOLEBOLS---PTAFNSLSLQVLANMSH 529
DB 423 -----NSFHS--MPETCQWPERKMKYLNLSRTHSVTCGIP-----KTLIELIDVSN 466
OY 530 N--NFFSLD-----TFP--YKCLNSLOVLDYSLNHMTSKQELQHPSSL 571
DB 467 NNILNLFSLNLPOLKELEYISRNMKMTLPDASLLPMLVLKISRNAITTFPSKEQLDSF--HTL 525
OY 572 AFLNLTQNDPACTGCEHOSFLQWIKQOROLVBEV-----ERMECAPSDKQGMPLSLNIT 626
DB 526 KTLBAGGNPFCSCFPLSFTQ---EQALAKVLIDWPANYLSDPSHVRGOQVODVRLS 581
OY 627 ---COMKNTIIGVSLVSVVAVLVYKFX--FHLMLAGCIKYGK-----GENI-Y 674
DB 582 VSECHRIALVSGMCALFLILITLTVGLCHRHGLMWMKMMAMWLQAKRKPAPSRNICY 641
OY 675 DAFVYSSQDEBWDVWNELVKNLEEGVPPQOLCLHYRDPFGVAIAANIIEGHFKSRKYI 734
DB 642 DAFVYSERDAYWVENLWQELFNPNPFKCLHXRDFIPGKIIDNII--DSIEKSHKTV 700
OY 735 VVVSQHFIQSRKCFEYELAQTWQFLSBRAGIIFIVLOKVEKTLIRQO--VELYRLSRNT 793
DB 701 FVLSENFKSEWCKYELDPSHRLFDENNDAIILILEPIEKKALPDRFCXLRKIMNTKT 760
OY 794 YLEWEDSVLGRHIFWRRLRKAL 815
DB 761 YLEWPMDEARQREGFWVNLRAAI 782

RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

Query Match 12.4%; Score 539; DB 4; Length 775;
Best Local Similarity 26.6%; Pred. No. 1,66-40;
Matches 218; Conservative 120; Mismatches 264; Indels 218; Gaps 37;

OY 48 IPDNLPESTKNLDLSFNPLRLHGSYSPFPELOVLDLSRCEIQITBEDAVQSLSHTL 107
DB 81 IPSGITEAVKSIDLSNNRITYISNGLDQRCVNLQALVLTLSNGINTIEEDPSLSLEHL 140
OY 108 ILTNGPISLALGASGSLQK-----VAVENTLASLENFPGLHKT----- 151
DB 141 DLSTVYLSNLSWSWKPSLFLNLLGNPKYTLGSETLSFSLTLQILRVGNDMTFKXI 200
OY 152 -----LKELVAVANHLIQSFCLPEYFSNLTLBHLDSNKK-----IQSI 190
DB 201 QKROPAGLTFLELEIDASDLSQSYE-PKSLKSIGVSHLILHMKQHILLLEIFVDVITSSV 259
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OY 191 YCTDLRVLHQPLNLNLSLDSLNPMNF--IQPGAFKEIRLHKTLRLN--NFDSL-NVMK 244
DB 260 ECLER-----DITLDTFHFSSELSTGETNSI--IKKFPFRVWKITDESILFYVMK 306
OY 245 TC--IQGLAGLEVHRLV---GEFRNENLEKPKSKALLEGICNLTIEFRLA--YLDVYL 297
DB 307 LLNOISGLELEFPDDCTLVNGVGNFRASDNDNRVIDPGKVE--TLTIRLHLPREFLYE-- 361
OY 298 DDIIDLFPNCLTNVSSFSLSVSTIERVDFSYNFGMOHLELVNCKFGQFPPLKLSLRLT 357
DB 362 -DLSTVLSITERVK-----RTVENSKYF-----LVPCLLSQ----- 392
OY 358 FTSNKGNAFSEVDLPSEFLDLSRN---GLSPKCCGSSDPTGTSKLYDLSFNGVI 412
DB 393 -----HKSLEYLDLSENLMVEEYLRNSAC--EDWAPSLQTLILIRON--- 432
OY 413 TMSNPLGLEBQLEHLDPOHSNLSKOMSEPSVLSLRNLIYDLSHTHTVAENGIPNGLSS 472
DB 433 -----HL-----ASLEKTEG--TLTTLKNTLNIDISK----- 457
OY 473 LEVLKMGNSFOENFLPDIFTELRLNLTFLDLSQCOLEBOLS---PTAFNSLSLQVLANMSH 529
DB 458 -----NSFHS--MPETCQWPERKMKYLNLSRTHSVTCGIP-----KTLIELIDVSN 501
OY 530 N--NFFSLD-----TFP--YKCLNSLOVLDYSLNHMTSKQELQHPSSL 571
DB 502 NNILNLFSLNLPOLKELEYISRNMKMTLPDASLLPMLVLKISRNAITTFPSKEQLDSF--HTL 560
OY 572 AFLNLTQNDPACTGCEHOSFLQWIKQOROLVBEV-----ERMECAPSDKQGMPLSLNIT 626
DB 561 KTLBAGGNPFCSCFPLSFTQ---EQALAKVLIDWPANYLSDPSHVRGOQVODVRLS 616
OY 627 ---COMKNTIIGVSLVSVVAVLVYKFX--FHLMLAGCIKYGK-----GENI-Y 674
DB 617 VSECHRIALVSGMCALFLILITLTVGLCHRHGLMWMKMMAMWLQAKRKPAPSRNICY 676
OY 675 DAFVYSSQDEBWDVWNELVKNLEEGVPPQOLCLHYRDPFGVAIAANIIEGHFKSRKYI 734
DB 677 DAFVYSERDAYWVENLWQELFNPNPFKCLHXRDFIPGKIIDNII--DSIEKSHKTV 735
OY 735 VVVSQHFIQSRKCFEYELAQTWQFLSBRAGIIFIVLOK 774
DB 736 FVLSENFKSEWCKYELDPSHRLFDENNDAIILILEPI 775

RESULT 6
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NOVEL LNSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-09-063-950-5

Query Match 7.3%; Score 316; DB 3; Length 605;
Best Local Similarity 24.4%; Pred. No. 4,1e-20;
Matches 157; Conservative 94; Mismatches 242; Indels 150; Gaps 23;

OY 33 VPNTIYQCEINLFKIPDNLPESTKNLDLSFNPLRLHGSYSPFPELOVLDLSRCEIQ 92
DB 53 VNELSVYCSRRNLRLDGPGLGTOALWLDNSNLSIPPAFRULSSLAFLNLOGGOLGS 112
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Qy 93 IEDGAYQSLSHSTLITGNPIQSIALGAFS-----GLSSL 128
Db 113 LEPQALLGLENLCHLHLEBNOLRLSLAVGTFAATPALALLGSSNNRLSLREDOGLFEGGLCNL 172
Qy 129 QKLVAVETNLASLENFPIGHLKTKELNVANHLLIOSFLLPEFNSLTNLEHLDSSNKIQ 188
Db 173 WDLNIGNSLAVLPDAARFGLGGLRELVLVAGNRL-AYLOPALFSGLAELRELDSSRNALR 231
Qy 189 SIYCTDLRVLHQPMLNLSLDLSLNPNNFIQGAKEIR-LHKLTLRNNFDSLNWKTCTI 247
Db 232 AI-----KANVAPQLPRLQ-KLYIDRLNLIAAVAPGALGLKALRWLDLSHN-RVAGLLEDTF 286
Qy 248 QGLAGLEVHRLVGLFEFNEGNLEKDKSALBGLCNLTIEFRLAYLDYLDIIDLFNCL 307
Db 287 PGLGLRLVRL-----SHNAIASLRPTFEDL-----HFLEEL----- 319
Qy 308 TNVSFSLVSTIERVKDPSYNGWHLVLVNCCKGQFPPLTKLSLKRLLFTS--NKGN 365
Db 320 -----QIGHNRIRQLAERSFE-GLGQLEVLTLDNQLOEVKVGAFGLGTVNAVNNLSGN 372
Qy 366 AFSEVDLPSEFLDLR-NGLSFKGCC-----SQSDFGTSLKYLDLSFNGVITMSSNFL 419
Db 373 CLR--NLPEQVFRGLKLSHLBESSCLGRIRPHFTGSLGRLLFKDNGLVGIEBQSL 430
Qy 420 -GLEQLEHLDPOHSNLMKMSSESVFLSLRNLIYLDISHHTRVAFNGIPLNGLSLEVLKM 478
Db 431 WGLELLELDLTNSQL-----THLP--HQLFOGLGKLEYLL 465
Qy 479 AGNSQENFLP-DIFTELRLNLFELDLSOCOLBOLSPAFNSLSLOVNMSSNPFSLDT 537
Db 466 SHNRILAE--LPADALGPLQRAFWLDVSHNRLEALGSLASLGRIRYLNLRN--SLRT 520
Qy 538 FPKYKLSNLQVLDVSLNHNMTSKOELQHPSSLAFLNLTONFACTECHO----- 589
Db 521 FTPQ-----PGLERLMLBGNPMWCSCLKALRPFALON 554
Qy 590 -----FLQMT--KQORQLVEVERMECATPSPDKQMPVLSTL 623
Db 555 PSAVRFVOALCEGDDCOPPYTYNNITCASPEVAVGLDLRL 597

RESULT 7
US-09-949-016-10995
; Sequence 10995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10995
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10995

Query Match 7.0%; Score 305; DB 4; Length 623;
Best Local Similarity 24.3%; Pred. No. 4,4e-19;
Matches 171; Conservative 96; Mismatches 260; Indels 178; Gaps 28;

Qy 4 ASRLA---GTILPAAFLSCVR--PESWE-----PCV---EVVPIIT 37
Db 16 ACRMLLRKGGALALLLLISWVALGPRSLGADPGTPGABGAPCAPACVCSYDDADELS 75

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Qy 38 YQCEMLNFPYKIPDNLPESTKNLDSFNPLRHLSYSPFSPPELOVLDLSRCEIQTIEDGA 97
Db 76 VFCSSRNLTRLPDVPGGTQALMLDGNNSLSVPPAAFGNLSLGLFNLQCGGLSLEPOA 135
Qy 98 YQSLSHSTLITGNPIQSIALGAFS-----GLSSLQKVA 133
Db 136 LLEGLNCHLHLEBNOLRLSLAVGTFAATPALALLGSSNNRLSLREDOGLFEGGLCNL 195
Qy 134 VETNLASLENFPIGHLKTKELNVANHLLIOSFLLPEFNSLTNLEHLDSSNKIQSYCT 193
Db 196 GMSNLAVLPDAARFGLGGLRELVLVAGNRL-AYLOPALFSGLAELRELDSSRNALR 251
Qy 194 DLRYLHQPMLNLSLDLSLNPNNFIQGAKEIR-LHKLTLRNNFDSLNWKTCTIQLAG 252
Db 252 KANVAPQLPRLQ-KLYIDRLNLIAAVAPGALGLKALRWLDLSHN-RVAGLLEDTFPGILG 309
Qy 253 LEVRLVGLFEFNEGNLEKDKSALBGLCNLTIEFRLAYLDYLDIIDLFNCLTNVS 312
Db 310 LRVRL-----SHNAIASLRPTFEDL-----HFLEEL----- 337
Qy 313 FSLVSTIERVKDPSYNGWHLVLVNCCKGQFPPLTKLSLKRLLFTS--NKGNAFSEV 370
Db 338 -QIGHNRIRQLAERSFE-GLGQLEVLTLDNQLOEVKVGAFGLGTVNAVNNLSGNCLR-- 393
Qy 371 DLPSEFLDLR-NGLSFKGCC-----SQSDFGTSLKYLDLSFNGVITMSSNFL-GLEQ 423
Db 394 NLPEQVFRGLKLSHLBESSCLGRIRPHFTGSLGRLLFKDNGLVGIEBQSLMGLAE 453
Qy 424 LEHLDPOHSNLMKMSSESVFLSLRNLIYLDISHHTRVAFNGIPLNGLSLEVLKMGNSF 483
Db 454 LLELDLTNSQL-----THLP--HRLFOGLGKLEYLLSLRNL 488
Qy 484 QENFLP-DIFTELRLNLFELDLSOCOLBOLSPAFNSLSLOVNMSSNPFSLDTPPYKC 542
Db 489 AE--LPADALGPLQRAFWLDVSHNRLEALGSLASLGRIRYLNLRN--SLRTFTQ- 542
Qy 543 LNSLQVLDVSLNHNMTSKOELQHPSSLAFLNLTONFACTECHOSEFLQMTK- 596
Db 543 -----PGLERLMLBGNPMWDCGP--LKALRPFALON 573

RESULT 8
US-08-190-802A-49
; Sequence 49, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: 265
; CURRENT APPLICATION NUMBER: US/08/190,802A
; PRIOR FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:

```

NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
MOLECULE TYPE: unknown
TOPOLOGY: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49

Query Match 7.0%; Score 303; DB 1; Length 605;
Best Local Similarity 24.4%; Pred. No. 6,4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;
QY 40 CMEINFYKIDNLPSTKNLDSFNPRLHLSYSFSPPELYQVLDLSRCETQTEDGAYQ 99
DB 60 CSSRNLTRLPDVGPGTQALMDGNLSSVPPAFQNLSSLGFLNLQGGQGSLEPQALL 119
QY 100 SLSHLSTLITGNPIOSIALGAFS-----GLSLQKLYAVE 135
DB 120 GLENLCHLHERNQKSLALGTFPAHTPALASLGNNRSLRLBDLFEGLSMDNLNGW 179
QY 136 TNLASLENPIGHLKTLKELVANHLIOSFKLPEYFSNLTNLEHLDSNKKIOSICTDL 195
DB 180 NSLAVLPDAFRGSGSLRELVLGAGNRL-AYLQPALFSGLAELREIDLSRNALRAI---KA 235
QY 196 RVLHOMPLNLSLDLSNPNMFIOGAFKEIR-LHKLTLRNPNDSLNWKTCTIOGLAGLE 254
DB 236 NVFVQLPRLO-KLYIDRNLIAAVAPGAFGLKALRWLDSHN-RVAGILDTFPGILGLR 293
QY 255 VHRVLVGEFNEGNLEKFDKSALEGLCNLTIEFRRLAYLDYLDIDLFNCLTNVSSFS 314
DB 294 VLR-----SHNAIASLRPRTFKDL-----HLEEL-----Q 320
QY 315 LVSTIERVDFSYNFGQHLIELVNCCKFGQPTLKLSLKLTFTS--NKGNAFSEVDL 372
DB 321 LGHNRIRQLAERSFE-GLGQLEVLITLDHNQLEVYAGAFGLITNVAVMNLSGNCIR--NL 377
QY 373 PSLEFLDLSR-NGLSFKGCC-----SOSDFGTTSLKXYLDLSPNGVITMSSNFL-GLGLE 425
DB 378 PEQVFRGLGKLSHLSBSCIGRIRPHTFTTGLSGIRLFLKONGLVGIEBOSLWGLLELL 437
QY 426 HLDFOHSLKQMSSESVFLSLRNLITLIDISHTTRVAENGIFNGLSLLEVLKMAGNSFOE 485
DB 438 ELDTLSNQL-----THLRP--HRLFOGKLELYLLLRNRLAE 472
QY 486 NFLP-DLFTELRNLTFLDLSQCLBOUSPTAFNSLISQVIMGNHNFPSLDTPPYKCLN 544
DB 473 --LPADLGLPQRAFVWLDVSHNRLEALPNSLIAPLGRIRYLSLRNN--SLRTFTPO--- 524
QY 545 SLQVLDVSLNIMTSSKKQELQHPSSSLAFLNLITQNDPACTCEHOSFLQWIMD----- 596
DB 525 -----PPGLERLWLBEQPMDCGP-----LKALDFALQNPESA 557
QY 597 -QROLLVEVERMECATPSDKQMPVLSLNITQNMKTIIGSV 638
DB 558 VPRFVQALCEBGDCQPAYTYN-----NITCASPREVVGIDL 594

RESULT 9
US-08-477-346-49
Sequence 49, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
MOLECULE TYPE: unknown
TOPOLOGY: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-477-346-49

Query Match 7.0%; Score 303; DB 3; Length 605;
Best Local Similarity 24.4%; Pred. No. 6,4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;
QY 40 CMEINFYKIDNLPSTKNLDSFNPRLHLSYSFSPPELYQVLDLSRCETQTEDGAYQ 99
DB 60 CSSRNLTRLPDVGPGTQALMDGNLSSVPPAFQNLSSLGFLNLQGGQGSLEPQALL 119
QY 100 SLSHLSTLITGNPIOSIALGAFS-----GLSLQKLYAVE 135
DB 120 GLENLCHLHERNQKSLALGTFPAHTPALASLGNNRSLRLBDLFEGLSMDNLNGW 179
QY 136 TNLASLENPIGHLKTLKELVANHLIOSFKLPEYFSNLTNLEHLDSNKKIOSICTDL 195
DB 180 NSLAVLPDAFRGSGSLRELVLGAGNRL-AYLQPALFSGLAELREIDLSRNALRAI---KA 235
QY 196 RVLHOMPLNLSLDLSNPNMFIOGAFKEIR-LHKLTLRNPNDSLNWKTCTIOGLAGLE 254
DB 236 NVFVQLPRLO-KLYIDRNLIAAVAPGAFGLKALRWLDSHN-RVAGILDTFPGILGLR 293
QY 255 VHRVLVGEFNEGNLEKFDKSALEGLCNLTIEFRRLAYLDYLDIDLFNCLTNVSSFS 314
DB 294 VLR-----SHNAIASLRPRTFKDL-----HLEEL-----Q 320
QY 315 LVSTIERVDFSYNFGQHLIELVNCCKFGQPTLKLSLKLTFTS--NKGNAFSEVDL 372
DB 321 LGHNRIRQLAERSFE-GLGQLEVLITLDHNQLEVYAGAFGLITNVAVMNLSGNCIR--NL 377
QY 373 PSLEFLDLSR-NGLSFKGCC-----SOSDFGTTSLKXYLDLSPNGVITMSSNFL-GLGLE 425

Db 378 PEQVFRGKGLSHLBSGCLGRIRPHFTFTGLSGRLFLKONGLVGIEBOSLWGIAEL 437
Qy 426 HLDFOHNLKQMSSEFVFLSLRNLIYLDISHHTVAVANGIPNGLSLEVLKMGANSFOE 485
Db 438 ELDLTSNQL-----THLP---HRLFQGLKLEYLLSLNRRLAE 472
Qy 486 NFLP-DIFTELRLNLTFLDLSOCQLEBQSPFAFNSLSLQVLMNSHNFFSLDTPPYKCLN 544
Db 473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRIRYLSLRNN---SLRTFTPO--- 524
Qy 545 SLQVLDYSLNIMTMSKQELQHPFSSLAFLNLTQNDFACTCEHOSFLOWIKD----- 596
Db 525 -----PGLERLMLBGNPMDCCP---LKALRDFALQNPBA 557
Qy 597 -QROLLEVERMECATPSDKQGMPLSLNITQNMKTIIGSV 638
Db 558 VPRFVQACEGDDCQPPAYTYN-----NITCASPPEVVGDL 594

RESULT 10

US-08-473-089-49
; Sequence 49, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-473-089-49

Qy Query Match 7.0%; Score 303; DB 3; Length 605;
Best Local Similarity 24.4%; Pred. No. 6.4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;
Qy 40 CHELNFYKIDNLPSTYKLDLSPNRLHLSYSPFPELOVLDLSREITIEDGAVO 99
Db 60 CSSRMVTRLPDGVPGTQALWLDGNLSSVPPAFQNLSSLOPLNLTQGGQSLSPQALL 119

Qy 100 SLSHLSTLLTNGNBIQSIALGAFS-----GLSSLOKLVAVE 135
Db 120 GLENLCHLHERNQLRSIALGTFAHTPALASGLNNRLSLBEDGLFEGLSLMDLNLGW 179
Qy 136 TNLASLENFPIGHTKLKELVANVNLIOSFGLPYFSNLTNLEHLDSSNNIQSICYCDL 195
Db 180 NSLVLPPAARFGISIRELVLAQNR--AVIQPALFSGLABLRELDLSRNALRAL--KA 235
Qy 196 RVLQMPPLNLSLPLNPMFIQGAPEKIR-LHKLTLRNPPSLNVMKTCIOGLAGLE 254
Db 236 NVFQQLPRLQ-KLVDRNLIAAVAPGALGKALRMWLDLSN-RVAGLEBTFPRLGLR 293
Qy 255 VHRVLGFERNGLKEPKDSEGLCNLTIEFRFLAVLDYDLDIIDLFNCLTNVSSFS 314
Db 294 VLRL-----SHNVLASLRRTFKDL-----HFLBEL-----Q 320
Qy 315 LVSTYTERVKDFSNFGQHLVYCNCKFGQPTLKLSIKRLTFTS--NKGNAFSEVDL 372
Db 321 LGHNRIRQLAESFE-GIGQLEVLTLDNQIQEVKAGAFGLGTLVVAVNNLSGNCIR--NL 377
Qy 373 PSLFELDLR-NGLSFKGCC-----SOSDFGTSLSKYLDLSFNGVITWSSNFL-GLBOLE 425
Db 378 PEQVFRGKGLSHLBSGCLGRIRPHFTFTGLSGRLFLKONGLVGIEBOSLWGIAEL 437
Qy 426 HLDFOHNLKQMSSEFVFLSLRNLIYLDISHHTVAVANGIPNGLSLEVLKMGANSFOE 485
Db 438 ELDLTSNQL-----THLP---HRLFQGLKLEYLLSLNRRLAE 472
Qy 486 NFLP-DIFTELRLNLTFLDLSOCQLEBQSPFAFNSLSLQVLMNSHNFFSLDTPPYKCLN 544
Db 473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRIRYLSLRNN---SLRTFTPO--- 524
Qy 545 SLQVLDYSLNIMTMSKQELQHPFSSLAFLNLTQNDFACTCEHOSFLOWIKD----- 596
Db 525 -----PGLERLMLBGNPMDCCP---LKALRDFALQNPBA 557

RESULT 11

US-08-487-072A-49
; Sequence 49, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:

APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratSeqFormatter Version 0.9
SEQ ID NO: 1325
LENGTH: 662
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q14392
US-09-538-092-1325

Query Match 6.9%; Score 299.5; DB 4; Length 662;

Best Local Similarity 25.9%; Pred. No. 1.6e-18;
Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

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QY 28 PCVEVVPNITYQCEMELNPFYKIPDNLPFSTKNLDSFNPRLHSGSYSPFSPPELQVLDLSR 87
DB 25 PCRWVKKVVS--CQVIGLQVPSVLPPTETLDSGNGRLSIASPLGFTYLRHLDST 82
QY 88 CEIQTIEDGAYQSLSHTLITGNPQISLALGAFSGSLQKLVAVETNLAS-----LE 142
DB 83 NEISFLQGAFOALTHLEHLSLANHRLAMATLASGGLPRLVTSLDLSGNSLYSGLE 142
QY 143 NPPIGHLTKELVANHLIOSFKLPXY-FSNLTNLEHLDSSNKGISYCTDLEVLHOM 201
DB 143 RL-LGEAPSLHTLSLAENSLT--RLTRHTFRDMPALBQDLHSNVLMDIEDGAFGLPRL 199
QY 202 PLNLNS-----LDLSNPNMFI-----QPGAKEIRLHKLTLRNN----- 236
DB 200 THLNLSRNSLTCTISDFSLQQLRVLDLSCNSIEAFQTASQPOA--EFQLTWLDLRNKLIH 257
QY 237 FDSLNVMTCTIOGLAGLEVHRLVIGEPRN-----EGNLEKFDKSL 277
DB 258 FPDLAALRLIYLNLSNNILRLPTGPPODSKGIHAPSEGSMSLPLSAPSGNAGRPLSQL 317
QY 278 EGLCNLTIEFRFLAVLDYLDIIDL-----NCLTVSSFSLSVITERYKDPSPYNG 331
DB 318 LNL-DLSYNEIEL-IPDSFLEHLTSLCPNLNSRNCLRTFEARRLSLPCLMLDLDSHN-A 374
QY 332 MOHLELVNCKFGQFPFLKLSKRLTFTSNKGNAFSEV-----DLPSLEFLDLSRNGI 385
DB 375 LETLELGARALGSLRTLLQ-----GNLRDLPPTYTPANLASLQKLNLOQNRV 422
QY 386 S-----FKGCCSGSDFGTTSIKYVLDLSFNGVITMSSNFLGLEQLEHLDFOHSNLKQ 436
DB 423 SPCGGPDERPGSGCAVPS--GITSLRSLSLVNDEI-----ELRAGAFLLTPPLE 470
QY 437 MSEFVFLSLRNLIYLDISHHTTRVAFNGIFNGI--SSLEVLKMAQNSPQ--ENFLPDIFT 493
DB 471 -----LDLSSNPGLEVATGALGSLASLEVALIQNGMLVLDVDPFCFC 515
QY 494 ELRNLTFLDLSQCCEQLSPFAFNSLSLOVLMNSHNNFSLDTPPYKCLNSLOVLDYSI 553
DB 516 ----LKRLNLLENRLSHL--PAWTOAVSLEVDL--RNNSSFSL--LPGSAMGLE----- 560
QY 554 NHIMTSKQOELQHPSSSLAFLNLTQNDPACTCEHOSFLOWIKQ--ROLIVAYERME--C 609
DB 561 -----TSLRRLYLQGNPLSC--CGN-----GMLAAQLHOGKVDVADATODLIC 600
QY 610 ATPSDKQGPVLSLNTIT-----QGMN--KTIIGSVLSVLSVAVLVYKFFHMLLAG 663
DB 601 RPSOBE-----VSLSHVRPEDECKGKLNINILITITFLVSAIL-----LTTTLA 647
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QY 664 C 664
DB 648 C 648

RESULT 14

US-09-949-016-6619

; Sequence 6619, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: C1001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 6619

; LENGTH: 662

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-6619

Query Match 6.9%; Score 299.5; DB 4; Length 662;

Best Local Similarity 25.9%; Pred. No. 1.6e-18;
Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

```
QY 28 PCVEVVPNITYQCEMELNPFYKIPDNLPFSTKNLDSFNPRLHSGSYSPFSPPELQVLDLSR 87
DB 25 PCRWVKKVVS--CQVIGLQVPSVLPPTETLDSGNGRLSIASPLGFTYLRHLDST 82
QY 88 CEIQTIEDGAYQSLSHTLITGNPQISLALGAFSGSLQKLVAVETNLAS-----LE 142
DB 83 NEISFLQGAFOALTHLEHLSLANHRLAMATLASGGLPRLVTSLDLSGNSLYSGLE 142
QY 143 NPPIGHLTKELVANHLIOSFKLPXY-FSNLTNLEHLDSSNKGISYCTDLEVLHOM 201
DB 143 RL-LGEAPSLHTLSLAENSLT--RLTRHTFRDMPALBQDLHSNVLMDIEDGAFGLPRL 199
QY 202 PLNLNS-----LDLSNPNMFI-----QPGAKEIRLHKLTLRNN----- 236
DB 200 THLNLSRNSLTCTISDFSLQQLRVLDLSCNSIEAFQTASQPOA--EFQLTWLDLRNKLIH 257
QY 237 FDSLNVMTCTIOGLAGLEVHRLVIGEPRN-----EGNLEKFDKSL 277
DB 258 FPDLAALRLIYLNLSNNILRLPTGPPODSKGIHAPSEGSMSLPLSAPSGNAGRPLSQL 317
QY 278 EGLCNLTIEFRFLAVLDYLDIIDL-----NCLTVSSFSLSVITERYKDPSPYNG 331
DB 318 LNL-DLSYNEIEL-IPDSFLEHLTSLCPNLNSRNCLRTFEARRLSLPCLMLDLDSHN-A 374
QY 332 MOHLELVNCKFGQFPFLKLSKRLTFTSNKGNAFSEV-----DLPSLEFLDLSRNGI 385
DB 375 LETLELGARALGSLRTLLQ-----GNLRDLPPTYTPANLASLQKLNLOQNRV 422
QY 386 S-----FKGCCSGSDFGTTSIKYVLDLSFNGVITMSSNFLGLEQLEHLDFOHSNLKQ 436
DB 423 SPCGGPDERPGSGCAVPS--GITSLRSLSLVNDEI-----ELRAGAFLLTPPLE 470
QY 437 MSEFVFLSLRNLIYLDISHHTTRVAFNGIFNGI--SSLEVLKMAQNSPQ--ENFLPDIFT 493
DB 471 -----LDLSSNPGLEVATGALGSLASLEVALIQNGMLVLDVDPFCFC 515
QY 494 ELRNLTFLDLSQCCEQLSPFAFNSLSLOVLMNSHNNFSLDTPPYKCLNSLOVLDYSI 553
DB 516 ----LKRLNLLENRLSHL--PAWTOAVSLEVDL--RNNSSFSL--LPGSAMGLE----- 560
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Qy 554 NHMTSKQELQHPSSLAFLNTQNDFACTCEHOSFLQWIKQ-QQLLVEVERME---C 609
Db 561 -----TSLRRLYLQGNPLSC-CGN-----GMLAQHQGRVDVDAQDILIC 600
Qy 610 ATPSDKQAMPVLSINIT-----COMN--KTIIGVSLVSVVAVLVYKFFPHMLLAG 663
Db 601 RFSQGE-----VLSHVRPDECKGKGNINLIITLFIIVSAIL-----LTTLLA 647
Qy 664 C 664
Db 648 C 648

RESULT 15
US-09-949-016-10710
; Sequence 10710, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10710
; LENGTH: 665
; TYPE: PR
; ORGANISM: Human
US-09-949-016-10710

Query Match 6.9%; Score 299.5; DB 4; Length 665;
Best Local Similarity 25.9%; Pred. No. 1.6e-18;
Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

Qy 28 PCVEVENITTYQCHELNAYKIPDNLPSTKULDISFNPRLHLSYSPFPELOVLDISR 87
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Qy 88 CEIQTEEDGAYOSLSHTLITGNPIQSALGAFSGLSLOKLVAVETNLAS-----LE 142
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Db 146 RL-LGEAPSLHTLSLAENSLT-RLTRHTFRDMPALBQDLHSNVLMIDEDGAFEGLPRL 202
Qy 202 PLNLS-----LDLSLNPMPFI---QGAFKETIRLHKLTLRNN--- 236
Db 203 THMLNSRSLCTISDFSLQQLRVLDLSGNSIEAFQASQPOA--EFQLTWLDLRENKLIH 260
Qy 237 FDSLNWMTCTIOGLAGLEVHRLVIGEPFN-----EGNLEKFDKSAI 277
Db 261 FPDLAALPRLIYLNLSNNLRPLPGPODSKGIIHAPSEGSALPLSAPSGNAGRPLSQI 320
Qy 278 EGLCNLTIEEFRLAYLDYDIDILF-----NCLTNVSSFSLSVVTIERVKDFSYNFG 331
Db 321 LNL-DLSYNEIEL-IPDSFLEHLTSLCFNLNRSNCLRTFEARLGSPLCMLLDLSHNT-A 377
Qy 332 WQHLLEVNCCKGQPPTLKLSKRLTFTSNKGNAFSEV-----DLPSEFLDLSRNGI 385
Db 378 LETLELGARALGSRLTLIQ-----GNALRDLPPYTFANLASLQRLNLQGNRV 425
Qy 386 S-----FKGCCSQSDPFGTTSGLKYLDLSFNGVITMSSNPLGLEQLEHLDPOHSNLIKQ 436

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Db 426 SPCCGDEPBGSGCVAFS--GITSLSLSLVNDIEI-----ELLRAGAFIHTPLTE 473
Qy 437 MSFSEVFLSLRNLIYLDISHTRVAFNGIFNGI-SSLEVLKMAGNSFO--ENFLPDIFT 493
Db 474 -----LDLSSNPGLEVATGALGGIEASLEVIALQGNGLMVLQVLDLPCFIC 518
Qy 494 ELRNLTFLDLSQCEBLSPLAFNSLSLOYLNKSHNPFSLDTFPYKCLANSLOVLDYSL 553
Db 519 -----LKRINLAENRLSHL--PAWQAVSLLEVLDL-RNNSFSL--LPGSAMGGLE----- 563
Qy 554 NHMTSKQELQHPSSLAFLNTQNDFACTCEHOSFLQWIKQ-QQLLVEVERME---C 609
Db 564 -----TSLRRLYLQGNPLSC-CGN-----GMLAQHQGRVDVDAQDILIC 603
Qy 610 ATPSDKQAMPVLSINIT-----COMN--KTIIGVSLVSVVAVLVYKFFPHMLLAG 663
Db 604 RFSQGE-----VLSHVRPDECKGKGNINLIITLFIIVSAIL-----LTTLLA 650
Qy 664 C 664
Db 651 C 651

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Search completed: March 12, 2005, 19:58:48
Job time : 27.0639 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:55:29 ; Search time 74.2496 Seconds
(without alignments)
3727.157 Million cell updates/sec

Title: US-09-396-985B-2

Perfect score: 4355
Sequence: 1 MMSASRLAGTLIPAMAFISC.....SMNDEGTGTCGNQGEATSI 839

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

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- 19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	4335.5	99.6	837	10	US-09-950-041-26
2	4141	95.1	799	10	US-09-950-041-8
3	4141	95.1	799	14	US-10-128-166-7
4	4141	95.1	799	16	US-10-732-563-8
5	4141	95.1	799	16	US-10-732-796A-8
6	663	15.2	661	15	US-10-038-854-135
7	663	15.2	661	13	US-10-037-417-107
8	629.5	14.5	661	13	US-10-114-893-10
9	629.5	14.5	661	15	US-10-038-854-134
10	603.5	13.9	784	10	US-09-950-041-4
11	603.5	13.9	784	15	US-10-456-947-46
12	602.5	13.8	784	14	US-10-095-627-12
13	602.5	13.8	784	16	US-10-732-563-4

14	602.5	13.8	784	16	US-10-732-796A-4	Sequence 4, Appli
15	602.5	13.8	784	17	US-10-741-600-1390	Sequence 1390, Ap
16	602.5	13.8	784	17	US-10-741-600-1391	Sequence 1391, Ap
17	599.5	13.8	784	13	US-10-145-014-23	Sequence 23, Appl
18	580.5	13.3	1032	10	US-09-954-987B-192	Sequence 192, App
19	580.5	13.3	1032	14	US-10-272-502A-31	Sequence 31, Appl
20	580.5	13.3	1032	15	US-10-407-952-32	Sequence 32, Appl
21	567	13.0	1050	10	US-09-954-987B-175	Sequence 175, Appl
22	567	13.0	1050	14	US-10-272-502A-22	Sequence 22, Appl
23	567	13.0	1050	15	US-10-407-952-26	Sequence 26, Appl
24	534	12.3	1032	9	US-09-950-041-37	Sequence 37, Appl
25	534	12.3	1032	9	US-09-864-761-38325	Sequence 38325, A
26	534	12.3	1041	10	US-09-954-987B-184	Sequence 184, App
27	534	12.3	1041	10	US-09-954-987B-186	Sequence 186, App
28	534	12.3	1041	14	US-10-272-502A-26	Sequence 26, Appl
29	534	12.3	1041	15	US-10-407-952-28	Sequence 28, Appl
30	534	12.3	1041	16	US-10-732-563-16	Sequence 16, Appl
31	534	12.3	1041	16	US-10-732-796A-16	Sequence 16, Appl
32	533	12.2	1041	9	US-09-168-978-3	Sequence 3, Appli
33	533	12.2	1041	9	US-09-978-295A-498	Sequence 498, App
34	533	12.2	1041	9	US-09-978-697-498	Sequence 498, App
35	533	12.2	1041	9	US-09-978-192A-498	Sequence 498, App
36	533	12.2	1041	9	US-09-999-832A-498	Sequence 498, App
37	533	12.2	1041	10	US-09-978-189-498	Sequence 498, App
38	533	12.2	1041	10	US-09-978-608A-498	Sequence 498, App
39	533	12.2	1041	10	US-09-978-585A-498	Sequence 498, App
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41	533	12.2	1041	10	US-09-978-403A-498	Sequence 498, App
42	533	12.2	1041	10	US-09-978-564A-498	Sequence 498, App
43	533	12.2	1041	10	US-09-999-833A-498	Sequence 498, App
44	533	12.2	1041	10	US-09-981-915A-498	Sequence 498, App
45	533	12.2	1041	10	US-09-978-824-498	Sequence 498, App

ALIGNMENTS

RESULT 1
US-09-950-041-26
Sequence 26, Application US/09950041

Publication No. US20030302090A1

GENERAL INFORMATION:

APPLICANT: Hardiman, Gerard T.

APPLICANT: Rock, Fernando L.

APPLICANT: Bazan, J. Fernando

APPLICANT: Kaestlein, Robert A.

APPLICANT: Ho, Stephen W.K.

APPLICANT: Liu, Yong-Jun

TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

FILE REFERENCE: DX0724XK1

CURRENT APPLICATION NUMBER: US/09/950,041

CURRENT FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: 09/728,540

PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 60/207,558

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 09/073,363

PRIOR FILING DATE: 1999-06-05

PRIOR APPLICATION NUMBER: 60/044,293

PRIOR FILING DATE: 1997-05-07

PRIOR APPLICATION NUMBER: 60/072,212

PRIOR FILING DATE: 1998-01-22

PRIOR APPLICATION NUMBER: 60/076,947

PRIOR FILING DATE: 1998-03-05

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn version 3.1

SEQ ID NO 26

LENGTH: 837

TYPE: PRT

ORGANISM: Homo sapiens

US-09-950-041-26

Query Match 99.6%, Score 4335.5, DB 10, Length 837;

Best Local Similarity 99.9%; Pred. No. 0; Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 1 MSASRLAGTLIPAMAFISCVPESMEPCVE-VPNITTCQCEMLNFYKIPDNLPFSTKXLDL 59

QY 62 SPNRLHLSYSPFSPPELQVLDLSRCEIQTIEDGAYQSLSHTLITLGNPIQSALGA 121
Db 60 SPNRLHLSYSPFSPPELQVLDLSRCEIQTIEDGAYQSLSHTLITLGNPIQSALGA 119

QY 122 FSGSLSQKVAVAVETNLASLENFPIGHLKTLKELVANAHLIQSFKLPEYPSNLNLHLD 181
Db 120 FSGSLSQKVAVAVETNLASLENFPIGHLKTLKELVANAHLIQSFKLPEYPSNLNLHLD 179

QY 182 LSSNKIOSICTDRLVHOMPLNLSDLSLNPNNFIOPGAFKIRLHKLTLRNPNPSLN 241
Db 180 LSSNKIOSICTDRLVHOMPLNLSDLSLNPNNFIOPGAFKIRLHKLTLRNPNPSLN 239

QY 242 VMKTCIOGLAGLEVHRLVLSGEPNENLEKFDKSGALEGLCNLTIEFRLAYLDYDDII 301
Db 240 VMKTCIOGLAGLEVHRLVLSGEPNENLEKFDKSGALEGLCNLTIEFRLAYLDYDDII 299

QY 302 DLEFCLTNVSSFSLSVTIERVKDPSYNGMHLVNCCKRGOPPTLKLSLKLFTSN 361
Db 300 DLEFCLTNVSSFSLSVTIERVKDPSYNGMHLVNCCKRGOPPTLKLSLKLFTSN 359

QY 362 KGGNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTSLKYLDLSFNGVITMSSNFG 421
Db 360 KGGNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTSLKYLDLSFNGVITMSSNFG 419

QY 422 EOLEHLDFOHNSLKQMBSEFVLSLRNLITLIDSHTRVAFNGIFNGLSLEVLAKAGN 481
Db 420 EOLEHLDFOHNSLKQMBSEFVLSLRNLITLIDSHTRVAFNGIFNGLSLEVLAKAGN 479

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Db 540 CLNSLQVLDYSLNHIMTSKQELQHPSSLAFLNLTONDFACTCEHOSFLQWIKDQRL 599

QY 602 VEVERMECATPDSKQMPVLSLNTTCQMNKTIIGVSVLSVLVSVAVLVYKFPYHML 661
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Db 720 IIEGFHKSRYIVVVSQHFQSRMCIFEYELAQTWQFLSRAGIIFVLOKVEKTLIRQ 779

QY 782 QVEYLRLSRTTYEMEDSVLGRHIFWRRLKALLDGKSNPESTVGTCNMQATSI 839
Db 780 QVEYLRLSRTTYEMEDSVLGRHIFWRRLKALLDGKSNPESTVGTCNMQATSI 837

RESULT 2
US-09-950-041-8
; Sequence 8, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XK1

CURRENT APPLICATION NUMBER: US/09/950,041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-8

Query Match 95.1%; Score 4141; DB 10; Length 799;
Best Local Similarity 100.0%; Pred. No. 0; Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 281 CNLTIEFRLAYLDYDDIIDLPCNLTNVSFSLSVTIERKYDPSYNGMHLVNC 340
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Db 301 KFGOPPTLKLSLKLFTSNKGGNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTTS 360

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Db 361 LKYLDSFNGVITMSSNFGLEBQLEHLDFOHNSLKQMBSEFVLSLRNLITLIDSHTR 420

QY 461 VARENGITNGLSSEVLKMAGNSFOENFLPDIETELRNLTFLDLSQCOLEOLSPFAFNSLS 520
Db 421 VARENGITNGLSSEVLKMAGNSFOENFLPDIETELRNLTFLDLSQCOLEOLSPFAFNSLS 480

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QY 581 FACTCEHOSFLQWIKDQRLVEVERMECATPDSKQMPVLSLNTTCQMNKTIIGVSVLS 640
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Db 781 WNPBGIVGTGCMQOEATSI 799

RESULT 3
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US2003007729A1
; GENERAL INFORMATION:
; APPLICANT: ARDITI, MOSHE
; APPLICANT: RAJAVASHISTH, TRIPATHI
; APPLICANT: SHAH, PREMIDAN K
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
; TITLE OF INVENTION: TOLL-LIKE RECEPTOR-4
; FILE REFERENCE: 81476-0255398
; CURRENT APPLICATION NUMBER: US/10/128,166
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-166-7

Query Match          95.1%; Score 4141; DB 14; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 MELNFYKIPDNLPESTKNLDSFNPRLHLSYSFSPPELQVLDLSRCEIQTIEDGAYQS 100
Db 1 MELNFYKIPDNLPESTKNLDSFNPRLHLSYSFSPPELQVLDLSRCEIQTIEDGAYQS 60

Qy 101 LSHLSTLILGNPIQSIALGAFSGLSLQKLVAVETNLASLENPPIGHLTKLKELVNAHN 160
Db 61 LSHLSTLILGNPIQSIALGAFSGLSLQKLVAVETNLASLENPPIGHLTKLKELVNAHN 120

Qy 161 LIQSFKLPEYFSNLTNLEHLDLSNKKIOSIYCTDLRVLHQPMLNLSLDSLNPMNF1QP 220
Db 121 LIQSFKLPEYFSNLTNLEHLDLSNKKIOSIYCTDLRVLHQPMLNLSLDSLNPMNF1QP 180

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Db 181 GAFKEIRLHLKTLRNNDPSLNVMKTCIOGLAGLEVHRLVIGEPRNEGULEKFDKSALEGL 240

Qy 281 CNLTIEEFRLAYLDYDDIIDLFNCLTNVSSFSLSVSTIERVADFYNFGMQLHELVNC 340
Db 241 CNLTIEEFRLAYLDYDDIIDLFNCLTNVSSFSLSVSTIERVADFYNFGMQLHELVNC 300

Qy 341 KFGQFPLTKLSLKRLLFTSNKGNAPSEVDLPSELEFLDLSRNGLSFKGCCSQSDFGTTS 400
Db 301 KFGQFPLTKLSLKRLLFTSNKGNAPSEVDLPSELEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy 401 LKTYLDSFNGVITMSSNFIQLBOLEHLDPQHSNLKOMSESVFLSLRNLIYLDISHHTHR 460
Db 361 LKTYLDSFNGVITMSSNFIQLBOLEHLDPQHSNLKOMSESVFLSLRNLIYLDISHHTHR 420

Qy 461 VAFNGIRNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCCOLEQSPAPFNSLS 520
Db 421 VAFNGIRNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCCOLEQSPAPFNSLS 480

Qy 521 SLQVLANSHNNFSLDTPPYKCLNSLOVLDVSLNHLNMTSKKQELQHPSSIAFLNLTQND 580
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Qy 581 PACTCEHOSFLQWKDQROLIVVERMECATPSPDKQMPVLSLNTQOMKTIIGVSVLS 640

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Db 601 VLWVSVAVLVYKFFPHMLLAGCIKYGRGENIVDAFIYVSQDEDMWRNELYNLEBGV 660
Qy 701 PPFOLCHYRDFIPGVAIAANIIEGFKRSKRVIVVVSQHFIOGRWCIFEYEIAQTWQPL 760
Db 661 PPFOLCHYRDFIPGVAIAANIIEGFKRSKRVIVVVSQHFIOGRWCIFEYEIAQTWQPL 720

Qy 761 SSRAGIIFIVLQKVEKTLRQOVELYRLSRNTYLEWEDSVLGRHIFRRRLKALDOKS 820
Db 721 SSRAGIIFIVLQKVEKTLRQOVELYRLSRNTYLEWEDSVLGRHIFRRRLKALDOKS 780
Qy 821 WNPBGIVGTGCMQOEATSI 839
Db 781 WNPBGIVGTGCMQOEATSI 799

RESULT 4
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Taron K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 5818300003
; CURRENT APPLICATION NUMBER: US/10/732,563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-563-8

Query Match          95.1%; Score 4141; DB 16; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 MELNFYKIPDNLPESTKNLDSFNPRLHLSYSFSPPELQVLDLSRCEIQTIEDGAYQS 100
Db 1 MELNFYKIPDNLPESTKNLDSFNPRLHLSYSFSPPELQVLDLSRCEIQTIEDGAYQS 60

Qy 101 LSHLSTLILGNPIQSIALGAFSGLSLQKLVAVETNLASLENPPIGHLTKLKELVNAHN 160
Db 61 LSHLSTLILGNPIQSIALGAFSGLSLQKLVAVETNLASLENPPIGHLTKLKELVNAHN 120

Qy 161 LIQSFKLPEYFSNLTNLEHLDLSNKKIOSIYCTDLRVLHQPMLNLSLDSLNPMNF1QP 220
Db 121 LIQSFKLPEYFSNLTNLEHLDLSNKKIOSIYCTDLRVLHQPMLNLSLDSLNPMNF1QP 180

Qy 221 GAFKEIRLHLKTLRNNDPSLNVMKTCIOGLAGLEVHRLVIGEPRNEGULEKFDKSALEGL 280
Db 181 GAFKEIRLHLKTLRNNDPSLNVMKTCIOGLAGLEVHRLVIGEPRNEGULEKFDKSALEGL 240

Qy 281 CNLTIEEFRLAYLDYDDIIDLFNCLTNVSSFSLSVSTIERVADFYNFGMQLHELVNC 340
Db 241 CNLTIEEFRLAYLDYDDIIDLFNCLTNVSSFSLSVSTIERVADFYNFGMQLHELVNC 300

Qy 341 KFGQFPLTKLSLKRLLFTSNKGNAPSEVDLPSELEFLDLSRNGLSFKGCCSQSDFGTTS 400
Db 301 KFGQFPLTKLSLKRLLFTSNKGNAPSEVDLPSELEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy 401 LKTYLDSFNGVITMSSNFIQLBOLEHLDPQHSNLKOMSESVFLSLRNLIYLDISHHTHR 460
Db 361 LKTYLDSFNGVITMSSNFIQLBOLEHLDPQHSNLKOMSESVFLSLRNLIYLDISHHTHR 420

Qy 461 VAFNGIRNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCCOLEQSPAPFNSLS 520

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Db      421 VAFNGIFNGSLSSLEVLKMAGNSFOENFLPDIFTELRLNLTFLDLSQCQLEQLSPTAFNSLS 480
Qy      521 SLOVLANSHNNFSLDTPFPYKCLNSLOVLDYSLNHMTSKQELQHPSSLAFLNTQND 580
Db      481 SLQVLANSHNNFSLDTPFPYKCLNSLOVLDYSLNHMTSKQELQHPSSLAFLNTQND 540
Qy      581 FACTCHQSFLQWKDQROLLEVERMECATPSDKQMPVLSLNTQMKTTIIGSVYLS 640
Db      541 FACTCHQSFLQWKDQROLLEVERMECATPSDKQMPVLSLNTQMKTTIIGSVYLS 600
Qy      641 VLAVSVAVLVYKFFPHMLLAGCIKYGGENITYDAFIYSSODEDWVRNELYKNEEGV 700
Db      601 VLAVSVAVLVYKFFPHMLLAGCIKYGGENITYDAFIYSSODEDWVRNELYKNEEGV 660
Qy      701 PPQOLCHYRDFIPGVAIAANIHEGFHKSARKVIVVVSQHFIOGRWCIFEYELAQWQFL 760
Db      661 PPQOLCHYRDFIPGVAIAANIHEGFHKSARKVIVVVSQHFIOGRWCIFEYELAQWQFL 720
Qy      761 SSRAGIIFIVLOKYEKTLRQOVELYRLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 820
Db      721 SSRAGIIFIVLOKYEKTLRQOVELYRLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780
Qy      821 MNPEGTIVGTGCNNQOEATSI 839
Db      781 MNPEGTIVGTGCNNQOEATSI 799

RESULT 5
US-10-732-796A-8
; Sequence 8, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732.796A
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-732-796A-8

Query Match      95.1%; Score 4141; DB 16; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      41 MEINFYKIPNLPSTKNDLSFNPRLHLSYSPFSFPELQVLDLSRCEIQTIEDGAYQS 100
Db      1 MEINFYKIPNLPSTKNDLSFNPRLHLSYSPFSFPELQVLDLSRCEIQTIEDGAYQS 60
Qy      101 LSHLSTILTGNIPIQSIALGAFSGLSLOKLVAVETNLASLENPFGHKLTKELNVAHN 160
Db      61 LSHLSTILTGNIPIQSIALGAFSGLSLOKLVAVETNLASLENPFGHKLTKELNVAHN 120
Qy      161 LIOSFKLPEYFSLNLTNLEHLDLSNKIQSYCTDILRLHQMPLNLSLDSINPMNTOP 220
Db      121 LIOSFKLPEYFSLNLTNLEHLDLSNKIQSYCTDILRLHQMPLNLSLDSINPMNTOP 180
Qy      221 GAFKEIRLHKLTLRNNFDSLNVMKTCIOGLAGLEVHRLVGEFPEBGNLEKFPKSALEGL 280
Db      181 GAFKEIRLHKLTLRNNFDSLNVMKTCIOGLAGLEVHRLVGEFPEBGNLEKFPKSALEGL 240
Qy      281 CNLTIEBFRLAYDYDYDIDILFNCUTNVSSFSVLVTIERVDFSYNFGWQHLELVNC 340
Db      241 CNLTIEBFRLAYDYDYDIDILFNCUTNVSSFSVLVTIERVDFSYNFGWQHLELVNC 300
Qy      341 KFGQPTLKLSKRLFTSNKGNAPSEVDLSLEFLDLSRNGLSFKGCCSOSDFGTTTS 400

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Db      301 KFGQPTLKLSKRLFTSNKGNAPSEVDLSLEFLDLSRNGLSFKGCCSOSDFGTTTS 360
Qy      401 LKTYDLSFNGVITMSSNPLGLLEQLEHDPQSHNLKOMSEFSVFLSLRNLTYLDLSHTHTR 460
Db      361 LKTYDLSFNGVITMSSNPLGLLEQLEHDPQSHNLKOMSEFSVFLSLRNLTYLDLSHTHTR 420
Qy      461 VAFNGIFNGSLSSLEVLKMAGNSFOENFLPDIFTELRLNLTFLDLSQCQLEQLSPTAFNSLS 520
Db      421 VAFNGIFNGSLSSLEVLKMAGNSFOENFLPDIFTELRLNLTFLDLSQCQLEQLSPTAFNSLS 480
Qy      521 SLOVLANSHNNFSLDTPFPYKCLNSLOVLDYSLNHMTSKQELQHPSSLAFLNTQND 580
Db      481 SLOVLANSHNNFSLDTPFPYKCLNSLOVLDYSLNHMTSKQELQHPSSLAFLNTQND 540
Qy      581 FACTCHQSFLQWKDQROLLEVERMECATPSDKQMPVLSLNTQMKTTIIGSVYLS 640
Db      541 FACTCHQSFLQWKDQROLLEVERMECATPSDKQMPVLSLNTQMKTTIIGSVYLS 600
Qy      641 VLAVSVAVLVYKFFPHMLLAGCIKYGGENITYDAFIYSSODEDWVRNELYKNEEGV 700
Db      601 VLAVSVAVLVYKFFPHMLLAGCIKYGGENITYDAFIYSSODEDWVRNELYKNEEGV 660
Qy      701 PPQOLCHYRDFIPGVAIAANIHEGFHKSARKVIVVVSQHFIOGRWCIFEYELAQWQFL 760
Db      661 PPQOLCHYRDFIPGVAIAANIHEGFHKSARKVIVVVSQHFIOGRWCIFEYELAQWQFL 720
Qy      761 SSRAGIIFIVLOKYEKTLRQOVELYRLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 820
Db      721 SSRAGIIFIVLOKYEKTLRQOVELYRLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780
Qy      821 MNPEGTIVGTGCNNQOEATSI 839
Db      781 MNPEGTIVGTGCNNQOEATSI 799

RESULT 6
US-10-038-854-135
; Sequence 135, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vermet, Corine
; APPLICANT: Bisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malynkar, Uriel M
; APPLICANT: Shimkete, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kektuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimirt Y
; APPLICANT: Gangoili, Basha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine B
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Miller, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29

```



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;; PRIOR APPLICATION NUMBER: 60/259,415
;; PRIOR FILING DATE: 2001-01-02
;; PRIOR APPLICATION NUMBER: 60/259,785
;; PRIOR FILING DATE: 2001-01-04
;; PRIOR APPLICATION NUMBER: 60/269,814
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/279,832
;; PRIOR FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/279,833
;; PRIOR FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/279,863
;; PRIOR FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/283,889
;; PRIOR FILING DATE: 2001-04-13
;; PRIOR APPLICATION NUMBER: 60/284,447
;; PRIOR FILING DATE: 2001-04-18
;; PRIOR APPLICATION NUMBER: 60/286,683
;; PRIOR FILING DATE: 2001-04-25
;; Remaining Prior Application data removed - See file Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 411
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 135
;; LENGTH: 661
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-10-038-854-135

Query Match      15.2%; Score 663; DB 15; Length 661;
Best Local Similarity 28.7%; Pred. No. 4.1e-44;
Matches 196; Conservative 116; Mismatches 289; Indels 82; Gaps 16;

QY 14 AMAFLSC-VRPESWPCVAVVNNITTYQCMELNFKYKIPDNLPSTKNLDLSPNPLRHLSGY 72
DB 12 ALFLASCRATSSDQCKIEKVNKTNCENGLNRIPTGLPSTCEFSFNVLPITQNT 71
QY 73 SFSPFPELVQVILSRCEIQITEDGAYQSLSHLSTILITGNITQSLALGAFGLSLQKLY 132
DB 72 TFSRLINTFLDLPRCQIYWHEDFQSHRLDTLVLTANPLIFMAETALSGPKALKILF 131
QY 133 AVETNLASLENFPICHTLKLKELNVAHNLIOFPLPEYFSLTMLEHDLSSNKLQSYIC 192
DB 132 FICIGISIDIPILHNOKTLESYIGSNHISIKLPKFPF-EKLVKVDFOHNAIHYISK 190
QY 193 TDLFVLHQMPLNLISLDSINPMNFIQGAFAKEIRLKLTLRNFDLSNWKTCIOGLAG 252
DB 191 EDMSSLOQ--ATNLSLNLNGNDIAGIEBGAFDSAFOGL---NFGGTONILVIFKGLKN 244
QY 253 LEVRLVIGFERRNGNEKEPKSALBGLCNTIEFRLAYDYIIDLIIDFNCLTNVSS 312
DB 245 STIOSLWGTETEDMD-EDISPAVEBGLCENSVSINL-QKHYPFNISSTNFCFS--- 298
QY 313 FSLSVTIERKDYKDSYNGMQLLELVNCKFGQFPT--LKLKSLKRLFTSNKGN--AFS 368
DB 299 -----GLOBLDTATHLSLPSGLVGLSTLKKLVLSANKPRLCOIS 340
QY 369 EVDLPSEF-----LDSRNGLSFGKCCSQSDFTGTSKY 403
DB 341 ASNPSTLTHLSIKNKTRELGTGCLNEMLRHLDISHDDIETSDCCNLQRLNLSHLS 400
QY 404 LDSFNGVITMSSN-FLGLEHLDHPHNSLTKOMSESVLSLRNLTYLDISHTHRYA 462
DB 401 LNLSPNPLSLKTAPEKCPQLELDLAFTRLKYVDAQSPQONHLKLVNLSSHLDIS 460
QY 463 FNGIFNGLSLEVLKMGNSFOENFL--PDIFTELRLNLTFFDLSCQOLHOLSPYAFNSLS 520
DB 461 SEQFDPDIPALQHNILQGNHFPKGNIOKTNLSQTLGRLEILVLSFCULSDIDQAFYSLK 520
QY 521 SLQVLNNSHNFFELDFPYKCLNSLO--VLDSLNHIMTSKKOELQHPSSLAFL--- 574
DB 521 MNHNVADLSHNR---LTSSEIALSHLKGIVNLNLSNHSIT-----LPDLPLLSQOR 570
QY 575 --NLTONDFACTCHOSFLOWIKQOROLLVEVERMECTPBDKQGMPLVLSNITTCQNMKT 632
DB 575 --NLTONDFACTCHOSFLOWIKQOROLLVEVERMECTPBDKQGMPLVLSNITTCQNMKT 632
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DB 571 TINRQNDCTCSNIYFLENYKENMOKLEDTEDTLCENPPLRGVRLSDVTLSCSMAAV 630
QY 633 IIGVSVLTVSVAVLVYKFX 655
DB 631 GIFPLIVLVFALLILPAVKYF 653

RESULT 7
US-10-037-417-107
Sequence 107, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
;; APPLICANT: Kekuda, Ramesh
;; APPLICANT: Alsobrook II, John P
;; APPLICANT: Tchernov, Velizar T
;; APPLICANT: Liu, Xiaohong
;; APPLICANT: Spytek, Kimberly A
;; APPLICANT: Paturajan, Meera
;; APPLICANT: Grose, William M
;; APPLICANT: Lepley, Denise M
;; APPLICANT: Burgess, Catherine E
;; APPLICANT: Verner, Corine A.M.
;; APPLICANT: Li, Li
;; APPLICANT: Gorman, Linda
;; APPLICANT: Edinger, Shlomit R
;; APPLICANT: Sciore, Paul
;; APPLICANT: Ellerman, Karen
;; APPLICANT: Malyanekar, Uriel M
;; APPLICANT: Rothenberg, Mark
;; APPLICANT: Stone, David J
;; APPLICANT: Boldog, Ferenc L
;; APPLICANT: Guo, Xiaojia
;; APPLICANT: Shenoy, Suresh G
;; APPLICANT: Anderson, David W
;; APPLICANT: Padigaru, Muralidhara
;; APPLICANT: Taupier Jr, Raymond J
;; APPLICANT: Miller, Charles E
;; APPLICANT: Eileen, Andrew J
;; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;; FILE REFERENCE: 21402-235
;; CURRENT APPLICATION NUMBER: US/10/037,417
;; CURRENT FILING DATE: 2002-09-20
;; PRIOR APPLICATION NUMBER: 60/260,018
;; PRIOR FILING DATE: 2001-01-05
;; PRIOR APPLICATION NUMBER: 60/260,360
;; PRIOR FILING DATE: 2001-01-08
;; PRIOR APPLICATION NUMBER: 60/272,411
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: 60/272,817
;; PRIOR FILING DATE: 2001-03-02
;; PRIOR APPLICATION NUMBER: 60/291,186
;; PRIOR FILING DATE: 2001-05-15
;; PRIOR APPLICATION NUMBER: 60/303,231
;; PRIOR FILING DATE: 2001-07-05
;; PRIOR APPLICATION NUMBER: 60/305,060
;; PRIOR FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: 60/318,405
;; PRIOR FILING DATE: 2001-09-10
;; PRIOR APPLICATION NUMBER: 60/318,700
;; PRIOR FILING DATE: 2001-09-12
;; NUMBER OF SEQ ID NOS: 227
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 107
;; LENGTH: 661
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-10-037-417-107

Query Match      15.2%; Score 663; DB 15; Length 661;
Best Local Similarity 28.7%; Pred. No. 4.1e-44;
Matches 196; Conservative 116; Mismatches 289; Indels 82; Gaps 16;

QY 14 AMAFLSC-VRPESWPCVAVVNNITTYQCMELNFKYKIPDNLPSTKNLDLSPNPLRHLSGY 72
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; SEQ ID NO 10
; LENGTH: 661
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-114-893-10

Query Match      14.5%; Score 629.5; DB 13; Length 661;
Best Local Similarity 29.7%; Pred. No. 2e-11;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

12 ALPLASCAATTSSPQCKICEKVENKTYNCENGLNEIPGLTLPNSTECLFSSFNVLPTIQNT 71
13 SEFSPPELQVLDLSCEIQTIEDGAYOSLSHSTLILGNPIQSLALGAFGLSLQGLV 132
72 TFSRLINLTFDLTRCQIYWHEDTFQSHRDLTVLTPANLIFAAETLALGPPKALKHLF 131
133 AVETNLASLENFPIGHLTKLELVANHLIOSFKLPEYFSLNLTNLEHDLSSNKIQSIYC 192
132 FIQGISIDPLPLHQKTESLYLGSNHSIKLPKFPF--EKLKVLDPQNNAIHYLSK 190
193 TDRLVHOMPLINSLDLSLAMPNFIQGAKEIRLHKLTLRNNFDSLNMKTCIQGLAG 252
191 EDMSSLQO--ATNLSLNLNGNDIAGIEPDAFSDAVFQSL---NFGQTQNLVLVFKGHN 244
253 LEVRLVLVEFRNEGNLEKPKSALGECNLTIEFRFLAYLDYVLDIIDLFPNCLTNVSS 312
245 STISLWLTGEDMD--EDISPAVEGLCEMSVESLNQ--QKHYPFNISNTFHCPS---- 298
313 FSLVSVTLIERVYKDPSPYNGWQHLBVLNCKFGQFPF--LKLKSLKRLTFTSNKGN--AFS 368
299 -----GLQELDLTATHLSLPSGLVGLSTLKKLVLSANKFENLQGIS 340
369 EVDLPSELF-----LDLSRNGLSFRGCCSQSDPRTTSLKY 403
341 ASNPFSLTHLSIKGNTKRLBELGTGCLLENLRBLDISHDIIETSDCCNLQLRNLSHLOS 400
404 LLSLFGNGVITSSN--FLGLEQLEHLDFOHNSMLKQWSEPSVFLSLNLYLDISHTHTVA 462
401 LNLVYNELSLKTAFAKCPQLELDLDAFLTKLYKDAQSPFQNLHLVLYLSHSLDIS 460
463 FNGJFNGLSLEVLKMAGNSFOENFL--PDIFTELRLNLTFLDLSQCOLEQSPFAFNSLS 520
461 SEQFDGLPALQHLNLQGNHFPKGNIQKTNLSLQTLGRLEILVLSFCDDLSIDQAFTSLK 520
521 SLQVLMNSHNPFSLDTPPYKCLANSIQ--VLDYSLNHTMTSKQELQHPFSSLAFL---- 574
521 MNMNVHVDISHNR---LTSSEIALSHLKGILYLNLAHNSHISII-----LPSILTLISQOR 570
575 --NLTONDFACCHQSFQWIKDORQLLVEVERMECATPSPDKQGMPLVSLNTCOMNKT 632
571 TINLRQNPDLCTCSNIYLEWYKEMQKLEBDEDTLTCENPFLKGVRLSDVTLSCMAAV 630
633 IIGVSLVSVLVSVVAVLVYKPY 655
631 GIFFLVFLVFLVFLAILLPAVKYF 653

RESULT 8
US-10-114-893-10
; Sequence 10, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Meberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OR INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCES: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114, 893
; EARLIER FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 10
; LENGTH: 661
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-114-893-10

Query Match      14.5%; Score 629.5; DB 13; Length 661;
Best Local Similarity 29.7%; Pred. No. 2e-11;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

25 SWEP-CYEVVPNTTYQCMELNFKIPDNLPESTNLDLSNPRLHLSYSFSPPELQVL 83
23 SWDMCKICEKANKTYNCENGLSEIPDLTPNTEFFLESFNFPLPTIHRKTFSLMNLTF 82
144 PRIGHLTKLELVANHLIOSFKLPEYFSLNLTNLEHDLSSNKIQSIYCTDLRVLHQMPL 203
143 IPVHNLNLSLYLGSNHSIKFPKDFP--ARNLKVLDPQNNAIHYISREDMSLEQ--A 199
204 LNLSDLSLAMPNFIQGAKEIRLHKLTLRNNFDSLNMKTCIQGLAGELVRLVYGSF 263
200 INLSLNFNGNNVKGIELGAFTVFOSL---NFGTPNLSVIFNGLQNSTTOSLWLTGF 255
264 RNEGNLEKPKSALGECNLTIEFRFLAYLDYVLDIIDLFPNCLTNVSSPSLVSVTIER 322
256 EDIIDL--EDISSAMLKGLCEMSVESLNQ--EHRSDISSTTFQCFQTOLELDLTATHLKG 312
323 VKDPSYNGWQHLBVLN-----CKF--GQPPFL-----KLKSLKRLTFTSN 361
313 LPS-----GKMGNLNLTKLVLSVNHFPQLQISANFPSTLHYIRGNVKKHLGVGCL 367
362 KGNASEVLDLPSEFLDLSRNGLSFRGCCSQSDPRTTSLKYDLSNGVITSSN--FLG 420
368 KLGK-----LQTLDLSHNDIEASDCSLQKNSHLOTLNLSNEBPGLSQSAFKE 418
421 LEQLEHDFQ-----HSNLKQWSEPS--VPLSLRLYI--LDISHTHTRVAFNGJFNGLS 472
419 CPQLELDLDAFLRHTIAPQ--SPQNLHFLQVNLTYTCFLDTSNQ-----LIALGIPV 470
473 LEVLKMAGNSFOENFL--PDIFTELRLNLTFLDLSQCOLEQSPFAFNSLSLQVLMNSH 530
471 LRHLNKGHFPQDGTIKTNMLQTVGSLVLYLSSCGLLSIDQAFTSLGMSHVDISHN 530
531 NFF--SLDTPPY-----KCLNSLOVLDYSLNHTMTSKQELQHPFSSLAFLNLTONDF 581
531 SLTCDSDLSLSHKGIYLNLAHNSHISII-----SQOSTINLSHNPL 579
582 ACTCEHQSFLQWIKDORQLLVEVERMECATPSPDKQGMPLVSLNTCOMNKTIIQVSVLSV 641
580 DCTCSNHLPLTWYKENHKLKESGETTCANPPLRGKLSDVLSGCI--TALGIFPLIV 637
642 LVSVVAVLVY 652
638 FLV-LTALILF 647

RESULT 9
US-10-038-854-134
; Sequence 134, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vermet, Corine
; APPLICANT: Eissen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malysankar, Urieal M
; APPLICANT: Shumkov, Richard A
; APPLICANT: Tchernetev, Velizar
```

[illegible]

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Cy      48  IPDNUPSTKUNLDSFNPRLRHGSGSFSFSPFLQVLDLSRCRQIQTEDEDAQYSLSTLT 107
Db      46  IPSGLTGKWSKLDLSNNRITYSNSDRLQRCVNLQALVLTNSGINTIEEDSFSLSLEHL 105

          13.9%; Score 603.5; DB 10; Length 784;
          Beat Local Similarity 27.0%; Pred. No. 3,1e-39;
          Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38

          / SEQUENCE: US-09-950-041-4
          / Publication No. US20030032090A1
          / GENERAL INFORMATION:
          / APPLICANT: Hardiman, Gerard T.
          / APPLICANT: Rock, Fernando L.
          / APPLICANT: Bazan, J. Fernando
          / APPLICANT: Kasteleijn, Robert A.
          / APPLICANT: Ho, Stephen W.K.
          / APPLICANT: Liu, Yong-Jun
          / TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
          / FILE REFERENCE: DX0724XKI
          / CURRENT APPLICATION NUMBER: US/09/950,041
          / CURRENT FILING DATE: 2002-05-06
          / PRIOR APPLICATION NUMBER: 09/728,540
          / PRIOR FILING DATE: 2000-11-28
          / PRIOR APPLICATION NUMBER: 60/207,558
          / PRIOR FILING DATE: 2000-05-25
          / PRIOR APPLICATION NUMBER: 09/073,363
          / PRIOR FILING DATE: 1999-06-05
          / PRIOR APPLICATION NUMBER: 60/044,293
          / PRIOR FILING DATE: 1997-05-07
          / PRIOR APPLICATION NUMBER: 60/072,212
          / PRIOR FILING DATE: 1998-01-22
          / PRIOR APPLICATION NUMBER: 60/076,947
          / PRIOR FILING DATE: 1998-03-05
          / NUMBER OF SEQ ID NOS: 45
          / SOFTWARE: PatentIn version 3.1
          / SEQ ID NO 4
          / LENGTH: 784
          / TYPE: PRT
          / ORGANISM: Homo sapiens

          / US-09-950-041-4

```


RESULT 12
US-10-095-627-12
Sequence 12, Application US/10095627
Publication No. US20030027260A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
Gadowski, Paul J.
Gurney, Austin
Mark, Melanie
Yang, Ruy-Bing
TITLE OF INVENTION: Human Toll Homologues
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,627
FILING DATE: 11-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/105,413A
FILING DATE: 26-Jun-1998
APPLICATION NUMBER: 60/083322
FILING DATE: 28-Apr-1998
APPLICATION NUMBER: 60/065311
FILING DATE: 13-Nov-1997
APPLICATION NUMBER: 60/062250
FILING DATE: 17-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marechang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1154-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acids
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-095-627-12
Query Match 13.8%; Score 602.5; DB 14; Length 784;
Best Local Similarity 27.0%; Pred. No. 3.7e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

245 TC--IQGLAGLEVRHVLV---GFRPANGNLEKPKSALLEGCLNLTIERFRLA--YLDYVL 297
272 LNIQISGLLELEFPDCTINGVGNFRASDNDVDVDPGRKE---TLTIRLAIHPRLFLFY-- 326
298 DDIIIDFVCLINNVSSFSLSVSTIERVKDPSYVFGQHELVNCKRGQFPPLKLSKRLT 357
327 -DLSTLYSLTERVK---RITVENSKVF-----LVPCLLSQ----- 357
358 FTSNKGNAFSEVDLPSELPDLNRN-----GLSEFGCCSOSDFGTSLSKYLDLSPNGVI 412
358 -----HKSLEVIDLSENLMVEEYLNKSNAC---EDAMPSELQTLILNQ--- 397
413 TWSSNFIQLEQLLEHLDFOHSLNKKOMSEFSVLSRLNLIYLDISHTHTVVAENGIRNGSS 472
398 -----HL-----ASLEKKG---TLTLKLNLTNIDISK----- 422
473 LEVLMAGNSFOENLPDIFTELNRNLTFLDISQOQLBOLS---PFAFNSLSLOYLNMNH 529
423 -----NSFHS--MPETQMPKMKYLNLSSTRHSVTCIP-----KLEILDVSN 466
530 N--NFFSLD-----TFP--YKCLNSLOVLDYSLNHIMTSKKOELQHPPSL 571
467 NNALNLSNLPLQKELYISRNKMLTLPDASLLPMLVLKISRNALTTSKQDLSF-HTL 525
572 AFLNLTQNDPACTCEHOSFLOWIKDQRLVEV-----ERNECATPSDKQGNPVLISNIT 626
526 KLEAGNNFICSCFELSFTQ---EQQALAKVLIDWPANYLCDSPSHVRCQOVQDVRLS 581
627 ---QMNKTIIGVSLVSVVSVVAVLYKKY--PHMLLAGCIYKGR-----GENI-Y 674
582 VSECHRTALVSGMCCALFLLLTGLCHRGHLMYMMAMALQAKKPRAPSRNICY 641
675 DAFVYSQDDWVWNELVKNLEBGPPOCLAHYRDFIPGVALANIIHBSGPHSKRYI 734
642 DAFVYSERDAYWVENLMVQELNENPPFKCLHGRDIIPEGWIIDNII-DSIEKSHKV 700
735 VVVSQHFIQSRWCIFEYELAQTWQFLSRAGIIFIVLQKVEKTLRQO-VELYRLISNT 793
701 FVLSNFVSEMKCEYELDFSHFRLEPDENNDAILLILPEIKKAIPOQFCRLKIKMTWT 760
794 YLEWEDSVLGRHIFWRRLKAL 815
761 YLEWPMDEAQREGEFVNLRAAI 782
Db 761 YLEWPMDEAQREGEFVNLRAAI 782
RESULT 13
US-10-732-563-4
Sequence 4, Application US/10732563
Publication No. US20040132079A1
GENERAL INFORMATION:
APPLICANT: Gupta, Shalley K.
APPLICANT: Ghosh, Tarnu K.
APPLICANT: Fink, Jason R.
TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
FILE REFERENCE: 58183WO003
CURRENT APPLICATION NUMBER: US/10/732,563
CURRENT FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 784
TYPE: PRT
ORGANISM: Homo sapiens
US-10-732-563-4
Query Match 13.8%; Score 602.5; DB 16; Length 784;
Best Local Similarity 27.0%; Pred. No. 3.7e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

48 IPDNLPESTKRLDLSFNLRLHSGSFFSPELOVLDLSRCIQITIEDGAYQSLSLSTL 107
46 IPSGLTBAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSGNITIEDSFSSLSLEHL 105

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QY 108 LUTGPIQSLALGATSGSLQKL-----VAETNLASLENPIGHLK----- 151
Db 106 DLSTAYLSTLSSWFEKPLSTFLPNLGNPYKTLAGTTSFSLTKQLQILRVGNMDPTFKI 165
QY 152 -----LLELVANHLIOSFKLPEYFSNLTNLEHLDSGNK-----IQSI 190
Db 166 QKRDPAGLTFLELEIDASDLQSYE-FKSLKSIQVNSHLILHKKHILLEIFVDTTSSV 224
QY 191 YCTDLRYLHOMPLNLISDLSPNMF--IQGAFKEIRLHKLTNRN--NFDSL-NVMK 244
Db 225 ECLER-----DITDITFHSLSIGETNSL-ICKTFPNVAKITBESLPQVMK 271
QY 245 TC--IQGLAGLEVHRLVU--GEFRRBGLLEKDKSALGLGMLTTEEPRLA--YLDYYL 297
Db 272 LLNQISGLELEFDDCTLNGVGNFRASDDRYIDPKVE--TLTIRRLHIPFFLYFY- 326
QY 298 DOIIDLFNCLITVSSFSFLSVTIERKDPFSYNGWHLLEVCKFCQFPFLKLSIKRLT 357
Db 327 -DLSTLYSLTERVK-----RITVENSKVF-----LYPELDSQ----- 357
QY 358 FTSNKGNAFSEVDLPSEFLDLSR-----GLSFEGCCSQSDPFGTTSKLYLDLSNGYI 412
Db 358 -----HLKSLBYLDLSENLWVEEYLKNSAC-----EDAMPSTQTLILRON-- 397
QY 413 TMSNFIQLEQLEHDFQHSNLTKOMSEFSVPISLRYLIDTISHTTRAVAFNIGFGLSS 472
Db 398 -----HL--ASLEKGE--TLTLKMLTNIDISK----- 422
QY 473 LEVLMAGNSFOENFLPDIFTELRLTLFLDLSQCCOLEDS--PTAFNSLSLOLVNMSH 529
Db 423 -----NSFHS--MPEFCQMPKKKYLNLSTRISHVTCGP-----KTLIELDVSN 466
QY 530 N--NFSLD-----FPP-YKCLNSLOYLDYSLNHTSKKOBELQHPSSL 571
Db 467 NNUNLPSNLPLQKELYSRNKLMTLPLDASLLPMLLVTKISRRAITTFSEQDISE-HTL 525
QY 572 AFLNLTONDFACTCEHOSFLQWIKDOROLIVEY-----ERMCAQTPSDQKQMPVLSLNT 626
Db 526 KTLBEGGNNTFICSCFLSTQ---EQQLAYLIDWPANYLIDCSNHRGQGVQDVRLS 561
QY 627 ---COMAKTIIGVSVLSVLVSVAVLVYKFY--FHLMLLAGCIKXGR-----GENI-Y 674
Db 582 VSECHRTALVSGMCALFLLILTLTGVLCHRFGMLWTKMMWMLQAKRKRKXAPSNI CY 641
QY 675 DAFVYSSODEBVMVNEVLKYNLEEGVRRPOLCLHTRDFIPGVALANIIHGGHRSRKYI 734
Db 642 DAFVYSRDAWYVENLWQELBENFPKPLCLHKKDFIPGKMIIDNII-DSTIEKSHKV 700
QY 735 VVVSQPIQSRWCICEYEYEAQTOFSLSPAGIIFLYQKVEKTLIRQO--VELYRLSRNT 793
Db 701 FVLSENFPKSEKCKEELDPHSRPLRDENNDAIILILEIEKKAIQRRCCKLRKINMTYT 760
QY 794 YLEWEDSVLGRIHFWRRLKAL 815
Db 761 YLEWPMDEAOREGEFWMNLEAAI 782

RESULT 14
US-10-732-796A-4
; Sequence 4, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Taron K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732,796A
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4

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; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-796A-4

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Query Match 13.8%; Score 602.5; DB 16; Length 784;
Best Local Similarity 27.0%; Pred. No. 3.7e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38

QY	48	PDNI,PFSTKNLDLSFNLRLHLSGSPSPSPPELQVLDLSRCSIQTEIDEAQOSLSHLSTL	107
Db	46	IPSGITLAVKSDLSNNRIITYISNDBLQCVNLQALVLTNSGINTIIEBSPSGLSEHL	105
QY	108	ILTGNPIQSLALGAFSGSLQKLT-----VAETNLASLENPFGLKLT----	151
Db	106	DLSTVYLSNLTSSSWFKPPLSTFLNLGNPKYTLGETSLSFHLTKQLDRVGNMDFTKI	165
QY	152	-----LKELVANHLIOSFCLPEYFSNLTYLLEHDLSSNK-----IQSI	190
Db	166	QRKDPAGTLPEELETSDLSQSYE-PSXLSIQVSHSLIMKHIIILILEIPVDVTSSV	224
QY	191	YCTDLRVLHQPMLNLTSLDLSLMPNMF--IQGAFKEIRLHKLTLRN--NFPDSL-NVWK	244
Db	225	ECLER-----DITDLTFHSELSGTEINSL-IKFTFRNVKITJESLQFQWK	271
QY	245	TC--IQIAGLEVHVLV--GEPPNEGULEKFDKSALEGLCNLTIEBRRLA--YIDYTL	297
Db	272	LINOISGLELEFDDCTLNGVGNFPASDNDRVIDGKYE--TLIRLRHIRFRFYLFY--	326
QY	298	DDIIDLFNCLTNVSSPFLSVATYIERVKDQSVNFGQHLVNCCKGQFPFLKLKSLRLT	357
Db	327	-DLSTVSLTRVK-----RITVENSKFY-----LVFCLLSQ-----	357
QY	358	FTSNKKGNAFSEVDLPSEPLDLSRN-----GLSKGCCSOSDFGTTSLKYLDLSFNGVI	412
Db	358	-----HLKSLLEYLDLSENLWVEEYLKNSAC-----EDAMPSTQTLILRON--	397
QY	413	TMSNPLGLBQLEHLDPHSLNKKOMSESVFLSINLTYDLSHTHTRAFNFIENGJLS	472
Db	398	-----H-----ASLEKGE--TLITLKNLTNNIDISK-----	422
QY	473	LEVLKMGNSFOENFLPDIFTELRLNLTPLDLSQCLQELS--PTAFNSLSLQVLMNSH	529
Db	423	-----NSPHS--MPETQMPREMKYLNLSSTRIHSTGICP-----KTLIEDVEN	466
QY	530	N--NFPSLD-----TFP--YKCLNSIQVLDYSLNHNTSKKQELQHPSSL	571
Db	467	NNLWFLSINTLPOLKELYISRNKMLTLPASLLPMLLVKISNNAITTSKEDLSDF-HTL	525
QY	572	AFNLITQNDFACTCEHOSFLOWIKDOROLAVE-----ERMECATPSDKQAPVSLNT	626
Db	526	KTLBAGGNFICSGEPLSTQ-----EQALAKVLIDWPANYICDPSHYRQGOVDYRIS	581
QY	627	---COMNKTIIGVSVLSVSVAVLVYKFY--PHMLLACIKYGR-----GENT-Y	674
Db	582	VSECHRTALVSGMCCAFLLITLLTGVLCHRFHGLMMYMMAMWLQAKKPRKPRASNICY	641
QY	675	DAFYYSQDSDWWRNBLVKYLEGVSVPFOCLNHRDPLPGVAILANIHHBGFHSRKYI	734
Db	642	DAFYYSRDRYWMENLWQLEJENFPFKCLHGRDITPGKWIIDNII-DSIESHKTV	700
QY	735	VVVSQHFLOSRCFYEYELAQTFWQFLSRAGIIFVLQKVEKTLDRQO--VELYRLLSRNT	793
Db	701	FVLSENFVKSQCYELDFSHFRLEFDENNDAAILLEPIEKALPQRCKRLKIMNTXT	760
QY	794	YLEWEDSVLGRHITWRRLKAL	815
Db	761	YLEWPMDEAQREGFWNLRAAI	782

RESULT 15
US-10-741-600-1390
; Sequence 1390, Application US/10741600

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Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: C1001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1390
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1390

Query Match      13.8%; Score 602.5; DB 17; Length 784;
Best Local Similarity 27.0%; Pred. No. 3.7e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

QY 48 IPDNLPESTKNDLSEFNPLRHLSYSPFSPPELOVLDLRCEIQTIEDGAYOSLSHLSTL 107
DB 46 IPSGLTEAVKSLDLNNRTIYSNSDLQRCVNLQALVLTSGNINTEBDSFSSLSLEHL 105
QY 108 ILTGNPISGLAIGAFSGSLLOKL-----VAEINLASLENFPIGHLKT--- 151
DB 106 DLSYNYLTSSSWFKPLSLFTFLNLGNPYKTLGTSLSFSLTKLQILRVGNMDTFYKI 165
QY 152 -----LKELVANLLOSFKLPEYFSNLTEHDLSSNK-----IQSI 190
DB 166 QKQDPAGLTFLEBELIDASDLQSYE-PSKLSIQNVSHLILMKOHILLLEIFVDVTSSV 224
QY 191 YCTDLRVLHOMPLNLSDLSINPMNF--IQGAFKEIRLHKLTLRN--NFDST-NVMK 244
DB 225 ECLER-----DTDLDTFHFSLSGTETNSL-IKKEFTFRNKITDESILFQYWK 271
QY 245 TC--IQGLAGLEHRLV--GEPRNENLEKFDKSALEGLCNLTIEFRILA--YLDYYL 297
DB 272 LNLQISGLLELEFDDCTLNGVNFPRASDNDRVIDPKVE--TLTIRRLHIPRYLFY-- 326
QY 298 DDIDLFNCLTNVSSFSLSVTEIRVKDPSYVFGWQHLELVNCKFGQPTLKLKSLKRLT 357
DB 327 -DLSTLYSLTERVK-----RITVENSKVF-----LVPCLLSQ----- 357
QY 358 FTSNKGNAFSEVDLPSELEFLDLSPN-----GLSPKCCSOSDFGTTSLKYLDLSPNGVI 412
DB 358 -----HLKSLLEYLDLSENLMWEYLKNSAC---EDAMPSLQTLILRN--- 397
QY 413 TMSNFFLGLEQLEHLDFOHSNLKQMSPEFSVLSLNLIVLDISHTHTRAVFNGLSS 472
DB 398 -----HL-----ASLEKTGE--TLTLTKNLTNIDISK----- 422
QY 473 LEVLKMGNSFQENLPDIFTELRLTLFLDSQCQLEOLS---PFAFNSLSLOVLNMSH 529
DB 423 -----NSFHS--MPEFCQMPKRYLNLSSTRIHSVTGCP-----KTLLEILDVSN 466
QY 530 N--NFFSLD-----TFP--YKCLNSLOVLDSYSLNHIIMTSKQELQHPSSLT 571
DB 467 NNLMNLFSLNLPQLKELYISRNKMLMTPDASLLPMLLVKLKISRNALTTFSKEQDLSF-HTL 525
QY 572 AFLNLTQNDFACTGHQSFLOMKQKQRLVEV---ERMECATPSDKQGNPVLNLNIT 626
DB 526 KTLKNGKNNFICSCHEFLSFTQ---EQQALAKVLIDWPANYLCDSPSHVRGQOVQDVRLS 581
QY 627 ---COMNKTIIIGVSLVSVVAVLVYKPY--PHLMVLACIKYGR-----GENI-Y 674
DB 582 VSECHRTALVSGMCALFLILTLITGLCHRFHGLMYMGMAMALQAKRKRKAPSRNICY 641
QY 675 DAFVITYSQDDEWVNNELVKNLEBGPFPOLCLAYRDFIPGVAIANIIEHGFHRSRKYI 734
DB 642 DAFVYSERDAYVWENLWQLELENFNPPFKCLCHKRDPFGKWIIDNII-DSIEKSHKTV 700
QY 735 VVSGHFIQSRWCIFEYELAQTWQPLSRBAGIIFIVLOKEKTLIRQO-VBLVRLLSRNT 793
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DB 701 FVLSNFVYSWECKYELDFSHFRLLFDENNDAIILILEPIEKKAIPORFCKLRKIMNTYT 760
QY 794 YLEWEDSVLGRHIFWRRLRKAL 815
DB 761 YLEWPMDEAQRGEFVNLRAAI 782
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Search completed: March 12, 2005, 20:27:48
Job time : 78.2496 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: March 12, 2005, 19:34:01 ; Search time 21.6477 Seconds
(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985B-2

Perfect score: 4355
Sequence: 1 MMSASRLAGTLIPAMAFISC.....SMNPGVTGTCGNQGEATSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	15.2	661	2	156258
2	474	10.9	786	2	T08664
3	454	10.4	1097	2	A29943
4	433	9.9	1389	2	T13852
5	421	9.7	1385	2	T13887
6	396	9.1	1066	2	T15864
7	333.5	7.7	1134	1	A29944
8	316	7.3	605	2	JC5239
9	305	7.0	853	2	T17461
10	303	7.0	605	2	A41915
11	299.5	6.9	662	2	S42799
12	299.5	6.9	1531	2	T42218
13	296.5	6.8	994	2	H96510
14	296	6.8	603	2	JC1282
15	295	6.8	907	2	JG0193
16	294	6.7	845	2	T07039
17	292.5	6.7	603	2	T24315
18	292.5	6.7	907	2	JE0176
19	290	6.7	907	2	JC6128
20	290	6.7	855	2	T07015
21	289.5	6.6	1112	2	T10504
22	289	6.6	855	2	T17460
23	284.5	6.5	1134	2	TJ0457
24	281.5	6.5	1134	2	JC7973
25	280	6.4	890	2	T00800
26	279	6.4	1027	2	B85089
27	278.5	6.4	1019	2	C96519
28	278	6.4	1091	2	A58532
29	276.5	6.3	768	2	T17462

ALIGNMENTS

30	276	6.3	983	2	G84524	probable disease r
31	275	6.3	1523	2	T13953	MEG5 protein - ra
32	272	6.2	1469	2	B36665	slit protein - pre
33	272	6.2	1480	2	A36665	slit protein 1 pre
34	270	6.2	1143	2	T10636	hypothetical prote
35	268	6.2	910	2	G84648	probable disease r
36	267	6.1	766	2	T01817	hypothetical prote
37	267	6.1	1784	2	C96615	hypothetical prote
38	266	6.1	863	2	A55173	cf-9 protein precu
39	263.5	6.1	967	2	T48210	hypothetical prote
40	262.5	6.0	1109	2	T18536	receptor-like prot
41	261.5	6.0	1051	2	T13174	gp150 protein - fr
42	260	6.0	1064	2	B86465	probable protein k
43	259	5.9	1029	2	T00712	protein kinase hom
44	257.5	5.9	738	2	T19938	hypothetical prote
45	256	5.9	771	2	T02565	disease resistance

RESULT 1
156258
RP105 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 156258
R.Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A>Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a m
A/Reference number: 156258; M01D:95204928; PMID:7897216
A/Accession: 156258
A>Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-661 <RES>
A/Cross-references: UNIPROT:062192; GB:J37797; NID:9761711; PIDN:BA07043.1; PID:9761712

Query Match 15.2%; Score 663; DB 2; Length 661;

Best Local Similarity 28.7%; Pred. No. 1.4e-33;

Matches 196; Conservative 116; Mismatches 289; Indels 82; Gaps 16;

QY	14	MAAFISC-VREPSMPCVAVVNTTYOCMEINFPYKIPDNLPSTKNDLSEFPLRHISGY	72
DB	12	ALFLASCATYSSDDCKIEKVNKTYNCENGINPGLPSTCELEFSFVNLPTIQNT	71
QY	73	SFFSPPELOVDRSCETIOTIEDGAYOSLSHSTLILNGNPISALGAFSGLSLOKLY	132
DB	72	TFSRLINLTFEDLTCQIYWIHEDTFOSQHRIDTLVLTANPLIFMAETRLSGPKALKLF	131
QY	133	AVETMLASLENPFGHILKTLKELANYAHNLIOGFKLPEYFSNLNLNHLDLSSNKIQSIYC	192
DB	132	FIQTGISIDFIPLNQNTLSLYGSNNHISIKLPKGPPT-EKLVKVDFOANNAHYLSK	190
QY	193	TDLRVLYHQPMLNLSLSDLPNMFIOGAFKEIRLHKLTLLNNPDSNLNMTKTCIOGLAG	252
DB	191	EDMSSLOQ--ATNLISLNLNGNDIAGIEGAPSAFAVOSL---NNGGTQNLVLVIFGKLN	244
QY	253	LEHVLVYGEFFRNENLEKFKSALGKCNLIEBPRALVLDYDDIIDLFNCLTNVSS	312
DB	245	STTQSLMTGTFEDMD-EDISPAVEFGCENSVESINL-QKAYFFNISNTHTCS----	298
QY	313	FSLVSVTTERVADPSYFNFGMQLIELVNCFKGQPTT-LTKLSIKRLTYTSNKGNN-AFS	368
DB	299	-----GLQELDLTATHTSLPSGLVLSLTKLVASANKFENLCQS	340
QY	369	EVDLPSLEF-----IDLSENGLSFKCCSQSPGTTSLKY	403
DB	341	ASNPFSLTSLISIKGNTKRLLETGCLLENLEMLRELDLSHDDTETSDDCCMLQRLNLSHLS	400
QY	404	LDLSPGVATWSSN-FLGLEOLEHLDPQSNLKQMSFVSFLNRLYLIDISHTTTRVA	462
DB	401	LDLSTNEPLSTKTEAPKPCQLELDLDAFTRLVKDAQSPFONHLKLVNLNLSHLLDIS	460

Db 573 IQLVGHVHKPOYSRQFKLRTDLVCSQNPVLEGTPEVROI EPQTLLCPDLSDDPERKCP 632
 Qy 388 KGC-CSQSDFGTSLKYLDLSPNGVITWSSNFLGLEOEHLDFOHSNKKOMSEFSVFTSL 446
 Db 633 RGCNCHVATYD---KALVINCH-----SGNLTHTVPRLPNL---HKMQLME-----LHL 675
 Qy 447 RNLVLDISHHTTRVAFNGIFNGLSLEVLKMGAGNSFOENFLPDI FTBLRLITFLDLSQC 506
 Db 676 ENNTLLRLPSANT-----PGYESVTSIHLAAG-----NLTSIDVQDL 712
 Qy 507 QLEQLSPFAFNSLSLQVLNASHNNFPSLDTPPYKCLNSLOVLDSLNHMTSKQEOLOH 566
 Db 713 -----PL-----NLTH-----LDISMNHL-----QMLN- 730
 Qy 567 FPSLAFLN-----LTQNDFACTCEHOSFLOMIDQROLVLEVERMECATPSDKQ 617
 Db 731 -ATVIGFLNRTMKRSVLSGNPMWCCTAKPLLFTQDNPERIGDRHEMCAVNAEMPT 789
 Qy 618 MPVLSLNTTQMNKTI-IGVSV---LSVLVSVVAVALYKF-----YFHLMLLAGCI 665
 Db 790 MVELSTNDICPAEKGVFIALAVIALTGLAGFTAAIYKFTQETIKIMLYAHNLL----- 845
 Qy 666 KYRGENT-----YAPFIYSSQDEDDWRANLEYKULEGCVPPPOCLAHYRDPITGVATA 720
 Db 846 WFTVEEDLDKDKKFDAPFISYSHKQDSFTEDYLPQLEHGPOKFOLCVHERDMLVGHIP 905
 Qy 721 NIHEGFHKSRKVIYVVOHFIOSRMCIFEYEAICTWOPLSRAGIIFIV---LQKVEKT 777
 Db 906 NIM-RSVADSRRTTIVLSONFIKSEMARLEFPAAHRSALNBSKRSIIYIISDIDGVEK- 963
 Qy 778 LLRQOVELYRLSRNTYLEMEDSVLGRHI FWRRLKALLDGKSNPEGVGTG 830
 Db 964 -LDEELKAY-LKMTYTLKMGDP-----WFMDKLAFALPHRR---PVGNGIG 1005

RESULT 4

113852
 gene wheelier protein - fruit fly (Drosophila melanogaster)
 C.Species: Drosophila melanogaster
 C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C.Accession: T13852
 R.Eidson, E.; Kooyer, S.; D'aveyln, D.; Duman, M.; Lawinger, P.; Botas, J.; Bellen, H.
 Development 120, 885-899, 1994
 A.Title: The Drosophila 18 wheelier is required for morphogenesis and has striking simila
 A.Reference number: Z17796; MUID:95524375; PMID:7600965
 A.Accession: T13852
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-1389 <EID>
 A.Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:9415682; PID:91019104; PIDN:AAA7920
 C.Genetics:
 A.Gene: wheelier
 A.Cross-references: FlyBase:FBgn0004364

Query Match 9.9%; Score 433; DB 2; Length 1389;
 Best Local Similarity 24.4%; Pred. No. 7.2e-19;
 Matches 217; Conservative 138; Mismatches 356; Indels 178; Gaps 34;

Qy 59 LDLSNPPLRHGYSFFPELQVLDLSRCIQTIEDGAYQSLSHLSTLITGNPIQSLA 118
 Db 338 LNLNNALTRIGSKTFKELYFLQIILDMRNNSIGHIEGAFPLVNLHTLNLAEHLHTLD 397
 Qy 119 LGAFGLSLQKLVAVETNLAST-ENFPIGHAKTKELVANNLQSFPLPEYFNTNL 177
 Db 398 NRIFNGLYVLTU-LLNNLVSVISOAFRNCSDKELDLSN--QTEVPAVODLSML 454
 Qy 178 EHLDSNNKIOSYCTDLRLVHQMPLNL-----SLDISNPMNF 217
 Db 455 KTLUDGEMQISEFKNTTNNLQGLRLIDNRIGNITVGMFODLPRLSVNLANKRIGS 514
 Qy 218 IOPGAF-KEIRLAKTLRNNPDSLANKVCTCIGLAGLEVHRLVGEFRNE----- 266
 Db 515 IERGAFTKTEIARLDRNF-----LTDINGIFATLASLMLNLSEHNLVWFYAFIP 568

Qy 267 GNLEKFD--KSAELGCLNL--TIEFRLAVLDYLDIIDLFNCLTNVSSFSVSVTIER 322
 Db 569 SNLKMLDHNGYIALGNYVYGLQEEIRVTTLDASHNRITETI-GAMSVNSIELLEFINNI 627
 Qy 323 VKDPSYN--FGMQLHELKNCFGQPTLKSLKRLFTSNK-----GNAPS----- 368
 Db 628 IGOIQANTFVDKTRLARVDLVANVLSKISLALVAPVSAKPVPEFYLGDPFCDGCSM 687
 Qy 369 -----EVDLPSEFL-----DLRNGLSERK-----GC 390
 Db 688 EMLQRLNLTTRQHPHYVDLNLIECLMPHRSAPLRPLASADPFVKYSHCPPTGHC 747
 Qy 391 CSQSDFGTSLKYLDLSPNGVITWSSNFL--GLBOLHLDFOHSNKKOMSEFSVFLSRN 448
 Db 748 CEYECCECEVLCFNGCSCFHDATWATNIVDCGQDLAAL-----PNRIPOVSDIYLDGNN 803
 Qy 449 LIYLDISHHTTRVAFNGIFNGLSLEVLKMGAGNSFOENFLPDI FTBLRLITFLDLSQC 508
 Db 804 MPELEVGHLTGRRLRALYLNASNLMTLQNS-----LAQLVNLVHLLENKL 852
 Qy 509 EQLSPTAFNSLSLQVLNASHNNFPSLDTPPYKCLNSLOVLDSLNHMTSKQEOLOHP 568
 Db 853 TALBGTFRSLGLRELTYLHNNMLTHISNATPEPVSLEURLDNKRSLSPHLOYR-- 910
 Qy 569 SSLAFLNLTQNDFACTCEH--OSFLOMIDQROLVLEVERMECATPSDKQMPVL----- 621
 Db 911 -SLGLTLGRNAGSCROQLRELALQFVSDNMMVVRADHDIYCLDAGIRLELIGNLANG 969
 Qy 622 -----SLNITCOMNKT-ITG-----VSVLSVLVSVVAVALYKFYFHLMLLAGC 664
 Db 970 PDCSDLDASASNTSSQDLGAIGCPMPAVLVILFVLVLIIVFVRESVRMLFA-- 1027
 Qy 665 IKYG-----RGEN---IYDAFVYSSODEDWRANLEYKULEGCVPPPOCLAHYRDPITG 715
 Db 1028 -HYGRVCEPRPEDEGKLYDAIILHSEKDYFVCENIAELHGRPPRLCICQORD-LPP 1085
 Qy 716 VAIANITHEGFHKSRKVIYVVOHFIOSRMCIFEYEAICTWOPLSRAGIIFIVLQK-- 773
 Db 1086 QASHQLV-EGARASRKIIIVLTNLATENNRIEFRA-----FHESLRL-----AQTLV 1136
 Qy 774 -VEKTLRQOVELYRLSRNTYLEMEDSVLGRHI-----FWRRLKRL 815
 Db 1137 IIEETSVAEAEDEVAELS--PYLK---SVPSNRLLTCDRYEWEXKLRYAI 1180

RESULT 5

T13887
 tlr protein - fruit fly (Drosophila melanogaster)
 C.Species: Drosophila melanogaster
 C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C.Accession: T13887
 R.Chang, C.; Beachy, P.A.
 Mech. Dev. 47, 225-239, 1994
 A.Title: Expression of a novel Toll-like gene spans the parasite boundary and contrib
 A.Reference number: Z17805; MUID:95151581; PMID:7848870
 A.Accession: T13887
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-1385 <CHI>
 A.Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:9913247; PID:9913248; PIDN:AAB33383
 C.Genetics:
 A.Note: tlr
 A.Cross-references: FlyBase:FBgn0004364

Query Match 9.7%; Score 421; DB 2; Length 1385;
 Best Local Similarity 24.0%; Pred. No. 4e-18;
 Matches 213; Conservative 139; Mismatches 359; Indels 178; Gaps 33;

Qy 59 LDLSNPPLRHGYSFFPELQVLDLSRCIQTIEDGAYQSLSHLSTLITGNPIQSLA 118
 Db 338 LNLNNALTRIGSKTFKELYFLQIILDMRNNSIGHIEGAFPLVNLHTLNLAEHLHTLD 397

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Oy 119 LGAFSGLSLQKLVAVENTNLSL-ENFPIGHLKTLKEINVAHNLQSFKLPFYSNLTNL 177
Db 398 NRIENGVLVLTCL-TLNNLVSVIVESOAFRNCSIDKEIDLSNN--QLTEVPEAAQDLSML 454
Oy 178 EHLDSNKKIOSIYCTDLRYLHQMPLNL-----SLDISLNPNMF 217
Db 455 KTLDSGNOIISFKNTRNLNQLTGLRIDNRIGNITVGMFQDLPRLSVNLAKNRQIS 514
Oy 218 IQPGAF-KEIRLHKLTLRNPNDSLNMVMTKCIQGLAGLEVHRLVLFGEFRNE----- 266
Db 515 IERGFNDKNTIEAIRLDKFF-----LTDINGIATLASLMLNLSENHLWMPDYATIP 568
Oy 267 GNLEKFD--KSALEGLCNL--TIEFRLAYLDYLDIIDLFNCLTNVSSSLVSTTER 322
Db 569 SNLKMULDHGNVTEALGNVYKLOEBEIRVTLTLDASHNRITEI-GAMSVNSIELLEINNNI 627
Oy 323 VKDFSYN--FGMQLHELVNCKRGQFPPLTKLSLKLTFSTNK-----GGNAPS----- 368
Db 628 IGOIQANTFVDKTRLARVDLVANVLSKISLNLARVAPVSAEKVPEFYLGNGPFECDCSM 687
Oy 369 -----EVDLPSELPL-----DLNRNGLSEK-----GC 390
Db 688 EMLQRINNLTTRQHPHVVLDIGNIECLMPHSRSLPLASLSASFVCKYSHCPPTGHC 747
Oy 391 CSQSDFGTTSKLYLDLSFNGVITMSSNPL--GLEOLEHLDFOHSLKOMSEFVFLSRN 448
Db 748 CEYECSECEVIPCNGSCFHDATYATNIVDCGRQDLAL--PYRIQDVSIDLTDGNN 803
Oy 449 LIYLDISHTHTRVAFNGIFNGLSLEVLKMGNSQENFLPDIPTIELNLPTFLDSQQL 508
Db 804 MPELEVGLTGRRLRALYLNASNLMTLQNS-----LQVLNLRVHLHNNKL 852
Oy 509 EQLSPTAFNSLSLQVLNMSHNPFLDTFPYKCLNSLQVLDYSLNHTSKKQLOQFP 568
Db 853 TALCEFTERSGLRELVELYHNNMLTHISNATPEPLVLSLEVRLDONNRSLSLPHIQYRH-- 910
Oy 569 SSLAFNLNTQDNFACTGH--QSFLQWITQDQROLVEVERMECATSPSDQGMPLV----- 621
Db 911 -SLOGLTGRRNAMS-CRCQOLRELAQFVSDNMAVVDADHIYCLDAGIRBELIGNLANG 969
Oy 622 -----SLNTTCQKN-----KTIIGSVLSVVSVAIVLYKFFPHMLLAGC 664
Db 970 PDCSDLDLASNSNLSSSDLAGCYRLPLAAVLVLIPLDVLLITFVRESVRMLF-- 1027
Oy 665 IKYG-----RGEN---LYDAFVIYSQDBDVRNELKNEBGPVPLCLHYSDFI 715
Db 1028 -HYGRVCEPRFEDAGKLYDAIILHSEKDYEFVCNIAAELEHGRPPRLCIGORD-LRP 1085
Oy 716 VALANITHEGFHKSRYIVVVSQHFIQSRWCIFETIATQWQPLSPAGIIFVYLQK-- 773
Db 1086 QASHLQLV-EGARARSRKIIILVLRLLATEWNRLEFRNA---FHESLRGL---AQKLV 1136
Oy 774 -VEKTLRMOQVELRLSRNTYLEMEDSVLGRHI-----FMRRLRKAL 815
Db 1137 IIEETSVSAEADVAELS--PYLK---SVPSNRLLTCDRYMEKLRVAT 1180

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RESULT 6

hypochemical protein C56R6.6 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T15864
 R:Fulton, L.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans coamid C56R6.
 A:Reference number: S69019
 A:Accession: T15864
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1066 <FULL>
 A:Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIND:AAA810
 C:Genetics:

A:Gene: C56R6.6
 A:introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 9
 Query Match 9.1%; Score 396; DB 2; Length 1066;
 Best Local Similarity 26.9%; Pred. No. 1e-16;
 Matches 156; Conservative 100; Mismatches 227; Indels 98; Gaps 24;

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Oy 35 NITYQCEMLNFKYKPDMLPSTKNLDSFNLRLHSGSFSPFELQVLDLRCEIOTIE 94
Db 131 NITH-LMDTNEVTRESMKVLRN-----KNVRLDHSGSFSPFKIRELDISTNOIQVE 184
Oy 95 DGAVQSLSHSLTLLITGNPIQSLALGAPSGLSLQKLVAVETNLASLENPIGHLKTIKE 154
Db 185 DSSEFTVGHQMSLDLSYRIAYLRG-----MLKNF-----AKTLTKT 221
Oy 155 LNVAHNLISFKLREYSNLTNLEHLDSNKKIOSI-----YCTDLRYLHQMPLNLSTL 208
Db 222 LKLABNNITHA--TPEALRDLRLTLNLNGKRLNRIGDVLKGTDTLV-----EL 270
Oy 209 DLSLNPNFIQPGAFKEIRLHKLTLRNPNDSLNMVMTKCIQGLAGLEVHRLVLFGEFRNEGN 268
Db 271 FIANNYLEHPIHVLGSKK-----QLEHLDISKKIKMSL-----KKPTS 309
Oy 269 LEKFDKALBGLCNLTIEFRLAYLDYLDIIDLFNCLTNVSSSLVSTTERVYDPS 327
Db 310 LLSITKEETSTVRRLNLAGRNINMSDYL--IFEHMPLLTVVDFSFRIRFISPRVEKL 367
Oy 328 YNFGMQLHELVNCKFGQFPPLTKLSLKLTFSTN---KGNAPSEVDLPSELFLDSRN 383
Db 368 KNL--ESLFLQNNQLANPFLFRDQKRLMLDNNQIOKIDN-PSLADLPQLQSLAGN 424
Oy 384 GLSPKCCSQSDFGTTS---LKYLDLSFNGVITMS-NFLGLEOLEHLDFOHSLKOMSE 439
Db 425 QLDI---ITENMFSSSSSELKSLNLANKKHISSSFSDLNQLQRLSHNNIRTTTS 481
Oy 440 FSVFLSRNLTYLDISHTHTRVAFNGIFNGLSLEVLKMGNSQENFLPDIPTIELNLPT 499
Db 482 MT-PSNLRNRYLDLSHRITIKILPSALYQLPALDVHLHNNMNE-IDRDAFSPSFDLQ 539
Oy 500 FLDSQQLLEOLSTAFNSLSLQVLNMSHNPFLDTFPYKCL-NSLQVLDYSLNHT 558
Db 540 SLKLSHNAFRFSCFPISGSQVHQDLSSNOINEITIF--CARGIRKLISLANSVEK 596
Oy 559 SKQELQHPSPSLAFNLTON-----DPACTCEHOSFIQ 592
Db 597 INRKLQD-ATELTSIDISHNGIIVDSDAFCBCKKXSHK 636

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RESULT 7

chaptin precursor - fruit fly (*Drosophila melanogaster*)
 A:Accession: A29944
 A:Residues: 1-1134 <REI>
 A:Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M19012
 C:Species: *Drosophila melanogaster*
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
 C:Accession: A29944; A21123
 R:Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
 Cell 52, 291-301, 1988
 A:Title: Chaptin, a cell surface glycoprotein required for *Drosophila* photoreceptor cell
 A:Reference number: A29944; MUID:88135762; PMID:3124963
 A:Accession: A29944
 A:Molecule type: DNA
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 C:Species: *Drosophila melanogaster*
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
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 C:Species: *Drosophila melanogaster*
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
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 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
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 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
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 R:Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
 Cell 52, 291-301, 1988
 A:Title: Chaptin, a cell surface glycoprotein required for *Drosophila* photoreceptor cell
 A:Reference number: A29944; MUID:88135762; PMID:3124963
 A:Accession: A29944
 A:Molecule type: DNA
 A:Residues: 1-1134 <REI>
 A:Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M19012
 C:Species: *Drosophila melanogaster*
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
 C:Accession: A29944; A21123
 R:Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
 Cell 52, 291-301, 1988
 A:Title: Chaptin, a cell surface glycoprotein required for *Drosophila* photoreceptor cell
 A:Reference number: A29944; MUID:88135762; PMID:3124963
 A:Accession: A29944
 A:Molecule type: DNA
 A:Residues: 1-1134 <REI>
 A:Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M19012
 C:Species: *Drosophila melanogaster*
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
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 A:Accession: A29944
 A:Molecule type: DNA
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 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
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 A:Molecule type: DNA
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 C:Species: *Drosophila melanogaster*
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 A:Molecule type: DNA
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 C:Species: *Drosophila melanogaster*
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
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 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
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 Cell 52, 291-301, 1988
 A:Title: Chaptin, a cell surface glycoprotein required for *Drosophila* photoreceptor cell
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 C:Species: *Drosophila melanogaster*
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
 C:Accession: A29944; A21123
 R:Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
 Cell 52, 291-301, 1988
 A:Title: Chaptin, a cell surface glycoprotein required for *Drosophila* photoreceptor cell
 A:Reference number: A29944; MUID:88135762; PMID:3124963
 A:Accession: A29944
 A:Molecule type: DNA
 A:Residues: 1-1134 <REI>
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 C:Species: *Drosophila melanogaster*
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
 C:Accession: A29944; A21123
 R:Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
 Cell 52, 291-301, 1988
 A:Title: Chaptin, a cell surface glycoprotein required for *Drosophila* photoreceptor cell
 A:Reference number: A29944; MUID:88135762; PMID:3124963
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 C:Species: *Drosophila melanogaster*
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
 C:Accession: A29944; A21123
 R:Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
 Cell 52, 291-301, 1988
 A:Title: Chaptin, a cell surface glycoprotein required for *Drosophila* photoreceptor cell
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 A:Accession: A29944
 A:Molecule type: DNA
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 A:Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M19012
 C:Species: *Drosophila melanogaster*
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
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 A:Title: Chaptin, a cell surface glycoprotein required for *Drosophila* photoreceptor cell
 A:Reference number: A29944; MUID:88135762; PMID:3124963
 A:Accession: A29944
 A:Molecule type: DNA
 A:Residues: 1-1134 <REI>
 A:Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M19012
 C:Species: *Drosophila melanogaster*
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
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 A:Reference number: A29944; MUID:88135762; PMID:3124963
 A:Accession: A29944
 A:Molecule type: DNA
 A:Residues: 1-1134 <REI>
 A:Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M19012
 C:Species: *Drosophila melanogaster*
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
 C:Accession: A29944; A21123
 R:Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
 Cell 52, 291-301,

A: Introns: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
 C: Superfamily: chaperlin; leucine-rich alpha-2-glycoprotein repeat homology
 C: Keywords: cell adhesion; glycoprotein; membrane protein
 F:1-29/Domain: signal sequence #status predicted <Sig>
 F:30-1134/Product: chaoptin #status predicted <MAT>
 F:80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR>
 F:103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F:128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F:177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F:201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
 F:226-248/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
 F:250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
 F:279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
 F:303-325/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
 F:326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
 F:351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
 F:375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
 F:401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
 F:428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
 F:453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
 F:477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
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 F:551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
 F:577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
 F:601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
 F:625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
 F:649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
 F:673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>
 F:708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
 F:733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
 F:757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>
 F:781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>
 F:805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
 F:828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
 F:854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
 F:879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
 F:903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
 F:928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR35>
 F:949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR>
 F:973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
 F:996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
 F:1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
 F:1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Query Match 7.7%; Score 333.5; DB 1; Length 1134;
 Best Local Similarity 23.0%; Pred. No. 8, 4e-13;
 Matches 177; Conservative 114; Mismatches 249; Indels 231; Gaps 30;

50 DNLPSTKRLDLPNPLRHLSYSFSPPELOV-----L 83
 346 DSLVNSLQILDSSGNLTGLHKLNNFVLRVISMKDKIKIQKTEFNVAHTLKL 405
 84 DLS-----RCEIQTEDGA---YOSLS-----HLSTLILTGPNIQ 115
 406 DLSGRNDPTNQLTRMTRKMNRSLSISRLGSSVGPEDPKDGVLELDQITRASLS 465
 116 SLALGAFGLSLQGLVAVETVLASLEN---FPIGLKTLKELNVAHNLIOGFKLPEYS 172
 466 GIOSHAFKRVRLKRLDSENGISSISLENDAPHEIGL-SLISLKMHSVGSGALPAEPRL 523
 173 NLTNLEHLDLSNKKIOSICTDRLVLPOMPLNLSLDLSLNPNNFIOPGAFK---EIRHL 229
 524 HLTSLQELDFSNHHSMSDTSFHLKLNRL---LELHDKRIEQLVKTGFGDHSKLE 579
 230 KLTLENN-----PDSLNVKTCIOGLAEVHRLVLSGFNRNEGLKFKDSALBS- 279
 580 EISLTFNHLTISQHTFFDLALRK-----LHLDNDKIDKIRRAFAMNDELLEYLSIRGN 634
 280 -LONTIEBF-----SLAVDYLDLDI---IDLFNGLTNVSSFSLSVSTIEBVKDPSNPF 330
 635 KINNLADESFQNLPKLEILDMAPNLPNPNFYFDQVGTLSNIN-VNVSHNQIRQLMTNS 693

331 GWOHLELVNCKRGQPTLKLSLKLRLFTSNKGNVAFSEVDLPSEFLDLSNGLSF--K 388
 694 SW-----SGRHEHGMVYNSIKIKIDLSHNNSIILHP 724
 389 GCCSGSDSGTT-----SLKYLDSFNGVATSMNS-FLSGEQLH 426
 725 GFYPAEASLTHLHLYGNSLMTNTEDVGNMPEHLOMDSLSTYMHLELDFAKNTKQLQL 784
 427 LDFOHNSKMSSEFVPSLRILNLYLSDSHYTR--VAFNGIFNG-----469
 765 VFFGNVYSDLPQ-DIFKPVQGLRIVDSHNRKLPDNLFFNGMEKLDVSHMMKLP 843
 470 ---LSLEVLKMAGNSFOENFLP-----DIFTELNLTFDLSQCLBQSPAFNSLSS 521
 844 SSSLSLSLAALTCELHLNNFSTISHMDLSKFRSLAYLDSYNYLLRIDAVATMPK 903
 522 LQVLYMSNR-----NFF-----SLDPPYKCLNSLOVLDYSLNHIMS 559
 904 LAVLDLSNRDLKWKDKSEFMLENSLILKLGLENVLSLTPBELRKYLEFRFGVNE-LPS 962
 560 KROELQHPSSLAFLNLPNDPACTCEHQSFLOWIKDQRLVVERECATPSDKQ---616
 963 IPDELAKHMSNLRMLDLSNND-----LTNPVLTQALPHLRML 1002
 617 -GMPVLSNITTCOMNKTIIGSV-LSVLVSVVAVLVYKFFHMLLAGCT 665
 1003 SGNPITSLN-----NSFQVNEDEMLDISNFRLAYREV-----GCL 1040

RESULT 8
 JCS239
 Insulin-like growth factor acid-labile chain - baboon
 C: Species: Papio sp. (baboon)
 C: Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
 C: Accession: JCS239
 R: Delnathy, P.; Baxter, R.C.
 Biochem. Biophys. Res. Commun. 227, 897-902, 1996
 A: Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
 A: Reference number: JCS239; MUID:97040714; PMID:886027
 A: Contents: liver
 A: Accession: JCS239
 A: Molecule type: mRNA
 A: Residues: 1-605 <DE>
 C: Comment: This factor is structurally related to proinsulin and have insulin-like meta

Query Match 7.3%; Score 316; DB 2; Length 605;
 Best Local Similarity 24.4%; Pred. No. 4, 5e-12;
 Matches 157; Conservative 94; Mismatches 242; Indels 150; Gaps 23;

33 VNTIYQCMELNFKYKIPNPLPFTSGNLDSPNPLRHLSYSFSPPELOVLDLSRCEIQ 92
 53 VNELSVFSSRRULRLPGLIGEGTQALWDNSLSIPPAFRNLISLAFNLQGGQLS 112
 93 IEDGAYOSLSLSTLILTGPNIOSIATGAFS-----GLSGL 128
 113 LEPQALIGLEMLCHLHLERNQRLSLAVGFATPALALLGLSNRLSRLEDGLFGLGNL 172
 129 QKLVAVETNLASLENFPIGLKTLKELNVAHNLIOGFKLPEFSNLTNLEHLDLSNKKIQ 188
 173 WDLNKGMSLVLPLPAARFGGLGRLVLAIGRL-AIYQALFSGLAELRELDLSRNAR 231
 189 STYCTDLVLPOMPLNLSLDLSLNPNNFIOPGAFKIR-LHKTLRNPNFDSIATMKTCT 247
 232 AI---KANVPQQLPRLQ-KLYLDRLLIAAVAPRGLGKALRMLDLSIN-RVAGLLEDF 286
 248 QGLAEVHRLVLSGFNRNEGLKFKDSALBSGLCNLTIEBRRLAYLDYLDIDLFNCL 307
 287 FGLGLRVLRL-----SHNAIASLRPRTEEDL-----HFILEL-----319
 308 TNVSSFSLSVSTIEBVKDPSNPFQWOHLELVNCKRGQPTLKLSLKLRLFTS--NKGN 365
 320 -----QGHNRKIRQLAERSFS-GIGQLEVLTDHNOQVAVGAFGLTNVAVNNLSGN 372

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QY      366 AFSEVDLPSLEHLDLSR-NGLSFKGCC-----SQDFFGTSIAKYDLSFNGYITMSSNPL 419
Db      373 CLR--NLPEQVRGRGAKSHLSHLESGCLGRIRPHFPAGISGRIRFLKDNONGVGEESOL 430
QY      420 -GLEQLEHLDFQHSNLKOWSEFSVFLSLRNLIYLDISHTHTEVAENGJFNGLSLEVKM 478
Db      431 WGLAELLELDLTSNQI-----THLP--HQFGIGKLEYILL 465
QY      479 AGNSFOENFLP-DITELRNLIFFLDSCQLEQLSPFAINSLSIQLVLMSHNNFFSLDT 537
Db      466 SHNRILAE-LRPADALGPLORAFMLDVSHNRLEALGSLIASIGRRYINLRNN--SLRT 520
QY      538 PPKYCINSIQVLDVSYLNHIMTSKQEOLOHFPSSIAFLNLTQDNFACTCEHOS----- 589
Db      521 FTPQ-----PPGLERLWLEGNPMWCSCGPLKALRDFALQN 554
QY      550 -----FLQMT---KQKQLVVEVRMECATPTSDKQMPVLSL 623
Db      555 PSAVRPFVQALCEGDDCQPPVYTNINITCASPEVAAGLDLRL 597

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RESULT 9
T17461
disease resistance protein D - tomato
C.Species: Lycopersicon esculentum (tomato)
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T17461
R.Parniske, M.; Jones, J.D.
Proc. Natl. Acad. Sci. U.S.A. 96, 5850-5855, 1999
A.Title: Recombination between diverged clusters of the tomato Cf-9 plant disease resist
A.Reference number: Z18801; PMID:10318973
A.Accession: T17461
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-853 <PAA>
A.Cross-references: UNIPROT:Q9ZS82; EMBL:AF119040; NID:g4235640; PID:g4235641; PIDN:AADI
C.Genetics:
A.Gene: NIOD

[illegible]

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Db 454 ALLLHHNNISGHTSSAICNLKTFILINLKSNNIDEGTIPQCLGEMSSLQV-----LD 504
QY 454 ISHTHTRAFNENGIENGLSSLEVLKMAAGNSFOENLPIEDITELRNILTFELDLSOCOLEOLSP 513
Db 505 LSNNLSLGTMTNTFFSIGNPLHIIKLDWNKLQCKVPEPSLI--NCKKLELDLSDNNELNDTFP 563
QY 514 TAFNLSLSQVANNMESH-----NFSLDTFEPYKCLNSLQVL-- 549
Db 564 KWLGDPLPNLQVLFNFSRNSKLYGPIRITNNLFAKIRRVYDLSNGHSGD--LPVSFFENFEAMKI 622
QY 550 -----DYSLNHMTSKK---OELQHFPSSLAFLNLTQNDFACTCEH--OS 589
Db 623 NGENNGTRKYVADLYSDYKYNLYIVTTKGLDDELGRVLTQIIIDLSKXFE--GHIPN 679
QY 590 FLQWIKDQROLVERBERMECATPSPDKQGNPVL-----SLNTTCQNNKTIIGVSVLSVLV 643
Db 660 IIGDILGRTNLSSHNVLEGHIPAFQONLSVLESIDLSSNNKISGALPQOLASITFLLEVAN 739
QY 644 VSVVAVLVYKFFYHMLLAGCICKYRGENTIVDAFYVYSQDEWDWVNEVLKONLEEGVPPF 703
Db 740 LS-----HNHLV---GCIPIKXKQ---PDSFENSIVLNGDGLR-----GLPFS 775
QY 704 QLC 706
Db 776 RDC 778

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RESULT 10
A41915
Insulin-like growth factor-binding complex acid-labile chain precursor - human
N:Alternate names: Acid-Labile Subunit (ALS)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A41915
R:leong, S.R., Baxter, R.C., Camerato, T., Dai, J., Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A>Title: Structure and functional expression of the acid-labile subunit of the insulin-1
A:Reference number: A41915; MUID:92357025; PMID:1379671
A:Accession: A41915
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-605 <LEO>
A:Cross-References: UNIPROT:P35858; GB:M86826; NID:G184807; PIDN:AAA6047.1; PID:G184808
A:Experimental source: liver
A>Note: sequence extracted from NCBI backbone (NCBIP:110171)
F:95-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:219-244/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F:339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F:411-433/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F:483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

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Best Local Similarity 24.4%; Pred. No. 2.9e-11;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

40 CMEINFYKIDNIIPTSTKNIDLSFNPRLRHGYSFSPFELQVLDLSRCRIQTIEDGAYQ 99
DB 60 CSSRNLITRPDVGQTAQWLTGDNNTLSVPPAFQNLISGFTNLGGGGLSEPPALL 119

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RESULT 12
T42218
alt-1 protein homolog - rat
N:Alternate names: MEGP4 protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T42218
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomic 51, 27-34, 1998
A>Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z4126; MUID:9860089; PMID:9693030
A:Accession: T42218
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1531 <NA>
A:Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:g3449289; PDB:BAJ32460.1; PID:g3
A:Experimental source: strain Sprague-Dawley; brain
C:Genetic:
A:Gene: MEGP4
C:Superfamily: fruit fly alt protein; EGF homology; leucine-rich alpha-2-glycoprotein x

Query Match 6.9%; Score 299.5; DB 2; Length 1531;
Best Local Similarity 22.1%; Pred. No. 1.6e-10;
Matches 167; Conservative 95; Mismatches 260; Indels 233; Gaps 27;

4 ASRLAGTLIPAMAFSLCVRPESMBPCVAVPNITVQCMEINFYKIPDNLPSTKNLDSF 63
Db ACTLSSGSCPMNC-SC-----SNGIVDCRGKGLTALPALTPEMTETIRLEL 318

Qy 64 NPLRLGYSFPSPPELOVLDSRCETIEDGAYQSISSHSTLTITGNPIQSLALGAPS 123
Db 319 NGIKSIIPGASPSYKRLRIDLSNNQIAEIPDAFQGLRSINSLVLYGNKITTIDPRGVFG 378

Qy 124 GLSSLOXVAVETNLASLENPFIGHLKTLKELNVANHLIQSPKLPVEYSNLTNHEHLDLS 183
Db 379 GLYTLQHL-----LNA--NKINCIR-PDAQODIQNSLSLEY 413

Qy 184 SNKIQSI---YCTDLRVLHOMPLNLSDLSINPMNFITOPGAFKEIRLKLTLRNPNDSL 240
Db 414 DNKIQSLAKGFTTSRAIQ-----TLHLAQNPFICDCLMKLA-----DFLRT 456

Qy 241 NVMTCTICGLAGLEVHRLV--LGEPRNEGULEKDKALBGLCNLTIEBRLAYLDYLL 297
Db 457 NPIET--TGACASPRRLANKRIGQIKS---KKRCSAKE-----QYFIPGEDHLL 503

Qy 298 D-----DIIDFNCITNVSSFSVLVETIEBVKDFYNGVOMHLELNCKF-----GQFP 346
Db 504 NSECTSDVACPRKCKCEASVVECSGLKSKIPF-RIPQSTTELRLNNEIETLGTGLFK 562

Qy 347 TLKLSLRLRTFTSNKGNAPSEVDLPSEFLDLSRNLSPKCCSQSDFGTTSKLVDL 406
Db 563 --KLSHLKLKINLSNNK-----VSEIEDGTFE-----GATISSEHL 596

Qy 407 SPNGYITMSSN-FLGLEQLEHLDFOHSNLKOMSESVLSRLNLYLDISHTHTRVAANG 465
Db 597 TANQLESVRSQWFRGLDGLRTLMENNRISCIHNDG-FTGLRNVALSLVYDNIITTSIPG 655

Qy 466 IFNGLSLEVLKMAINSFOENP----- 487
Db 656 AFDITQALSTLNLNLPNRCQCLAMLGDMLEKRIYVGNPRCPDPLRQIPLODVAPP 715

Qy 488 -----LPIDITFEL----- 495
Db 716 DFRCEGQEBVGCLPRPCQPCACLDITVVRCSNHLQALPKGIPKANTETELDQNGFTL 775

Qy 496 -----RNLFTLDLSQCQLSEQLSPYAFNSLSISQVLTNMGHNNFSLDTPPYKCLNSIQ 547
Db 776 VPGQLSTFKYQLQVLDLSNNKISSLSNSSFTTMSQTLTTLISYNAQCIPIPLAFQGLRSIR 835

Qy 548 VLIDYSLNHTMSKQELQHPSSSLAFNLTLQNDFACTGEHOSFLOWINDQQLVVEVRM 607
Db 836 LLSLHGNDVSTLQBSGIFADV--TSLSHLAIGANPLYCDCHLRWLSWVTKYK--EPGIA 891

Qy 608 ECA-----TPSDK---QGMPEVLSLNTIC 627
Db 892 RCAGPPEMEGKLLTTPAKKKECGPPSLAVQAKC 926

RESULT 13
H96510
Probable disease resistance protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H96510
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federzpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitli, R.; Marzelli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96510
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-994 <STO>
A:Cross-references: UNIPROT:Q9C637; GB:AE005173; NID:g11321768; PDB:AAJ34245.1; GSPDB:GT
C:Genetic:
A:Gene: F2G19.6
A:Map position: 1

Query Match 6.8%; Score 296.5; DB 2; Length 994;
Best Local Similarity 23.0%; Pred. No. 1.4e-10;
Matches 161; Conservative 102; Mismatches 271; Indels 167; Gaps 31;

Qy 2 MSASRLAGTLIPAMAFSLCVRPESMBPC-----VEVVPNITVQCMEINFYKIPDNL 52
Db 213 MSSVDISAPPIEBSYVMSKSLTLKGCNLLGRFPNSVLIDIPNLSISLDHNL-----NL 267

Qy 53 PFSTKNLDSFNPLRHGYSY-----SFSFPPELOVLDSRCETIEDGAYQSISSHSTLTITGNPIQSLALGAPS 102
Db 268 EGSIPNP-LRNNSLKLKSIYNTSFGTIPNSISLKLTLSDKLOQSAFSGRIPSSLSLS 326

Qy 103 HLSTLITGNPIQSLALGAPSGLSLQKLVAVETNLASLENFP--IGHLTKELNVAHN 160
Db 327 HLSLVAVENNPFVEIIPSSVSNLQQLTLPVSDNNLNG--NPSLSLNTLNQRLRIDICSN 384

Qy 161 LIQSFKLPEYFNSLTNHEHLDLSNKKIQSYCTDLRVLHQNPF--LNLSS--LDLSLNP 214
Db 385 HFTGF-LPPTISQLSNLEFSPACDSFTG-----SIPSLFNISLITLGLSYNQ 433

Qy 215 MNFIPQAPFKEIRLKLTLRNPNDSLNVMTKTCICGLAGLEVHRLVLDGEPRNEGULEKFPDK 274
Db 434 LN-----DTNI-----KVISLHNLQ 451

Qy 275 SALEGLCNLTIEBRLAYLDYLDIIDLFNCLTNVSSFSIVSY--TIERVKDPSYNGF 331
Db 452 LLDLN-----NNKKAQVD-----LDVFLSLKRLVSLALSGPLPSTTNTISSEFS 499

Qy 332 WQHELVNCKFGQFPPTLKSLKRLFTSNKGNAPSEVD---LPSEFLDLSRNL 385
Db 500 LEVLELSCNIIPEPF-IRNQRLSSIDLSNNNIKQGVNMLWRLELSTVDISNNSLI 558

Qy 386 SFRKCCSQSDRGTTSLKYDLSFNGVITWSSN-----FLGLEQLEHLDFOHSNLKOMSE 439
Db 559 GFNG-----SLALSGSKIVMLDLSNAPQGLFMPPRGIQYFLSYNNFTGYIP 608

Qy 440 FSVLSLRLNLYLDISHTHTRVAFNGIFNGI-----SSLEVLKMAINSFOENP 490
Db 609 PSI-CGLANPLIIDLSS-----NNNLHGLIPRCLEAQMSLSLVNLRNNSL-DGSLPN 656

Qy 491 ITTELRLNLTLDLSQCQLSEQLSPYAFNSLSLQVLTNMGHNNFSLDTPPY--KCLNSLQV 548

Db 659 IFMAKAVLSLDVSNHTLEGKLPASLAGSALEITLAVESNNT--NDTFPFWLNLSLPKIQV 716
QY 549 LDYSLNHMTSKKQELQH-----FPSLAFINTQNDPACTCEHQSFLQWIKDQRQLL 601
Db 717 LVLRBNNF-----KGLHNVNDGVWFGFP--LLRITDVSHNDPVGTLTSDYIMMNTAISKS-- 769
QY 602 VEVERMECATPSD---KQMPVLSLNTTCQNNKTIIGSVL 639
Db 770 -ETELQYIGDPEDYGYTSLVLMNKGVSMEMQRIITKYTVI 809

RESULT 14

JC1282
Insulin-like growth factor-binding protein acid labile chain precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JCI282
R/Idat, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A/Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A/Reference number: JCI282; MUID:93038676; PMID:1384485
A/Accession: JCI282
A/Molecule type: mRNA
A/Residues: 1-603 <DAI>
A/Cross-references: UNIPROT:P35859; GB:S46785; NID:q258002; PIDN:AAB3770.2; PID:q570593
A/Experimental source: liver
A/Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 6.8%; Score 296; DB 2; Length 603;

Best Local Similarity 24.1%; Pred. No. 7.8e-11;

Matches 155; Conservative 84; Mismatches 243; Indels 162; Gaps 24;

QY 40 CMEINFPYKIPDNLPESTKNLDSFNPRLHLSYSPFPELOVDLSRCEIQTIEDGAYQ 99
Db 60 CSSKNLTHLPDIPVSTRALMLDGNLSSIPSAFQNLSSLDPLNLQGSWLSRLEPQLL 119
QY 100 SLSHSLTILTNPFIQSALGAFSGLSIQKVAVETNLASLENPIGHLKTLKELNVA- 158
Db 120 GLQNLVYLHLERNLRNLAVGLFTHPTSLASLSLSNLLGRLEBGLFQGLSHMLDNLGM 179
QY 159 -----NHLI-----QSFKLPEYFSNLTNLEHLDSKSKIOSICTDLR 196
Db 180 NSLVVLPDTPVPGGLGNLHVLVAGNKLTLQPALPCGLGELRELDLSRAALASV--KAN 236
QY 197 VLAHQPLNLTLSDLSLNPNNFIQPGAFAKEIR-LHKLTLRNPDSINVMKTCIQGLAGLEV 255
Db 227 VFWHLPRIQ-KLYLDRNLITAVAPGAFGLMKALRMLDLSHN-RVAGLMEDTFPGLLGLHV 294
QY 256 HRLV-----LGEFR-NEGNIKEPKDKALBGLCNLTIEEFLAYLYDYVL 297
Db 295 LRLANNAIASLRPRTFKDLHLEELQLGHNRIROLGEERTEEGLEGLEV---LTLNDNQI 350
QY 298 DDI-IDLNFCLTNVSSFSLSVTI---ERV---KDFSYNFGMQLHELVNCKFGQPTLX 349
Db 351 TEVRVAGSGFLNVAWNLNGCNLSLPRVFOGLDKHSLHLESCLGHVLAHTF--AG 408
QY 350 LKSLRLTFTSNKGNAPSEVD-----LPSLEFLDSHNGLSFKGCCSQSDPGTTSIX 403
Db 409 LSGRLRLFLRD-----NSISIEEQSLAGSELLELDLTNNRLTH--LPRQLFQGLGHLEY 462
QY 404 LDLSNNGVITMSSNPLGLEOLEHLDPOHSNKKOMSEFSVLSLRNLIYIDISHTTRVAF 463
Db 463 LLLSTNOULTTISAAYLG-----PLQAFWMLDISHNHLLETIA 498
QY 464 NCIFNGLSLEVLKMAAGNSFOENFLPDIPTFLRNLTFLDLSQCLEQSLPTAFNLSISIQ 523
Db 499 EQLFSSLGKVRVYLSLNNLSLQ--TFSP-----QGLERL----- 530
QY 524 VLMNSHNPFSLDTPPYKCLNSLQVL-DYSLNHMTSKKQELQHFPSSLAFLNLTQNDPA 582

Db 531 -----WIDANPWCSCPLKALRDPALQN-----PGVVPFVQT----- 563
QY 563 CTCHEQSFLQWIKDQRQLLVEVERMECATPSDKQMPVLSLNTI 626
Db 564 -VCE-----GDDCQGVYTYNNITTCAGPANVSGLDRDYSER 598

RESULT 15

JG0193

G protein-coupled receptor PRX - mouse

C/Species: Mus musculus (house mouse)

C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000

C/Accession: JG0193

R/Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.

Biochem. Biophys. Res. Commun. 254, 273-279, 1999

A/Title: Identification of a novel seven-transmembrane receptor with homology to glycopr

A/Reference number: JG0193; MUID:99121227; PMID:9920770

A/Accession: JG0193

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-907 <HER>

Query Match 6.8%; Score 295; DB 2; Length 907;

Best Local Similarity 23.0%; Pred. No. 1.5e-10;

Matches 167; Conservative 110; Mismatches 243; Indels 206; Gaps 32;

QY 11 LIPNAFPLSCVRPEWMECEVAVPN-----ITYQCEINFPYKIPDNLPRS 55
Db 9 LLSLALQLQVLAAGS-SPEPDATIPGCCSHCHCELDGMRLRVDCSDGLSPLNSLVF 67
QY 56 TKNLDSFNPRLHLSYSPFPELOVDLSRCEIQTIEDGAYQSLSH---LSTLLITLG 111
Db 68 TSYDLSMNNISQDPA-----SLHRLCTLEELRLAG 99
QY 112 NFIQSLAIGAFSGLSLQKLVAVETNLASLENPIGHLKTLKELNVAHNLIOSFKLPEYF 171
Db 100 NALTHIPKGAFTGLSLVLVLMQNNQKRVBEALQNLRSIQSLRLDANH-I-SYVPPSCF 158
QY 172 SNLTNLEHLDSNNGISQITCTDLRLVHQPLNLTLSDLSLNPNNFIQPGAFAKEI-RLHK 230
Db 159 SGLSHLRHMLDNNLTLVPVQAFPSLSALO---AMTLALKHINHIDYAGNLSLVV 214
QY 231 LTLRNN-FDSINVMKTCIQGLAGLEVHRLVLEGFENEGNLEKFDKSALEGLCNLTIEBER 289
Db 215 LHLHNNRHSLG--KKCFDGLHSLETLTL-----NYYNLDLF-PTALKTISN----- 258
QY 290 LAIYDYIIDIIIDL---FNCLTNVSSFSLSVTI--ERVKDFSYNFGMQLHELVNCKFGQ 344
Db 259 LKEIGFHSNNIRSIPIERAF-----VGNPSLITIHFDNDPIQFVGVSARQHLR-----E 306
QY 345 FPTLKLKSLKTLFTSNKGNAPSEVDLPISLEFLDLSNNGLSF--KGCSCSQSDPGTTSIX 402
Db 307 LRTLLTGASHITTEPHLTGTA-----TRESLTLTGAKLSLSPQAVCDQ---LPLNQI 355
QY 403 YLDSFNGVITMSSNPLGLEOLEHLDPOHSNKKOMSEFSVLSLRNLIYIDISHTTRVA 462
Db 356 VLDSLYNLEDLPS--LSGCQKLOKIDLRN----- 384
QY 463 FNGIFNGLSLEVLKMAAGNSFOENFLPDIPTFLRNLTFLDLSQCLEQSLPTAFNLSISL 522
Db 385 -----EIVIKSTFQQLF-----NLRSNLINLAWNKIATIHPPVAFSTLPSL 424
QY 523 QVLMNSHNPFSLDTPPYKCLNSLQVLDYSLNHMTSKKQELQ-----HPSSLAFLNLT 576
Db 425 IKLDLSN--LLSFPVTLG-----HGTLHLKLTGNRALQSLIPANFP-ELKTIEM 473
QY 577 TQNDPACT---CE--HQSFLQWIKDQRQLLVEVERMECA--TPSDKQMPVLSLNTIQM 629
Db 474 PSAYCCAFGCGENYKISNQMKDDGNSVDDIHKXQAGLQVQDERLEDLDFLEDEDL 533
QY 630 NK-----TIIGSVLSLVVS---VVAVLVYK---FYFILM 659

Db	534	NAHSHVQCSPRGPFKEHLEFGSWLIRIGVTTAVLILSCNALVALTVFRTPLYISSIK	593
Oy	660	LIAGCI	665
Db	594	LLIGVI	599

Search completed: March 12, 2005, 19:56:52
Job time : 30.6477 sec8

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 12, 2005, 19:34:46 ; Search time 21.9643 Seconds
(without alignments)
2715.523 Million cell updates/sec

Title: US-09-396-985B-4

Perfect score: 4141
Sequence: 1 MELNFKYKIPDNLPRSTKNLD.....SWNEGTGTCNNQGEATSI 799

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4141	100.0	844	US-09-949-016-9438	Sequence 9438, App1
2	599.5	14.5	784	US-09-982-308B-23	Sequence 23, App1
3	590	14.2	661	US-08-514-014-4	Sequence 4, App1
4	590	14.2	661	US-08-833-823-4	Sequence 4, App1
5	539	13.0	775	US-09-949-016-8799	Sequence 8799, App1
6	309	7.5	605	US-09-063-950-5	Sequence 5, App1
7	297	7.2	605	US-08-190-802A-49	Sequence 49, App1
8	297	7.2	605	US-08-477-346-49	Sequence 49, App1
9	297	7.2	605	US-08-477-346-49	Sequence 49, App1
10	297	7.2	605	US-08-487-089-49	Sequence 49, App1
11	297	7.2	605	US-09-538-092-1087	Sequence 1087, App1
12	297	7.2	623	US-09-949-016-10995	Sequence 10995, App1
13	290	7.0	603	US-08-190-802A-50	Sequence 50, App1
14	290	7.0	603	US-08-477-346-50	Sequence 50, App1
15	290	7.0	603	US-08-473-089-50	Sequence 50, App1
16	290	7.0	603	US-08-487-072A-50	Sequence 50, App1
17	289.5	7.0	1112	US-09-353-585-3	Sequence 3, App1
18	287.5	6.9	662	US-09-538-092-1325	Sequence 1325, App1
19	287.5	6.9	662	US-09-949-016-6619	Sequence 6619, App1
20	287.5	6.9	665	US-09-949-016-10710	Sequence 10710, App1
21	286.5	6.9	1525	US-09-191-647-2	Sequence 2, App1
22	286.5	6.9	1525	US-09-540-245A-2	Sequence 2, App1
23	286.5	6.9	1525	US-09-540-153-2	Sequence 2, App1
24	286	6.9	1112	US-09-353-585-2	Sequence 2, App1
25	284.5	6.9	907	US-09-170-496D-264	Sequence 264, App1
26	284.5	6.9	907	US-09-170-496D-278	Sequence 278, App1
27	283.5	6.8	1166	US-10-101-464A-900	Sequence 900, App1

28	279.5	6.7	1529	4	US-09-312-283C-396	Sequence 396, App1
29	277.5	6.7	1523	3	US-09-182-024A-2	Sequence 2, App1
30	273	6.6	620	4	US-09-907-794A-73	Sequence 73, App1
31	273	6.6	620	4	US-09-905-125A-73	Sequence 73, App1
32	273	6.6	620	4	US-09-902-775A-73	Sequence 73, App1
33	273	6.6	620	4	US-09-906-700-73	Sequence 73, App1
34	273	6.6	620	4	US-09-903-603A-73	Sequence 73, App1
35	273	6.6	620	4	US-09-904-920A-73	Sequence 73, App1
36	273	6.6	620	4	US-09-909-064-73	Sequence 73, App1
37	273	6.6	620	4	US-09-905-381A-73	Sequence 73, App1
38	273	6.6	620	4	US-09-906-618-73	Sequence 73, App1
39	270	6.5	1101	3	US-08-986-485-2	Sequence 2, App1
40	266.5	6.4	1091	3	US-08-986-485-5	Sequence 2, App1
41	265.5	6.4	863	2	US-08-666-271-2	Sequence 2, App1
42	265.5	6.4	1874	4	US-09-331-403-2	Sequence 2, App1
43	264	6.4	1480	3	US-09-191-647-7	Sequence 7, App1
44	264	6.4	1480	3	US-09-540-245A-7	Sequence 7, App1
45	264	6.4	1480	3	US-09-540-153-7	Sequence 7, App1

ALIGNMENTS

RESULT 1						
US-09-949-016-9438						
Sequence 9438, Application US/09949016						
Patent No. 6812339						
GENERAL INFORMATION:						
APPLICANT: VENTER, J. Craig et al.						
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED						
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF						
FILE REFERENCE: C1001307						
CURRENT APPLICATION NUMBER: US/09/949, 016						
CURRENT FILING DATE: 2000-04-14						
PRIOR APPLICATION NUMBER: 60/241, 755						
PRIOR FILING DATE: 2000-10-20						
PRIOR APPLICATION NUMBER: 60/237, 768						
PRIOR FILING DATE: 2000-10-03						
PRIOR APPLICATION NUMBER: 60/231, 498						
PRIOR FILING DATE: 2000-09-08						
NUMBER OF SEQ ID NOS: 207012						
SOFTWARE: FASTSEQ for Windows Version 4.0						
SEQ ID NO 9438						
LENGTH: 844						
TYPE: PRT						
ORGANISM: Human						
US-09-949-016-9438						
Query Match						
Best Local Similarity 100.0%; Score 4141; DB 4; Length 844;						
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	MELNFKYKIPDNLPRSTKNLDSPNRLHLSYSPFPELOVLDLSREIQTIENGAQS	60			
DB	46	MELNFKYKIPDNLPRSTKNLDSPNRLHLSYSPFPELOVLDLSREIQTIENGAQS	105			
QY	61	LSHSTLILTNPNISIALAFSGLSYQKVAVEYNLASLENPFIQHLKTLKELNVAHN	120			
DB	106	LSHSTLILTNPNISIALAFSGLSYQKVAVEYNLASLENPFIQHLKTLKELNVAHN	165			
QY	121	LIOGFKLPEYPSNLTNLEHLDSSNKSIOISYCTDLRVLAHQPLNLSIDLISLMPNFTOP	180			
DB	166	LIOGFKLPEYPSNLTNLEHLDSSNKSIOISYCTDLRVLAHQPLNLSIDLISLMPNFTOP	225			
QY	181	GAPEIRLHKTLTNNPNSLVMWTCCTOGAGLVHRVLVGEFNEGKLEKPDKSALEGL	240			
DB	226	GAPEIRLHKTLTNNPNSLVMWTCCTOGAGLVHRVLVGEFNEGKLEKPDKSALEGL	285			
QY	241	CNLTIEEFLAYLDYDDIDIDLFNCLTNVSSFSVLSTIERVXDFSYNFGMOHLELVNC	300			
DB	286	CNLTIEEFLAYLDYDDIDIDLFNCLTNVSSFSVLSTIERVXDFSYNFGMOHLELVNC	345			
QY	301	KFGQPTLKLSLRKLTFTSNKGNAPSEVDLPSELEFLDLSRNGLSFKGCCQSDFGTT	360			

Db 346 KFGPPTLKLKSLKLTFTSNKGNAPFSEVLPSELEFDLSRNGISFPGCCSQSDPFGTTS 405
Qy 361 LKYLDLSFNGVITWSSNFTLGELEHLDFOHSNLKOMSEFVLSLRNLIYLDISHHTR 420
Db 406 LKYLDLSFNGVITWSSNFTLGELEHLDFOHSNLKOMSEFVLSLRNLIYLDISHHTR 465
Qy 421 VAFNGIFNGLSLEVLKMGNSFOENFLPDIETELRNLTFLDLSQCOLEQSPPTAFNSLS 480
Db 466 VAFNGIFNGLSLEVLKMGNSFOENFLPDIETELRNLTFLDLSQCOLEQSPPTAFNSLS 525
Qy 481 SLOVLMNSHNNPFSIDTPPYKCLNSLOVLDVSLNHTMSKQOELHPPSSLAFLNLTOND 540
Db 526 SLOVLMNSHNNPFSIDTPPYKCLNSLOVLDVSLNHTMSKQOELHPPSSLAFLNLTOND 585
Qy 541 FACCEHOSFLOMIDQOLIVEVERMECAPSPDQOGMPVLSLNTTCOMNTIIGVSVLS 600
Db 586 FACCEHOSFLOMIDQOLIVEVERMECAPSPDQOGMPVLSLNTTCOMNTIIGVSVLS 645
Qy 601 VLVSVAVLVYKFFHMLLAGCIKYGRGENIYDAFIYSSODEDWVRLVKNLEBGV 660
Db 646 VLVSVAVLVYKFFHMLLAGCIKYGRGENIYDAFIYSSODEDWVRLVKNLEBGV 705
Qy 661 PPFQCLHYRPPFPAVAIAANIIEHGFYKSRKVIYVVSQHTIQSFWCIFFEYIAQTWQFL 720
Db 706 PPFQCLHYRPPFPAVAIAANIIEHGFYKSRKVIYVVSQHTIQSFWCIFFEYIAQTWQFL 765
Qy 721 SSRAGIIFIVAKVEKTLRQOVELYRLSNRTYLEMDSVLRGRIEMRLKALLDQKS 780
Db 766 SSRAGIIFIVAKVEKTLRQOVELYRLSNRTYLEMDSVLRGRIEMRLKALLDQKS 825
Qy 781 WNPBGTVGTGCMQGEATSI 799
Db 826 WNPBGTVGTGCMQGEATSI 844

RESULT 2
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
; APPLICANT: Dalle, Barbara
; APPLICANT: Fan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tan, Jimmy C.
; APPLICANT: Zavadny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: J80601QC
; CURRENT APPLICATION NUMBER: US/09/982.308B
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,163
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-308B-23

Query Match 14.5%; Score 599.5; DB 4; Length 784;
Best Local Similarity 27.0%; Pred. No. 2.5e-46;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

Qy 8 IPDNLPSTKMLDSFNLRLHGSYSPFPELOVLDLSRCEIQIETGGAQVQSHSTL 67
Db 46 IPGSLTEAVKSLDJSNNRITTYISNDLORCVNLQALVLTJNGINTIEEDSPSSLSLEHL 105

Qy 68 ILTGNPIQSIALGAFSGLSLQKL-----VAVENTNLSENPIGHLKT----- 111
Db 106 DLSYNYLSNLSSSWFKPLSLTFLNLGNPKYKLTGRTSLFSHLTKQLLRGVNDMTFTKI 165
Qy 112 -----LKEANVAHNLQSFKLPEYPSNLTNLEHLDSSNK-----IQSI 150
Db 166 QKDPFAGVTFLEBELEIASDLSQSYE-PKSLKSIGNVSHLILMHQHILLEIFVDVTSV 224
Qy 151 YCTDLRVLHQPPLNLTLSDLSINPMNF--IQGAFKEIRLHKLTURN--NFDST-NVMK 204
Db 225 ECLER-----DIDLOTFHSELSGTSTNL-IKKTFPRVKTIDESLPQVMK 271
Qy 205 TC--IQGLAGLEVRLV---GEFRNEGULEKFPKALBGLCNLTIEFRLA--YLDYLT 257
Db 272 LMQISGLLELEFPDCTINGVGNFRASDNDRVIDPGKYE--TLTIRRLHPRFLFY-- 326
Qy 258 DDIIDFNCLTNVSSFSLVSTYIRVDFPSNPFQWQLELVNCKFGQFPFLKLSKRLT 317
Db 327 -DLSTLYSLTERVK-----RTVENSKV-----LVPCLLSQ----- 357
Qy 318 FTSNKGNAFSEVLPSELEFDLSRN-----GLSFKGCSCSQSDPGTTSLSKYLDLSFNGVI 372
Db 358 -----HUKSELYLDSENLMEBYLKNASC---EDAWESLQTLIRON--- 397
Qy 373 TWSNPFGLBQLEHLDFQHSNLKOMSEFVFLSLRNLIYLDISHHTRVAFNGIFNGLS 432
Db 398 -----HL-----ASLEKTGE--TLTLKNTLNIDISK----- 422
Qy 433 LEVLMKNGSFQENFLPDIETELRNLTFLDLSQCOLEOLS---PTAFNSLSLOVLMNSH 489
Db 423 -----NSFHS--MBETQWPEKMKYLNLSSTRHSVGCIP-----KTLIELVSN 466
Qy 490 N--NFSILD-----TFP--YKCLNSLOVLDVSLNHTMSKQOELHPPSSL 531
Db 467 NNLANLPSLNLPOLKELYISRNKMTLPDASLPLMLVLKISRNALITFSKQLODSF-HTL 525
Qy 532 AFLNLTONDPACTCEHOSFLOMIDQOLIVEV-----ERMECAPSPDQOGMPVLSLNT 586
Db 526 KTLBAGNNFFICSCEFLSTQ---EQALAKVLIDWPANYLCPSPHVGQOVQDVRLS 581
Qy 587 -----COMKTIIGVSVLSVVSVAVLVYKFF--FHLMLAGCIKYGR-----GENI-Y 634
Db 582 VSECHRIALVSGMCALFLLILGLVCHRHGIMYKMMWAMLOARPKPRKADSRNICY 641
Qy 635 DAFVYSSODEDWVRLVKNLEBGVPPFQCLHYRPPFPAVAIAANIIEHGFYKSRKVI 694
Db 642 DAFVYSERDAYWENLMQELBNPFPKCLHAKRFIPGKWIIDNI-DSEKSHKTV 700
Qy 695 VVSQHTIQSFWCIFFEYIAQTWQFLSSRAGIIFIVAKVEKTLRQO-VELYRLSNRT 753
Db 701 FVLSSENVKSEWCYEDFSHFRLEDDNDAAILILLEPIEKKAIPORFCKLRKIMWTY 760
Qy 754 YLEWEDSVLRGRIEMRLKRL 775
Db 761 YLEWPKDEAQREGFWNLRAAI 782

RESULT 3
US-08-514-014-4
; Sequence 4, Application US/08514014
; Patent No. 5707829
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
STREET: 87 Cambridgepark Drive
CITY: Cambridge

```

STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514,014
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-514-014-4

```

Query Match 14.2%; Score 590; DB 1; Length 661;

Best Local Similarity 29.3%; Pred. No. 1.4e-45;

Matches 191; Conservative 107; Mismatches 266; Indels 88; Gaps 23;

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3 INFYKIPNDLPSTKNDLDSNPRLHLSYSPFSPPELOVLDLSRCEIQTEDGAYQSL 62
42 LGLSIPPTLNTBTEFLSFNFPLTINRTFSRLMNTFLDTRCQINWHEDEFGQHH 101
63 HLSTLLTGNPIQSLALGAFSGLSLQKLVAVENTMLASLENPIGHLTKLELVANHLI 122
102 QLTSLVLTGNPLIFMAETSLNGPKSLKHLFLIQGISNLEFPVHNLELSTLYGSHI 161
123 QSPKLEFYFNSMLTNEHLDLSNKKIOSIYCTDLRYLHQMPLNLSLDSINPMNFIOGCA 182
162 SSIRKPKPFP-ARNLKLVDPQNNALHYISREDMSLEQ-AINLSLNFNGNNGKIEIGA 218
183 FKEIRLHLKTLRNNPDSINVMKTCIQGLAGLEVHRLVGEFRNEGNLEKFDKSALEGICN 242
219 FDSYTFQGL----NCGTGNLSVIFNGIQNSTQSLMTGTPEDDID-EDISSAMKGLCE 273
243 LTIEFRLAYLDYLDIID-LFNCLTNVSSFSIVSVIERVKDFSYNGQHLELVN-- 299
274 MSVESLNLQ--EHRSDISSTTFQCFQLOLDELDTATHLKGLPS-----GKGLMLLKKL 326
300 -----CKF--GQFPTL-----KLKSLKLTFTSNGGNAFSEVLDPSLEFDL 340
327 VLSVNHDPOLCOISANPPSLTHLYIRGVKKLHLGVGLEKLGK-----LQTLDL 377
341 SRNGLSFGCCSQSPFGTTSLSKYLDSFNGVITGSSN-FLGLEQEHDFQ----HSNLK 395
378 SHNDLEADDCGSLQKLNLSHLDQNLNLSHNEPGLGSOAFKECPQLLELDLATRHLINAP 437
396 QMSFSS--VPLSLRLYI--LDISHTTRVAFNGIFNGLSLEVLKMAANSFOENFL--P 449
438 Q-SFQNLHFLQVNLVTCFLDTSNQH-----LLAGLPVLRHNLKGNHFDQGITRKT 489
450 DIFTELRLUTFLDLSQCOLEQLSPFAFNSLSLQVLNNSHNF--SLDTPFY----- 500
490 NLLQTVGLSEVLISSCGSLSDQQAFLSHLGMGSHVDLSHNSLTCDSIDSLSLKGIYLN 549
501 KCLNSLOLVDSYSLNIMTSKQELQHPFSLAFNLNTQNDFACTGCEHGSFLQWIKDQRL 560
550 LAANSINISPRLLIL-----SQOSTINLSHNPDLCTCSNHLFLTWYKENLAK 598
561 LVEVERMECATPSDKQMPVLSLNTTCQNNKTIIGSVSVLSVIVSVAVLVY 612

```

DB 599 LEGSEETTCANPSSLRGVKSVDVLSGCI--TAIGIFLYVFL-LLAIIILF 647

RESULT 4

US-08-833-823-4

Sequence 4, Application US/08833823

Patent No. 5969093

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS

TITLE OF INVENTION: ENCODED THEREBY

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: Genetics Institute, Inc. -- Legal Affairs

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,823

FILING DATE: 10-APR-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/514,014

FILING DATE: 11-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G16000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 661 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-833-823-4

Query Match 14.2%; Score 590; DB 2; Length 661;

Best Local Similarity 29.3%; Pred. No. 1.4e-45;

Matches 191; Conservative 107; Mismatches 266; Indels 88; Gaps 23;

```

3 INFYKIPNDLPSTKNDLDSNPRLHLSYSPFSPPELOVLDLSRCEIQTEDGAYQSL 62
42 LGLSIPPTLNTBTEFLSFNFPLTINRTFSRLMNTFLDTRCQINWHEDEFGQHH 101
63 HLSTLLTGNPIQSLALGAFSGLSLQKLVAVENTMLASLENPIGHLTKLELVANHLI 122
102 QLTSLVLTGNPLIFMAETSLNGPKSLKHLFLIQGISNLEFPVHNLELSTLYGSHI 161
123 QSPKLEFYFNSMLTNEHLDLSNKKIOSIYCTDLRYLHQMPLNLSLDSINPMNFIOGCA 182
162 SSIRKPKPFP-ARNLKLVDPQNNALHYISREDMSLEQ-AINLSLNFNGNNGKIEIGA 218
183 FKEIRLHLKTLRNNPDSINVMKTCIQGLAGLEVHRLVGEFRNEGNLEKFDKSALEGICN 242
219 FDSYTFQGL----NCGTGNLSVIFNGIQNSTQSLMTGTPEDDID-EDISSAMKGLCE 273
243 LTIEFRLAYLDYLDIID-LFNCLTNVSSFSIVSVIERVKDFSYNGQHLELVN-- 299
274 MSVESLNLQ--EHRSDISSTTFQCFQLOLDELDTATHLKGLPS-----GKGLMLLKKL 326

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Qy 300 -----CKF--GQFPTL-----KLSLRKLTFTSNKGGNAVEVDLPSELFLDL 340
Db 327 VLSVNHFDQLCOISAANPPLTLHYIRGNVKKLHLGVGCLERLGN-----LQTLIDL 377
Qy 341 SRNLSPFGCCSQSDPFTSLKLYLDSPNGVITMSSN-FLGLBQLEHLDPQ-----HSLTK 395
Db 378 SHNDIEASDCCSLQKLNLSHLOTLNLSHNEBPLQSOAFKCPQLEGLDLAFTRLHINAP 437
Qy 396 QMSFSS--VPLSLNLTLY--LDISHTHTRVAFNGIFNGLSLEVLMKMGNSFOENFL--P 449
Db 438 Q-SFQONHFLQVANTLYCFDITSNQH-----LLABLPLYRLHNLKGNHFOGOTITKT 489
Qy 450 DIFTELRLNLTLDLSQCEQLSPFAPNSLSLOYLNHNNFF--SLDTFPY-----500
Db 490 NLQTVGSLLEVTLISSCGLSIDQAFHSLGKMSHVDSLHNSLTCDSIDSLHKGILYN 549
Qy 501 KCLNSLOVLDYSLNHHMSSKQELQHPSSLAFLNTQNDPACFCENHSPLOMKDQROL 560
Db 550 LAANSINILSPRLPIL-----SQOSTINLSHNPDLDCSCSNHFLTWYKENLAK 598
Qy 561 LVEVERECATPSDKQMPVLSLNTITCOMKTIIGVSVLVSVAVALVY 612
Db 599 LESEETTCCANPPLSRGVKLSVDKLSGCI--TALGIFPLVFL-LALILF 647

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RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

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Query Match 13.0%; Score 539; DB 4; Length 775;
Best Local Similarity 26.6%; Pred. No. 9.9e-41;
Matches 218; Conservative 120; Mismatches 264; Indels 218; Gaps 37;

Qy 8 IPDNLPESTKNLDSFNPRLHLSYSFFSPPELOVLDLSRCEIQTIEDGAYQSLSHL 67
Db 81 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSGINTIIEBDSFSSLSLEHL 140
Qy 68 ILTGNPIQSIALGAFSGLSLOKL-----VAVENTIASLSENFPIGHKT-----111
Db 141 DLSYVLSNLSNNWKPPLSLTFLNLGLNPKYTLGETSYLFSHLTYLQILRVGNMDTFPTKI 200
Qy 112 -----LKEINVAHNLIQSFCLPEYFNSLNTLBEHLDSNNK-----10SI 150
Db 201 QKQFAGLTFLBELEIDSQSYE-PRSLKSIQVSHLILHMKQHILLEIPVDVSSV 259
Qy 151 YCTDLRVLHQPLNLNLSDLSLNPWF--IQGAFKEIRLHKLTIRN--NFDLI-NVWK 204
Db 260 ECLERL-----DTLDLDFHFELESTGETNSL-IKKFTFRNXYITDESIFQYMK 306
Qy 205 TC--IQGLAGLEVHRLV--GEPRNEGLKFPKSALEGONLTIEFRLLA--YLQVYL 257
Db 307 LNLQISGLLELPDDCTLVGNFPRASDNDRVIDPGKVE--TLTIRLHLIPRYLFY-- 361

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Qy 258 DDIIDLFCILTNVSSFSLSVSTIERVDFSYNFGMOHLELVNCKFGQPTTLKLSRLT 317
Db 362 -DLSTLYSLTERVK-----RITVENSXVF-----LVPCLLSQ-----392
Qy 318 FTSNKGNAASEVDLPSELFLDSRN-----GLSFKCCSQSDPFTSLKLYLDSPNGVI 372
Db 393 -----HLKSLVYLDISENLMVEEYLNKNSC--EDAWPSLQTLILRON--432
Qy 373 TMSNFIQLBQLEHLDPQHSNLKQMSSESVFLSLRNLYDLSHTHTRVAFNGIFNGLS 432
Db 433 -----HL-----ASLEKTB--TLTYLKNLTNIDISK-----457
Qy 433 LEVLKMGNSFOENFLPDIPTTELRLNLTLDLSQCEQLS-----PTAFNSLSLOYLNHNSH 489
Db 458 -----NSFHS--METQWPEKMKYLNLSSTRHSVTCGP-----KTLIELDVSN 501
Qy 490 N--NFSGLD-----TFP-YCLNSLOVLDYSLNHHMSSKQELQHPSSSL 531
Db 502 NNLNLFSLNLPOLKELYISRNKLTMLTPDASLLPMLVLKISRNAVITTFSEKLOLDSF-HTL 560
Qy 532 AFLNLTQNDPACFCENHSPLOMKDQROLVEV-----ERMECATPSDKQMPVLSLNTIT 586
Db 561 KTLBAGGNFTCSCEFLSFTQ---EQALAKVLDMPANYLCDSPSHRGQOVQDVRLS 616
Qy 587 ---COMKTIIGVSVLVSVAVALVYKRY--FILMLAGCIXGR-----GENI-Y 634
Db 617 VSECHRALVSGMCCALFLLILTLGVLCRPHGLMWKMMAMVLAQRKRKAPSRNICY 676
Qy 635 DAFVYSSQEDWRYNRLVKNLEBGVPPQCLHYRPFITGVAILNIHGFHKSRYI 694
Db 677 DAFVYSERAYWYENIMVLELBNFPPLCLHKKRPFIGKWIIDNI-DSEIKSRKY 735
Qy 695 VVWSQHFIOGRWCIFEYEIAQTWQFSSRAGIIFIVQKV 734
Db 736 FVLSNFVKSBCXELDFSHFLFDENNAIILILEPT 775

```

```

RESULT 6
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LNSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-09-063-950-5

```

```

Query Match 7.5%; Score 309; DB 3; Length 605;
Best Local Similarity 24.5%; Pred. No. 1.4e-19;
Matches 155; Conservative 92; Mismatches 225; Indels 150; Gaps 23;

Qy 4 NFYKIPDNLPESTKNLDSFNPRLHLSYSFFSPPELOVLDLSRCEIQTIEDGAYQSLSH 63
Db 64 NLTRLPDQIFQGTALWLDNSNNLSIPPAFRNLSLAFNLQCGQGLSEPQALGLEN 123
Qy 64 LSTIILTGNPIQSIALGAFS-----GLSSLOKLVAVENTRLA 99
Db 124 LCHLHIERNOJRLSLAVGTFAVTPALALLGSSNNRSLBEDGLPEGLGNLMDLNLGNSLA 183
Qy 100 SLENFPIGHKTLKEINVAHNLIQSFCLPEYFNSLNTLBEHLDSNNKSIQSYCTDLRVLH 159
Db 184 VLPDAAFRGGIGLRELVLAGNRL-AYLQPALFSGLABELRLDLSRNALRAL--KANVFA 239

```

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QY 160 QMPLNLSTLSDSLNPMNFIOGAFKEIR-LHKLTIRNPFDSLNVKTKCIQGLAGLEVRL 218
DB 240 QLPRLQ-KLYIDRNLIAAVAPGAFGLKALRWLDSHN-RVAGLLEDFPGILGRVRL 297
QY 219 VLGEFRNEGNLEKEDKSALEGLCNLTIEFRFLAYDYLDIIDLFCNLTWVSFSLVS 278
DB 298 -----SHNAIASLRPTFKDL-----HLEEL-----QLGHN 324
QY 279 TIEVKDFSYNFGMOHLELVNCKFGQFPPTLKLSKRLTFTS--NKGNAFSEVDLPSE 336
DB 325 RIQLAERSFE-GIGOLEVLTLDNQLOEVKAGFLGLTNVAVMNLSCNCR--NLPRQV 381
QY 337 FLDSR-NGLSFKGCC-----SQSDFGTSLKYLDLSNGVITMSSNPL-GLBQLEHLD 389
DB 382 FRGKGLSHLHESCGIRIRPHFAGISGRRLFLKONGVGIEQSLGIAELHLEIDL 441
QY 390 QHNLKQMSSEFVLSLNLTYLDISHHTVAFNGIFNGLSLEVLMAQNSFOENFLP 449
DB 442 TSNQL-----THLP--HQLFQGLKLEYLLSHRLAE--LP 474
QY 450 -DIFTELRLTLFDLSQCLEQLSPTAFNSLSLQVLNMSHNFPSLDTFPHYKCLNSIQV 508
DB 475 ADALGPQRAFWLDSVSHNRLEALPNSLALSGRLRYLNRN---SLRTFTPQ----- 524
QY 509 LDYSLNHMTSKQELQHPSSLAFLNLTQNDFACTCEHQS-----FLOWI 554
DB 525 -----PGLERLWLEGNPMDCSCLKALRDFALQNPASVPRFQAI 565
QY 555 ---KDORQLVEVERMECATPSDKQMPVLSL 583
DB 566 CEGDDCQPPVTTYNNITCASPEVAVGLDRL 597

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RESULT 7

```

US-08-190-802A-49
; Sequence 49, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190, 802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO

```

```

; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
; US-08-190-802A-49

```

```

Query Match 7.2%; Score 297; DB 1; Length 605;
Best Local Similarity 24.4%; Pred. No. 1.8e-18;
Matches 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;

```

```

QY 4 NFYKIPDNLPSTKNLDSFNPPLHLSYSFSPSELOVLDLSRCEIOTIEDGAYQSLSH 63
DB 64 NLTRLPQGVPGGTQALWLDGNNLSVPPAARQNSLSGLFNLQGGQSLSPQALGLLEN 123
QY 64 LSTLLGNPQISDALGAFS-----GLSSTLOKLVAVETNIA 99
DB 124 LCHLHLENNQARSALATGFAATPALASISLNNRSLRLEDGLFEGLSLMDNLGMSLA 183
QY 100 SLENPPIGHLKTYLELVANHLIQSFKLPEYFSNLTMLEHLDSNKKIQSIYCTDLRYLH 159
DB 184 VLPPAARFGISLRELVLAGNRL-AYLOPALFSGIAELREBIDLSRNALRAI---KANFV 239
QY 160 QMPLNLSTLSDSLNPMNFIOGAFKEIR-LHKLTIRNPFDSLNVKTKCIQGLAGLEVRL 218
DB 240 QLPRLQ-KLYIDRNLIAAVAPGAFGLKALRWLDSHN-RVAGLLEDFPGILGRVRL 297
QY 219 VLGEFRNEGNLEKEDKSALEGLCNLTIEFRFLAYDYLDIIDLFCNLTWVSFSLVS 278
DB 298 -----SHNAIASLRPTFKDL-----HLEEL-----QLGHN 324
QY 279 TIEVKDFSYNFGMOHLELVNCKFGQFPPTLKLSKRLTFTS--NKGNAFSEVDLPSE 336
DB 325 RIQLAERSFE-GIGOLEVLTLDNQLOEVKAGFLGLTNVAVMNLSCNCR--NLPRQV 381
QY 337 FLDSR-NGLSFKGCC-----SQSDFGTSLKYLDLSNGVITMSSNPL-GLBQLEHLD 389
DB 382 FRGKGLSHLHESCGIRIRPHFAGISGRRLFLKONGVGIEBOSLWGLAELEIDL 441
QY 390 QHNLKQMSSEFVLSLNLTYLDISHHTVAFNGIFNGLSLEVLMAQNSFOENFLP 449
DB 442 TSNQL-----THLP--HRLFQGLKLEYLLSHRLAE--LP 474
QY 450 -DIFTELRLTLFDLSQCLEQLSPTAFNSLSLQVLNMSHNFPSLDTFPHYKCLNSIQV 508
DB 475 ADALGPQRAFWLDSVSHNRLEALPNSLALSGRLRYLNRN---SLRTFTPQ----- 524
QY 509 LDYSLNHMTSKQELQHPSSLAFLNLTQNDFACTCEHQSFLOWID-----ORQ 559
DB 525 -----PGLERLWLEGNPMDCP---LXALRDFALQNPASVPRF 561
QY 560 LVEVERMECATPSDKQMPVLSLNTCCOMNKTIIIGSV 598
DB 562 VQALCEGDDCQPPVTTYNNITCASPEVAVGLD 594

```

RESULT 8

```

US-08-477-346-49
; Sequence 49, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:

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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/477,346
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/487,072
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MURASHIGE, KATE H.
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 2550-0025.20
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-0763
/ TELEFAX: (202) 887-0763
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 605 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: Insulin-like growth factor binding
/ protein complex, Fig. 32
/ US-08-477-346-49
```

Query Match 7.2%; Score 297; DB 3; Length 605;

Best Local Similarity 24.4%; Pred. No. 1.8e-18;

Matches 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;

```
QY 4 NFYKIPNLPSTKNLDSFNPLRHLSYSFSPPELQVLDLSRCETQITDGA YQSLSH 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 NLRLPGVGGGTQALWLDGNNLSVPPAFQNLSSIGFNLQGGQSGSLPPQALLGLE 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 LSTLILGNPIQSIALGAFS-----GLSLQKLVAVETNLA 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 LCHHLERNQRLSLALGTFAHTPALASIGLNNRLSRLEDGLFEGLSLMDLNGMSLA 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 100 SLENFPIGHLKTLELVANHLIOSFKLPEYFSNLTNLEHLDLSNNKIOSIYCTDL 159
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 VLPDAFRGSGSLRELVLAGNRL-AYLQPALFSGLAELREIDLSRNALRAI---KAN 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 160 QMPILNLSLDSLNPNMFIOGAFKEIR-LHKLTIRNPFSLNMMKTCIOGLAGLEV 218
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 240 QLPRLQ-KLYLDRNLIAVAPGAFGLKALRWLDLSHN-RVAGLLEDTFPGLGLRV 297
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 219 VLGEFRNEGNLEKFDKSLBGLCNLTIEEFLAVLDYLDIIDLFNCLTNVSSFSI 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 298 -----SHNAISLRPRTRKDL-----HFLBEL-----QLGHN 324
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 279 TIERVKDSYVNGQHLVELVNCCKFGQPTTLKLSIKELTPTS--NKGNAFSEVDP 336
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 325 RIRQLARSTF-GLGQLEVLTLDNHQLEVYKAGAFGLITVAVMNLGSCNCLR-- 381
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 337 FLIDLSR-NGLSFKCC-----SQSDFGTSLSKTYDLSNGVYTMSSNFL-GL 389
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 382 FRIGKLSHLSLESGCGIRIRPHTFTGSGRLRLFLDNKGVLVGEOSLWGLAELE 441
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 390 QHSLNKMSEFSVLSRLNIYLDISHTHTVANGIFNGLSLSLEVLMAGNSQENFL 449
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 442 TSNOL-----THLP--HRLFGGKLEVLILSLNRLAE--LP 474
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 450 -DIFTELRLNLTFLDLSOCQLEQSLPTAFNSLSLVNMSHNPFSLDTPFYKCI 508
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 475 ADALGPIQRAFWLVDVSHNRLEALPNSLLAPLGRRLRYLSLRNN---SLRT 524
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 509 LDYSLNHNIMTSKQELQHPSSSLAFLNLTQNDFACTEHOSEFLQWIID----- 559
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
DB 525 -----PPGLERLWLBGNPMDCCP-----LKALRDFAQNBSAVRPF 561
QY 560 LVAVERMECATPSDKQGMVPLSLNTCCQNNKTIIGSV 598
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 562 VQALCEGDDCCQPAYTYN-----NITCASPPPEVVGIDL 594
```

RESULT 9

US-08-473-089-49

Sequence 49, Application US/08473089

Patent No. 6342368

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,089

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.22

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 605 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHEICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Insulin-like growth factor binding

protein complex, Fig. 32

INDIVIDUAL ISOLATE: Insulin-like growth factor binding

protein complex, Fig. 32

US-08-473-089-49

Query Match 7.2%; Score 297; DB 3; Length 605;

Best Local Similarity 24.4%; Pred. No. 1.8e-18;

Matches 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;

```
QY 4 NFYKIPNLPSTKNLDSFNPLRHLSYSFSPPELQVLDLSRCETQITDGA YQSLSH 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 NLRLPGVGGGTQALWLDGNNLSVPPAFQNLSSIGFNLQGGQSGSLPPQALLGLE 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 LSTLILGNPIQSIALGAFS-----GLSLQKLVAVETNLA 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 LCHHLERNQRLSLALGTFAHTPALASIGLNNRLSRLEDGLFEGLSLMDLNGMSLA 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 100 SLENFPIGHLKTLELVANHLIOSFKLPEYFSNLTNLEHLDLSNNKIOSIYCTDL 159
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 VLPDAFRGSGSLRELVLAGNRL-AYLQPALFSGLAELREIDLSRNALRAI---KAN 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 160 QMPILNLSLDSLNPNMFIOGAFKEIR-LHKLTIRNPFSLNMMKTCIOGLAGLEV 218
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 240 QLPRLQ-KLYLDRNLIAVAPGAFGLKALRWLDLSHN-RVAGLLEDTFPGLGLRV 297
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```


QY 219 VLGERNNEGNEKPDKSLAEGICNLTIEFRFLAYIDYLDIIDLFNCLTNVSSFLSV 278
Db 298 -----SHNAIASLRPTFKDL-----HFLEEL-----QLGHN 324
QY 279 TIERKDFSYNFGMCHLELVNCKFGQFPPLKLSIKRLTFTS--NKGNAFSEVDLPGLE 336
Db 325 RIQLAERSFE-GIGQLEVLTLIDHNOLOEVKAGAFGLITVAVMNLSCNCR--NLPRQV 381
QY 337 FLIDLSR-NGLSFKGCC-----SQSDFGTSLKYLDLSFNGVITWSSNFL-GLEQLEHLP 389
Db 382 FRGGLKLSHLHESGCLIRIRPHFTGSLGRRLFLKONGLVGIEQGLMGLAELEIDL 441
QY 390 QHSNKKQMSERSVFLSLNLYLIDSHHTTRVANGINGSLSEVLKMAQNSFOENLP 449
Db 442 TSNQL-----THLP-----HRLFOGLKLEYLLSRRLAE--LP 474
QY 450 -DIFTELNLTLFLDLSQCOLRSLPTAFNSLSLOVLMNSHNPFSLDTPPYKCLNSLOV 508
Db 475 ADALGPLORAFWLDVSHNRLEALPNSLLAPLGRRLYLSLRNN--SLATFTTQ----- 524
QY 509 LDYSLNHTSKKQELQHPPSLAFNLTONDFACTCEHOSFLQWIKD-----ORQ 559
Db 525 -----PGLERLWLEGNPMDGCP-----LKALRDPALQNPASVPRF 561
QY 560 LLIIVERNECATPSDKQMPVLSLNTQCMKTIIGVSU 598
Db 562 VQAICEGDDCQPPAYTN-----NITCASPEVVGLDL 594

RESULT 10
US-08-487-072A-49
Sequence 49, Application US/08487072A
Patent No. 6423684

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theorof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32

US-08-487-072A-49
Query/Match 7.2%; Score 297; DB 4; Length 605;
Best Local Similarity 24.4%; Pred. No. 1.8e-18;
Matches 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;

QY 4 NFYKIPDNLPPSTYKNDLSFNPPLRLGYSFSPPELOVLDLSREIOTIEDGAYQASH 63
Db 64 NLTRLPDVPQGTQALWIDGNLSSVPPARQNLISGLFNLQGGQLSLPEQALLGLEN 123
QY 64 LSTLILTNPIQSIALGAFS-----GLSLQKLVAVETNIA 99
Db 124 LCHLHLERNQRLSLALGTFTATPALASIGLNNRSLRLEDGLFEGLSLMDLNGNSIA 183
QY 100 SIENPPIGLKTLKELVANAHLIOSFKLPEYFSNLTNLEHLDLSNKTQSIYCTDLRYLH 159
Db 184 VLPPDAFRGLSLRELVLVAGNRL--AYLOPALFSGLAELRELDLSNNALRAI--KANFV 239
QY 160 QPPLNLSLDLSLNPANFIQGAKEIR-LHKLTLRNNPDSLNWKTCTQGLAGLEVHRL 218
Db 240 QLPRLQ-KLYIDRNLIAVAAGAFGLKALRWLDLSHN-RVAGLEDETFPPGLGRVRL 297
QY 219 VLGERNNEGNEKPDKSLAEGICNLTIEFRFLAYIDYLDIIDLFNCLTNVSSFLSV 278
Db 298 -----SHNAIASLRPTFKDL-----HFLEEL-----QLGHN 324
QY 279 TIERKDFSYNFGMCHLELVNCKFGQFPPLKLSIKRLTFTS--NKGNAFSEVDLPGLE 336
Db 325 RIQLAERSFE-GIGQLEVLTLIDHNOLOEVKAGAFGLITVAVMNLSCNCR--NLPRQV 381
QY 337 FLIDLSR-NGLSFKGCC-----SQSDFGTSLKYLDLSFNGVITWSSNFL-GLEQLEHLP 389
Db 382 FRGGLKLSHLHESGCLIRIRPHFTGSLGRRLFLKONGLVGIEQGLMGLAELEIDL 441
QY 390 QHSNKKQMSERSVFLSLNLYLIDSHHTTRVANGINGSLSEVLKMAQNSFOENLP 449
Db 442 TSNQL-----THLP-----HRLFOGLKLEYLLSRRLAE--LP 474
QY 450 -DIFTELNLTLFLDLSQCOLRSLPTAFNSLSLOVLMNSHNPFSLDTPPYKCLNSLOV 508
Db 475 ADALGPLORAFWLDVSHNRLEALPNSLLAPLGRRLYLSLRNN--SLATFTTQ----- 524
QY 509 LDYSLNHTSKKQELQHPPSLAFNLTONDFACTCEHOSFLQWIKD-----ORQ 559
Db 525 -----PGLERLWLEGNPMDGCP-----LKALRDPALQNPASVPRF 561
QY 560 LLIIVERNECATPSDKQMPVLSLNTQCMKTIIGVSU 598
Db 562 VQAICEGDDCQPPAYTN-----NITCASPEVVGLDL 594

RESULT 11
US-09-538-092-1087
Sequence 1087, Application US/09538092
Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Manefield, Traci A.
APPLICANT: Giot, Loic
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratSeqFormatter Version 0.9
SEQ ID NO 1087
LENGTH: 605
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087

Query Match 7.2% Score 297; DB 4; Length 605;

Best Local Similarity 24.4%; Pred. No. 1.8e-18; Mismatches 240; Indels 152; Gaps 24;

Matches 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;

QY 4 NFYKIPDNLPSTKNDLSFNPDLRHLSGSYSPFPELOVDLSRCEIQTIEDGAYQSLSH 63
D 4 NTRLPDGVPGTQALWDGNNLSVPPAQNLSLGFNLQGGQSLSPQALLGLEN 123
QY 64 LSTLILGNPIQSIALGAFS-----GLSSIQKLVAVETNLA 99
D 124 LCHHLERNQRLSLATGFATTPALASLGSNNRLSLREDDLFEGISLMDNLNGMSLSA 183
QY 100 SLENPIGHLKTKELVAVANHLIOSFKLPEYFSNLTNLEHLDLSNKKIOSIYCTDLRYLH 159
D 184 VLPDAFRGSLRELVLAGNRL-AYLPALFSGLAELRELDLSRNALRAI---KANFV 239
QY 160 QMPLNLISLDSLNPMNFIQGAFAKEIR-LHKLTLRNPFDSLANKTCIOGLAGLEVRL 218
D 240 QLPRLQ-KLYIDRNLIAVAPGALGKALRWLDSHN-RVAGLEDTFFGLGLRVRL 297
QY 219 VLGEFRNEGNIKEPKSALBGLCNLTIEPRLAYLDYLDIIDLFNCLTNVSSFSIVSV 278
D 298 -----SHNAIASLRPTFKDL-----HFLEEL-----QLGHN 324
QY 279 TIERVKDPSYVFGQHLKELVAVANHLIOSFKLPEYFSNLTNLEHLDLSNKKIOSIYCTDLRYLH 336
D 325 RIRQLAERSFE-GIGQLEVLTLDNQLOEVYAGAFGLITVAVMNLGNCILR--NLPEQV 381
QY 337 FLIDLSR-NGLSFKGCC-----SOSDFGTSIKYLDLSFNGVITWSSNPL-GLBQLEHLD 389
D 382 FRGIGKLSHLBESSCLGRIRPHFTGSLGRILFLKONGLVGIEGSLWGLAELEIDL 441
QY 390 QHSNLIKQMSERSVFLSLRNLYLDISHTHTVAVENGIFNGLSLEVLKMAGNSFOENFLP 449
D 442 TSNQL-----THLP---HRLFGIGKLEVYLLSNRLAE--LP 474
QY 450 -DITTELRLNLTFLDLSQCEQLSPFLAFNSLSLOVLMGSHNPFSLDTPPYKCLNSIQV 508
D 475 ADALGPLQRAFWLDVSHNRLEALPNSILAPLGRIRYLSLRNN--SLRTFPQ----- 524
QY 509 LDVSLNIMTSKQELQHPFSSLAFLNLTQNDFACTCEHOSFLOMIXD-----QRQ 559
D 525 -----PPGLERLWLBGNPMDGCP-----LKAALDFALQNPASVPRF 561
QY 560 LLAVERMECATPSDKQGMVPLSLNITCQANKTIIGVSV 598
D 562 VQATCEGDDCQPPAYTYN-----NITCASPPEVVGDL 594

RESULT 12

US-09-949-016-10995
; Sequence 10995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10995
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10995

Query Match 7.2% Score 297; DB 4; Length 623;

Best Local Similarity 24.4%; Pred. No. 1.9e-18; Mismatches 240; Indels 152; Gaps 24;

Matches 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;

QY 4 NFYKIPDNLPSTKNDLSFNPDLRHLSGSYSPFPELOVDLSRCEIQTIEDGAYQSLSH 63
D 82 NTRLPDGVPGTQALWDGNNLSVPPAQNLSLGFNLQGGQSLSPQALLGLEN 141
QY 64 LSTLILGNPIQSIALGAFS-----GLSSIQKLVAVETNLA 99
D 142 LCHHLERNQRLSLATGFATTPALASLGSNNRLSLREDDLFEGISLMDNLNGMSLSA 201
QY 100 SLENPIGHLKTKELVAVANHLIOSFKLPEYFSNLTNLEHLDLSNKKIOSIYCTDLRYLH 159
D 202 VLPDAFRGSLRELVLAGNRL-AYLPALFSGLAELRELDLSRNALRAI---KANFV 257
QY 160 QMPLNLISLDSLNPMNFIQGAFAKEIR-LHKLTLRNPFDSLANKTCIOGLAGLEVRL 218
D 258 QLPRLQ-KLYIDRNLIAVAPGALGKALRWLDSHN-RVAGLEDTFFGLGLRVRL 315
QY 219 VLGEFRNEGNIKEPKSALBGLCNLTIEPRLAYLDYLDIIDLFNCLTNVSSFSIVSV 278
D 316 -----SHNAIASLRPTFKDL-----HFLEEL-----QLGHN 342
QY 279 TIERVKDPSYVFGQHLKELVAVANHLIOSFKLPEYFSNLTNLEHLDLSNKKIOSIYCTDLRYLH 336
D 343 RIRQLAERSFE-GIGQLEVLTLDNQLOEVYAGAFGLITVAVMNLGNCILR--NLPEQV 399
QY 337 FLIDLSR-NGLSFKGCC-----SOSDFGTSIKYLDLSFNGVITWSSNPL-GLBQLEHLD 389
D 400 FRGIGKLSHLBESSCLGRIRPHFTGSLGRILFLKONGLVGIEGSLWGLAELEIDL 459
QY 390 QHSNLIKQMSERSVFLSLRNLYLDISHTHTVAVENGIFNGLSLEVLKMAGNSFOENFLP 449
D 460 TSNQL-----THLP---HRLFGIGKLEVYLLSNRLAE--LP 492
QY 450 -DITTELRLNLTFLDLSQCEQLSPFLAFNSLSLOVLMGSHNPFSLDTPPYKCLNSIQV 508
D 493 ADALGPLQRAFWLDVSHNRLEALPNSILAPLGRIRYLSLRNN--SLRTFPQ----- 542
QY 509 LDVSLNIMTSKQELQHPFSSLAFLNLTQNDFACTCEHOSFLOMIXD-----QRQ 559
D 543 -----PPGLERLWLBGNPMDGCP-----LKAALDFALQNPASVPRF 579
QY 560 LLAVERMECATPSDKQGMVPLSLNITCQANKTIIGVSV 598
D 580 VQATCEGDDCQPPAYTYN-----NITCASPPEVVGDL 612

RESULT 13

US-08-190-802A-50
; Sequence 50, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Kon, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:

QY 220 -----IGERR-NEGNIKEPKXALBGLCNTIEEPRLAYDYLDI- 260
Db 299 HNAIASLRPTFKDLHFLEELQIGHNRIROGERTFEGQLQEV---LTINDQITEVR 354
QY 261 IDLFNCITNVSSFSLVSVTI---ERV---KDFSYNFGMOHLELVNCKFGPPTLKLSL 313
Db 355 VGAFSGLFNVAVMNLSGNCISLRPERVFGQDKHLSLHESCLGHVRLHTF--AGLSGL 412
QY 314 KRLTFTSNKGNNAFSEVD-----LPSEFLDLSHNGLSFKGCCSQSDFGTTSLSKYLDLS 367
Db 413 RRLFLRD---NSISIEQSLAGLSLELDLTNNRLTH--LPRQLFGQGHLEYLLLS 466
QY 368 FNGVITMSSNPLGLEQLHEDPQHSNKKOMSEFSVFLSKRLIYDISHTRVAFNGIF 427
Db 467 YNQLTTLSAEVLG-----PLQRAFWLDSHNLLETLAGELF 502
QY 428 NGLSLEVLKMGANSFOENFLPDIFTELRLNLTFLDLSQCOLEQSLPTAFNSLSLSQVLNM 487
Db 503 SSLGRVYLSLRNNSLQ--TFSP-----QPLERL----- 530
QY 488 SHNNFSLDTPPYKCLNSLOVL-DYSLNHMTSKKQELQHPSSLAFLNLTONDFACTCE 546
Db 531 -----WLDANPWCSCPLKALRDFALQ-----PGVPRFVQT-----VCE 566
QY 547 HQSFLQWIKDQROLLEVERMECATPSDKQGMVLSLNTIT 586
Db 567 -----GDDCQPVYTYNNITCAGPANVSGLDLDVSET 598

RESULT 15

US-08-473-089-50
Sequence 50, Application US/08473089

Patent No. 6342368

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OF INVENTION: Thee of

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,089

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.22

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 603 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Insulin-like growth factor bind.

US-08-473-089-50

Query Match

Best Local Similarity 24.1%, Pred. No. 7.8e-18;

Matches 154; Conservative 84; Mismatches 240; Indels 162; Gaps 24;

QY 4 NFYIIPDNLPPSTYNLDLSNPLRLHLSYSFSSFPPELQVLDLSCEIQTIEDGAYQSLSH 63
Db 64 NLTHLPDIPVSTRALWDGNNLSISPAAFOQNLSLDPLNTQSWRLSEPPQALLGION 123
QY 64 LSTLIILGNPISALAFSGLSLQKLVAVENTLASLENPIGHLTKIELNVA----- 118
Db 124 LYTHLEBRRLKRLNVAAGLFTTPSLASLSNLLGRLBGLFGCLSHLMDNLGMNSLV 183
QY 119 -----HNL-----QSFKLPEYFNLTNLEHLDSNKKIOSIYCTDLRYLVHQ 160
Db 184 VLPRTVFGQGNLHLEVLNAGKLTLYLQPALFCGELRELDLSNALSRSV---KANNFVH 240
QY 161 MFLNLSLDLSLNPWNFIQGAPEIR-LHKLTLRNPFSLNWKTCIOGIALGVEHRLV 219
Db 241 LPRLO-KLYIDRLNLTAVAGAFGMKALRWLDLSH-RVAGLMEDTFPGILGHVRLA 298
QY 220 -----IGERR-NEGNIKEPKXALBGLCNTIEEPRLAYDYLDI- 260
Db 299 HNAIASLRPTFKDLHFLEELQIGHNRIROGERTFEGQLQEV---LTINDQITEVR 354
QY 261 IDLFNCITNVSSFSLVSVTI---ERV---KDFSYNFGMOHLELVNCKFGPPTLKLSL 313
Db 355 VGAFSGLFNVAVMNLSGNCISLRPERVFGQDKHLSLHESCLGHVRLHTF--AGLSGL 412
QY 314 KRLTFTSNKGNNAFSEVD-----LPSEFLDLSHNGLSFKGCCSQSDFGTTSLSKYLDLS 367
Db 413 RRLFLRD---NSISIEQSLAGLSLELDLTNNRLTH--LPRQLFGQGHLEYLLLS 466
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Search completed: March 12, 2005, 19:58:59
Job time : 32.9643 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:55:29 ; Search time 70.7097 Seconds

(without alignments)
3727.157 Million cell updates/sec

Title: US-09-396-985B-4

Perfect score: 4141
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4141	100.0	799	14	US-10-128-166-7 Sequence 7, Appl1
3	4141	100.0	799	16	US-10-732-563-8 Sequence 8, Appl1
4	4141	100.0	799	16	US-10-732-796A-8 Sequence 8, Appl1
5	4141	100.0	837	10	US-09-950-041-26 Sequence 26, Appl1
6	625.5	15.1	661	15	US-10-038-854-135 Sequence 135, Appl1
7	625.5	15.1	661	15	US-10-037-417-107 Sequence 107, Appl1
8	603.5	14.6	784	10	US-09-950-041-4 Sequence 4, Appl1
9	603.5	14.6	784	15	US-10-456-947-46 Sequence 46, Appl1
10	602.5	14.5	784	14	US-10-095-627-12 Sequence 12, Appl1
11	602.5	14.5	784	16	US-10-732-563-4 Sequence 4, Appl1
12	602.5	14.5	784	16	US-10-732-796A-4 Sequence 4, Appl1
13	602.5	14.5	784	17	US-10-741-600-1390 Sequence 1390, Appl1

14	602.5	14.5	784	17	US-10-741-600-1391 Sequence 1391, Appl1
15	599.5	14.5	784	13	US-10-145-014-23 Sequence 23, Appl1
16	590	14.2	661	13	US-10-114-893-10 Sequence 10, Appl1
17	590	14.2	661	15	US-10-038-854-134 Sequence 134, Appl1
18	573	13.8	1032	10	US-09-954-987B-192 Sequence 192, Appl1
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ALIGNMENTS

RESULT 1
US-09-950-041-8
Sequence 8, Application US/09950041
Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kaszelen, Robert A.
APPLICANT: Ho, Stephen W.K.
APPLICANT: Liu, Yong-Jun
TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REFERENCE: DX0724XK1
CURRENT APPLICATION NUMBER: US/09/950,041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293
PRIOR FILING DATE: 1997-05-07
PRIOR APPLICATION NUMBER: 60/072,212
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 60/076,947
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 799
TYPE: PRT
ORGANISM: Homo sapiens
US-09-950-041-8
Query Match 100.0%, Score 4141, DB 10, Length 799;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 7, Application US/10128166
; Publication No. US2003007279A1
; GENERAL INFORMATION:
; APPLICANT: ARDITI, MOSHE
; APPLICANT: RAUVASHITSH, TRIPATHI
; APPLICANT: SHAH, PREMIMAN K.
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
; TITLE OF INVENTION: TOLL-LIKE RECEPTOR-4
; FILE REFERENCE: 81476-0255398
; CURRENT APPLICATION NUMBER: US/10/128,166
; CURRENT FILING DATE: 2002-04-23
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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 7
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-166-7

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
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; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 581830003
; CURRENT APPLICATION NUMBER: US/10/732,563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-563-8

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Db 781 WNPBGTGTGCMQDEATSI 799

RESULT 4
US-10-732-796a-8
; Sequence 8, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732,796A
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-796a-8

Query Match      100.0%; Score 4141; DB 16; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 661 PPQCLCHYRDPFIPGVAIAAANIHEGFHKSARKVIVVVSQHFIQSRMCIFEEYIAQTWQFL 720
Qy 721 SSRAGIIFIVLQKVEKTLRQOVELYRLSRNTYLEMEDSVLGRIHFWRLRKALLDGS 780
Db 721 SSRAGIIFIVLQKVEKTLRQOVELYRLSRNTYLEMEDSVLGRIHFWRLRKALLDGS 780
Qy 781 WNPBGTVGTGCMWQEAISI 799
Db 781 WNPBGTVGTGCMWQEAISI 799

RESULT 5
US-09-950-041-26
/ Sequence 26, Application US/09950041
/ Publication No. US20030032090A1
/ GENERAL INFORMATION:
/ APPLICANT: Hardiman, Gerard T.
/ APPLICANT: Rock, Fernando L.
/ APPLICANT: Bazan, J. Fernando
/ APPLICANT: Kaestlein, Robert A.
/ APPLICANT: Ho, Stephen W.K.
/ APPLICANT: Liu, Yong-Jun
/ TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
/ FILE REFERENCE: DX0724XK1
/ CURRENT APPLICATION NUMBER: US/09/950,041
/ CURRENT FILING DATE: 2002-05-06
/ PRIOR APPLICATION NUMBER: 09/728,540
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: 60/207,558
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 09/073,363
/ PRIOR FILING DATE: 1999-06-05
/ PRIOR APPLICATION NUMBER: 60/044,293
/ PRIOR FILING DATE: 1997-05-07
/ PRIOR APPLICATION NUMBER: 60/072,212
/ PRIOR FILING DATE: 1998-01-22
/ PRIOR APPLICATION NUMBER: 60/076,947
/ PRIOR FILING DATE: 1998-03-05
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 26
/ LENGTH: 837
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-950-041-26

Query Match 100.0%; Score 4141; DB 10; Length 837;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MELNFYKIPDNLPESTKNLDSLSPNPLRLHLSYSFFSPPELOVLDLSRCEIOTIEDGAYOS 60
Db 39 MELNFYKIPDNLPESTKNLDSLSPNPLRLHLSYSFFSPPELOVLDLSRCEIOTIEDGAYOS 98
Qy 61 LSHSLTILITGNPIQSLALGAFSGLSISQKLVAVETNIASLENPIGHLKTLKEINVAHN 120
Db 99 LSHSLTILITGNPIQSLALGAFSGLSISQKLVAVETNIASLENPIGHLKTLKEINVAHN 158
Qy 121 LIQSFKLPEYPSNLTNLEHLDLSNKTOSTYCTDLRVHQPMLNLSLDLSLNPNFQIP 180
Db 159 LIQSFKLPEYPSNLTNLEHLDLSNKTOSTYCTDLRVHQPMLNLSLDLSLNPNFQIP 218
Qy 181 GAFKEIRLHKLTLLNNPDSLNVMTKCIQGLAGLEVHRLVLGEFNNEGNLJEKFDKSALEGL 240
Db 219 GAFKEIRLHKLTLLNNPDSLNVMTKCIQGLAGLEVHRLVLGEFNNEGNLJEKFDKSALEGL 278
Qy 241 CNLTIEBRRLAYLDYDDIIDLFCNCLTNVSSFSVLVYTERIVKXDFSYNFGMÖHLEIVNC 300
Db 279 CNLTIEBRRLAYLDYDDIIDLFCNCLTNVSSFSVLVYTERIVKXDFSYNFGMÖHLEIVNC 338
Qy 301 KFGQFPLTKLSLRLTFTSNKGNAPSEVDLPSELNLSRNLSFRGCCSOSDFGTS 360
Db 301 KFGQFPLTKLSLRLTFTSNKGNAPSEVDLPSELNLSRNLSFRGCCSOSDFGTS 360
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Db 339 KFGQFPLTKLSLRLTFTSNKGNAPSEVDLPSELNLSRNLSFRGCCSOSDFGTS 398
Qy 361 LKYLDSLSPNGVITWSSNFGLEQLEHLDPQHSNLSKOMSEFSVFLSLNRLIYLDLSHTTR 420
Db 399 LKYLDSLSPNGVITWSSNFGLEQLEHLDPQHSNLSKOMSEFSVFLSLNRLIYLDLSHTTR 458
Qy 421 VAFNGIFNGLSLSEVLVMAGNSFOENFLPDI FTFLRNLTFLDLSQCOLBQISPTAFNSLS 480
Db 459 VAFNGIFNGLSLSEVLVMAGNSFOENFLPDI FTFLRNLTFLDLSQCOLBQISPTAFNSLS 518
Qy 481 SLOVLNMSHNNFSLDTPPYKCLNSLOVLYSLNHTSKQELQHPSSLAFLNLOND 540
Db 519 SLOVLNMSHNNFSLDTPPYKCLNSLOVLYSLNHTSKQELQHPSSLAFLNLOND 578
Qy 541 FACTCEHQSFLQWIKDOROLLVEVERMECATPSDKQMPVLSLNTCOMNTIIGVSVLS 600
Db 579 FACTCEHQSFLQWIKDOROLLVEVERMECATPSDKQMPVLSLNTCOMNTIIGVSVLS 638
Qy 601 VLVSVAVALVYKPYFHLMLLAGCIKXGRGENIYDAFVIYSSQDEDMWRNELVNLBEGV 660
Db 639 VLVSVAVALVYKPYFHLMLLAGCIKXGRGENIYDAFVIYSSQDEDMWRNELVNLBEGV 698
Qy 661 PPQCLCHYRDPFIPGVAIAAANIHEGFHKSARKVIVVVSQHFIQSRMCIFEEYIAQTWQFL 720
Db 699 PPQCLCHYRDPFIPGVAIAAANIHEGFHKSARKVIVVVSQHFIQSRMCIFEEYIAQTWQFL 758
Qy 721 SSRAGIIFIVLQKVEKTLRQOVELYRLSRNTYLEMEDSVLGRIHFWRLRKALLDGS 780
Db 759 SSRAGIIFIVLQKVEKTLRQOVELYRLSRNTYLEMEDSVLGRIHFWRLRKALLDGS 818
Qy 781 WNPBGTVGTGCMWQEAISI 799
Db 819 WNPBGTVGTGCMWQEAISI 837

RESULT 6
US-10-038-854-135
/ Sequence 135, Application US/10038854
/ Publication No. US20040022781A1
/ GENERAL INFORMATION:
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Li, Li
/ APPLICANT: Wolenc, Adam R
/ APPLICANT: Vernel, Corine
/ APPLICANT: Eileen, Andrew J
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Malyankar, Uriel M
/ APPLICANT: Shinkets, Richard A
/ APPLICANT: Tchiernev, Velizar
/ APPLICANT: Spaderna, Steven K
/ APPLICANT: Gorman, Linda
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Gusev, Vladimyr Y
/ APPLICANT: Gangoli, Baha A
/ APPLICANT: Guo, Xiaojia S
/ APPLICANT: Shenoy, Suresh G
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Casman, Stacie J
/ APPLICANT: Boldog, Ferenc
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Edinger, Shlomit R
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Gunther, Erik
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Millec, Isabelle
/ APPLICANT: MacDougall, John R
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-230
/ CURRENT APPLICATION NUMBER: US/10/038,854
/ PRIOR FILING DATE: 2003-01-22
/ PRIOR APPLICATION NUMBER: 60/258,928
/ PRIOR FILING DATE: 2000-12-29
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PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 135
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus
US-10-038-854-135

Query Match 15.1%; Score 625.5; DB 15; Length 661;
Best Local Similarity 28.5%; Pred. No. 2.6e-41;

Matches 186; Conservative 113; Mismatches 273; Indels 81; Gaps 15;

3 INFYKIPNLPSTKNLDSFNPRLHLSGYSFSPPELQVLDLSRCETQIEDGAYOSLS 62
42 LGANIEPGLPNSTECLERFSFNVLPITQNTTFSRLINLTFDLPTRCOQYWMHEDTFQSQH 101
63 HLSTLILGNPQISALGAFSGLSLOKLVAVETNLASLENFPIGHLKTLKELNVAHNL 122
102 RLDTLVLANPLIFMAETALSGPKALKHLPFQITQISSIDFPIHNOKTLESLYIGSNHI 161
123 OSFKLPEYFNSLNTNLEHDLSSNKLOSTICTDRLVHQMPNLNLSLDISINPMNFIORGA 182
162 SIKLPKGPPT-EKLKLVDPQNNALHYLSKEDMSLQO-ATNLNLNNGNDIAGIEPGA 218
183 FKEIRLHKLTLRNPNDSINVMKTCIQGLAGLEVHRLVGEFENEGNLEKFDKSALEGCN 242
219 FDSAVFQSL---NFGTQNLIVIRKGLKNSIQSLWGTGFEDMD-EDISAVFEGICE 273
243 LTIEFRLAYDYDDIIDLFCNLTNVSFSLVVTIERVKOFSTYNGMHLBVNCKF 302
274 MSVESINL-OKHYFENISSNTFHCS-----GLQRLDLTAVHL 310
303 GQFPT--LKLSIKRLFTSNKGN--AFSEVDLPLEF----- 337
311 SELPSGLVGLSTLTKLVLSANKFENLCOISANPSLSLTHLSIKGNTKRLLEGTCLENDLE 370
338 ----LDSRNGLSFPGCCSOSDFGTTSLKYLDLSFNGVITWSSN-FLGLEQLEHLDFOHS 392
371 NLRELDSHDDIETSDCCNLQJRNLSHLQSLNLSNEPLSLKTEAFKCPQLELDLAF 430
393 NLKQMSFVSPLSLNLIYLDISHTTRVAFNGIENGSLSEVLKMAQNSFOENFL--PD 450
431 RLKVDASQPFQNLHLKLVNLNLSHSLDISSEQLFDGRLAQHNLMOGHNFPKGIQKTN 490
451 IFTBLRNLTFLDSCOLEQSPTAFNLSLSLOVNLMSHNNFSLDTPRYKLNLSQ--V 508
491 SLQGTGRLEILVLSLCSIDQHAFTSLKMMNHVLSHNR--LTSSIELSLKGIY 547
509 LDYSLNHMTSKKQELQHFPSLAFL-----NLTONDFACTCEHQSFLOWIKDQROLIV 562
548 LNLASNHLSII-----LPSLPLTSLQOQRTINLQNPLDCCSNITYLEWKEKMQKLE 600
563 EVERNECATPSPKQMPVLASLNTITQANKTIIGVSVLSVLVSVAVLVYKF 615

DB 601 DTEDTLCEPNPLNGVRISDVTLSCSMAAVGIFLIVFLVPAILLITAVKYE 653

US-10-037-417-107

Sequence 107, Application US/10037417
Publication No. US20040052806A1

GENERAL INFORMATION:

APPLICANT: Kekush

APPLICANT: Alsbrook II, John P

APPLICANT: Tchermey, Velizar T

APPLICANT: Liu, Xiaohong

APPLICANT: Spytek, Kimberly A

APPLICANT: Patturajan, Meera

APPLICANT: Grosse, William M

APPLICANT: Lepley, Denise M

APPLICANT: Burgess, Catherine E

APPLICANT: Verne, Corine A.M.

APPLICANT: Li, Li

APPLICANT: Gorman, Linda

APPLICANT: Edinger, Shlomit R

APPLICANT: Sciore, Paul

APPLICANT: Ellerman, Karen

APPLICANT: Malynkar, Uriel M

APPLICANT: Rothenberg, Mark

APPLICANT: Stone, David J

APPLICANT: Boldog, Ferenc L

APPLICANT: Guo, Xiaojia

APPLICANT: Shenoy, Sureeh G

APPLICANT: Anderson, David M

APPLICANT: Padigaru, Muralidhara

APPLICANT: Taupier Jr, Raymond J

APPLICANT: Miller, Charles E

APPLICANT: Eisen, Andrew J

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-235

CURRENT FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: 60/260,018

PRIOR FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: 60/260,360

PRIOR FILING DATE: 2001-01-08

PRIOR APPLICATION NUMBER: 60/272,411

PRIOR FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: 60/272,817

PRIOR FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 60/291,186

PRIOR FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: 60/303,231

PRIOR FILING DATE: 2001-07-05

PRIOR APPLICATION NUMBER: 60/305,060

PRIOR FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: 60/318,405

PRIOR FILING DATE: 2001-09-10

PRIOR APPLICATION NUMBER: 60/318,700

PRIOR FILING DATE: 2001-09-12

NUMBER OF SEQ ID NOS: 227

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 107

LENGTH: 661

TYPE: PRT

ORGANISM: Mus musculus

US-10-037-417-107

Query Match 15.1%; Score 625.5; DB 15; Length 661;
Best Local Similarity 28.5%; Pred. No. 2.6e-41;

Matches 186; Conservative 113; Mismatches 273; Indels 81; Gaps 15;

3 INFYKIPNLPSTKNLDSFNPRLHLSGYSFSPPELQVLDLSRCETQIEDGAYOSLS 62
42 LGANIEPGLPNSTECLERFSFNVLPITQNTTFSRLINLTFDLPTRCOQYWMHEDTFQSQH 101
63 HLSTLILGNPQISALGAFSGLSLOKLVAVETNLASLENFPIGHLKTLKELNVAHNL 122

Db 102 RLDTVLTPANPLIFMAETLALSGPKALKHLPFIQTOTISSIDFLPHNOKTELSLYGSHNI 161
Qy 123 QSFKLPEYFNSLNTLNEHLDSNKKISQIYCTDLRYLHQWPLNLSLDLSLNMNFIOGA 182
Db 162 SSIKPKKPPPT-EKAKVLPDQNNALHYLSKEMMSLQQ--ATNLNLNANGDIADIBFGA 218
Qy 183 FKEIRLHKLTLYNNPDSINVMKTCIQIAGLAEVHRLVIGEFNNEGNELEKFDKSALEGICN 242
Db 219 FDSAVFQSL---NFGTQNLVLVIFKGLKNSTIQSLMTQTFEDMD-EDISPAVEGICE 273
Qy 243 LTIEFRRLAYLDYLDIIDLFCNLTNNVSSFLSVTIERVVDPSYNGMQLLEVNCXF 302
Db 274 MSVESINL-QKHYPFNISNTFCHPS-----GLDELDTATHTL 310
Qy 303 GQFPF-LKLSKLTFTSNKGN--AFSEVDLPSEF----- 337
Db 311 SELPGLVGLSTLKLVLASANKFEMLCQISANFSLTHLSIKGNTKLELGTCLENDL 370
Qy 338 ---LDSRNGLSFKGCCSQSDFGTTSKLYLDLSFNGVITWSSN-FLGLEOLEHLDPQHS 392
Db 371 NLRELDLHDIDLETSDCCNLQLRNLSHLQSLNLSYNEPLSLKTEAFKCEQPLELIDLAFT 430
Qy 393 NLKQMSFSPFLSLENLYLDISHTHTVAFNGIFNGSSLEVLKMGANSPOENFL--PD 450
Db 431 RLKVAQSPQNLHLVLNLSHSLDLISSEQLPDLGALQHLNLQNHFPKGNIOKTN 490
Qy 451 IFTELRNTFLDLSQCOLEOLSPRTAFNSLSLQVLNHNPNFSLDTEPPYKCLNSLQ--V 508
Db 491 SLQTLGRLEILVLSFCDLSIDQAHFTSLKMNHVLDLSNR---LTSSIELSLHKIY 547
Qy 509 LDVSLNHTMSKQELQHPSSLAFL---NLTONDPACTCEHQSFLOWIKDQROLIV 562
Db 548 LNLASNHSIIL-----LPSLPLISQORTINLEQNPLDCTCSNIYFLEWKEMQKLE 600
Qy 563 EVERNECATPBDKQMPVLSLNTQNMKTIIGVSVLSVVAVLVYKPY 615
Db 601 DTEDTLCPNPLLRGVRLSDVTLSCSMAVGIFFLIVELVAILLIPAVKPF 653

RESULT 8
US-09-950-041-4
; Sequence 4, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kaestlein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XK1
; CURRENT APPLICATION NUMBER: US/09/950,041
; PRIOR APPLICATION NUMBER: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-950-041-4
Query Match 14.6%; Score 603.5; DB 10; Length 784;
Best Local Similarity 27.0%; Pred. No. 1.9e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

Qy 8 IPDNLPESTKNLDSFNPRLHGSYSPFSPPELOVLDLSRCEIOTIEDGAYQSLSHLSTL 67
Db 46 IPSGLTEAVKSLDLSNNRITYIYNSDLQRCVNLQALVLTSGINTIBEDSPSSLSLEHL 105
Qy 68 ILTGNPIQSLALGAFSGSLSLQK-----VAVENLASLENPIGLHKT----- 111
Db 106 DLSYNYLSNLSWFKPLSLFTPLNLGNPKYKLGERTSLFSHLKLTQLIRVGNMDTFYKI 165
Qy 112 ---LKEINVAHNLQSFKLPYFENLNTLNEHLDSNKN-----IQSI 150
Db 166 QKQKPAGLTFEELIEIDASDQSTE-PKSLKSIGNVSHLILMHQHLLEIPVDYTSV 224
Qy 151 YCTDLRYLHQWPLNLSLDLSLNMNF--IQPGAKEIRLHKLTLYRN--NFDL-NYMK 204
Db 225 ECLERL-----DTDLDFHFSLSJSTGETNSL-IKKFTRVVKITDESLSFYMK 271
Qy 205 TC--IQGLAGLEVRLV---GEFRNEGNELEKFDKSALEGICNTTIEFRLA--YLDVYL 257
Db 272 LLMQISGLLEBFDCTLNGVFNRAADNDVIDPGKVE--TLTIRLHIPIREYLFY-- 326
Qy 258 DDIDLFCNLTNNVSSFLSVTIERVVDPSYNGMQLLEVNCXKFGQFPPLKLSKRLT 317
Db 327 -DLSTLYSLTRVK-----RTVENSKYF-----LVPCLSQ----- 357
Qy 318 FTSNKGNAFSEVDLPSEFLDLSRN-----GLSFKCCSQSDFGTTSKLYLDLSFNGVI 372
Db 358 ---HLKLELYLDLSENLMVEYLLKNSAC---EDAPSLQTLILRN--- 397
Qy 373 TMSNPLGLEBELELDQHSNLKQMSFVSFLSLRNLYLDISHTHTVAFNGIFNGSS 432
Db 398 ---HL---ASLEKTEG--TLTTLKNTLNIDISK----- 422
Qy 433 LEVLKMGANSPOENFLPDIPTELRNTFLDLSQCOLEOLS---PTAFNSLSLQVLNMSH 489
Db 423 ---NSFHS--METCQWPEKMKYLNLSRHSYVCGIT-----KTLEILDVSN 466
Qy 490 N--NPSLID-----TFP-YKCLNSLQVLDSLNHTMSKQELQHPSSL 531
Db 467 NNLMLFSLNLPQLKELYISRKLMTLTPDASILPWLVLKISRNALITFESKQLODSF-HTL 525
Qy 532 AFLNLQNDPACTCEHQSFLOWIKDQROLIVV-----ERNECATPBDKQMPVLSLNT 586
Db 526 KTLBAGGNFTCSCEFLSFTQ---EQDALAKVLDIMPANYLCPSPHVRQGVQDVRLS 581
Qy 587 ---QNMKTIIGVSVLSVVAVLVYKPY--FHLMLLAGCIIKGR-----GENI-Y 634
Db 582 VSECHRALVSGMCCALFILLILGLVCHRPHGLMYKMMWAMQAGRKPKKASRNICY 641
Qy 635 DAFVITYSSQDEWDYRNELVKNLEBGPVFPOLCLHYRDPFGVALIANIIEGFKSKRYI 694
Db 642 DAFVYSERDAYWVENIMQELBENFPFKCLHKRDPFGKWIINDII-DSIKSHKTV 700
Qy 695 VVVSQHFIQSRWCIFFEYIAQWTFPLSSRAGIIFIVQAKVEKTLRQO-VELYLLSRNT 753
Db 701 FVLSSENFVKSBCRYELDFSHFLFEENNDAIILILEPIEKKAIPORFCKLRKIMYKT 760
Qy 754 YLEWEDSVLGRHIFWRRLKRL 775
Db 761 YLEWPMDEAQRGEGFWVNLRAAI 782

RESULT 9
US-10-456-947-46
; Sequence 46, Application US/10456947
; Publication No. US2004005841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey

Db 106 DLSYNYLSSSMFKPLSLTLFLNLGNPYKTLGETSLPSHLTKQLIRVGNMDTFYKI 165
Qy 112 -----LKEINVAHNLIQSFKLPEYFSNLTNLEHLDSSNK-----IQSI 150
Db 166 QKDPAGTLFLEHIDASDQSYE-PKSLKSIQVSHLIMKHILLLEIFVDVTSV 224
Qy 151 YCTDLRVLHQMPLNLISLDSLNPMNF--IQGAFKEIRLHKLTLRN--NFDSL-NVMK 204
Db 225 ECLERL-----DTDLDTFHFSLSLSTGETNSL-IKKFTRRWKITYDESLFQYMK 271
Qy 205 TC--IQGLAGLEVHRLVLT--GEFRNENLEKFDKSALEGCLNLTIEFRLA--YLDYVL 257
Db 272 LLNQISGLELEFPDCTLNGVGNFRASDNDRIIDPKVE--TLTIRRLHPRFLYF-- 326
Qy 258 DDIIDLFNCLTNVSSFSLSVSTIERVKDFSYNFGMQLHELVNCKFGQFPTLKSLKRLT 317
Db 327 -DLSTLYSLTERVK-----RITVENSKYF-----LVPCLLSQ----- 357
Qy 318 FTSNKGNAFSEVDLPSEFLDLSRN-----GLSFKCCSOSDGTTSKLYLDSFNGVI 372
Db 358 -----HLKSLLEYDLSENLMVEEYLKNSAC--EDAMPSTQLTLIRQN-- 397
Qy 373 TMSNPLGLBQLEHLDFOHSLNKKOMSEFSVFLSLRNLYLDISHHTHVAFNGIFNGISS 432
Db 398 -----HL-----ASLEKTEG--TLTTLKLNLTNIDISK----- 422
Qy 433 LEVLKMGNSFOENFLPDIFTELRLNLTFLDLSQCLBOLS--PTAFNLSLSLOVLNMSH 489
Db 423 -----NSFHS--METCOQWPEKMKYLNLSSTRHISVTCIP-----KTLIEDVSN 466
Qy 490 N--NPFSLD-----TFP--YKCLNSLOVDYSLNHTMTSKQELCHFPSSL 531
Db 467 NNLNLFSLNLPOLKELYISRNKLMTLPDASLLPMLLVLIKISRNALITFSKQOLSF-HTL 525
Qy 532 AFLNLTQNDPACTCEHOSFLQWIKDQROLVEV-----ERMECATPSDKQMPVLSLNT 586
Db 526 KTLKAGNNTFCSCFPLSFTQ-----EQALAKVLIDMPANYLSDSPSHVHQOVDFRLS 581
Qy 587 ---COMKTTIIGVSVLSLVVSVAVLVYKFY--FHLMLAGCIKYGR-----GENI-Y 634
Db 582 VSECHRTALVSGMCCALFLILITLTVLCHRFHGLWYMMWMMAMQAKRKPRAKSRNICY 641
Qy 635 DAFVITYSSQDEBWRNELVKNLEBGPFPOLCLHYRDPFGVAIAIANIHHGFKSRKVI 694
Db 642 DAFVYSERDAYWVENLMVOELENFNPFKLCHKRDPFGKMIIDNII-DSIEKSHKTV 700
Qy 695 VVVSQHFIOQRWCIFEEYEIAQWQFLSRAGIIFIVLOKVEKTLRQO-VELYRLSRNT 753
Db 701 FVLSNFVKSERCKEYLDPSHFRLPDENNDAILILLEPIEKKAIPOKFCUKRKIMNTKT 760
Qy 754 YLEWEDSVLGRHIFWRRLRKAL 775
Db 761 YLEWPMDEAQRGEGFWNLRAAI 782

RESULT 11
US-10-732-563-4
; Sequence 4, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Taron K.
; TITLE OF INVENTION: Assays Relating to Toll-like Receptor Activity
; FILE REFERENCE: 58183W0003
; CURRENT APPLICATION NUMBER: US/10/732,563
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-732-563-4
Query Match 14.5%; Score 602.5; DB 16; Length 784;
Best Local Similarity 27.0%; Pred. No. 2,36-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;
Qy 8 IPDNLPTSTKNLDSFNPRLHLSYSPFPELOVLDSRCEIOTIEDGAYQSLSHSTL 67
Db 46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVYTSNGINTIEEDSPSSLSLEHL 105
Qy 68 ILTGNPISQIALGAFSGLSLQKL-----VAVENNLASLENFPIGHILKT----- 111
Db 106 DLSYNYLSSSMFKPLSLTLFLNLGNPYKTLGETSLPSHLTKQLIRVGNMDTFYKI 165
Qy 112 -----LKEINVAHNLIQSFKLPEYFSNLTNLEHLDSSNK-----IQSI 150
Db 166 QKDPAGTLFLEHIDASDQSYE-PKSLKSIQVSHLIMKHILLLEIFVDVTSV 224
Qy 151 YCTDLRVLHQMPLNLISLDSLNPMNF--IQGAFKEIRLHKLTLRN--NFDSL-NVMK 204
Db 225 ECLERL-----DTDLDTFHFSLSLSTGETNSL-IKKFTRRWKITYDESLFQYMK 271
Qy 205 TC--IQGLAGLEVHRLVLT--GEFRNENLEKFDKSALEGCLNLTIEFRLA--YLDYVL 257
Db 272 LLNQISGLELEFPDCTLNGVGNFRASDNDRIIDPKVE--TLTIRRLHPRFLYF-- 326
Qy 258 DDIIDLFNCLTNVSSFSLSVSTIERVKDFSYNFGMQLHELVNCKFGQFPTLKSLKRLT 317
Db 327 -DLSTLYSLTERVK-----RITVENSKYF-----LVPCLLSQ----- 357
Qy 318 FTSNKGNAFSEVDLPSEFLDLSRN-----GLSFKCCSOSDGTTSKLYLDSFNGVI 372
Db 358 -----HLKSLLEYDLSENLMVEEYLKNSAC--EDAMPSTQLTLIRQN-- 397
Qy 373 TMSNPLGLBQLEHLDFOHSLNKKOMSEFSVFLSLRNLYLDISHHTHVAFNGIFNGISS 432
Db 398 -----HL-----ASLEKTEG--TLTTLKLNLTNIDISK----- 422
Qy 433 LEVLKMGNSFOENFLPDIFTELRLNLTFLDLSQCLBOLS--PTAFNLSLSLOVLNMSH 489
Db 423 -----NSFHS--METCOQWPEKMKYLNLSSTRHISVTCIP-----KTLIEDVSN 466
Qy 490 N--NPFSLD-----TFP--YKCLNSLOVDYSLNHTMTSKQELCHFPSSL 531
Db 467 NNLNLFSLNLPOLKELYISRNKLMTLPDASLLPMLLVLIKISRNALITFSKQOLSF-HTL 525
Qy 532 AFLNLTQNDPACTCEHOSFLQWIKDQROLVEV-----ERMECATPSDKQMPVLSLNT 586
Db 526 KTLKAGNNTFCSCFPLSFTQ-----EQALAKVLIDMPANYLSDSPSHVHQOVDFRLS 581
Qy 587 ---COMKTTIIGVSVLSLVVSVAVLVYKFY--FHLMLAGCIKYGR-----GENI-Y 634
Db 582 VSECHRTALVSGMCCALFLILITLTVLCHRFHGLWYMMWMMAMQAKRKPRAKSRNICY 641
Qy 635 DAFVITYSSQDEBWRNELVKNLEBGPFPOLCLHYRDPFGVAIAIANIHHGFKSRKVI 694
Db 642 DAFVYSERDAYWVENLMVOELENFNPFKLCHKRDPFGKMIIDNII-DSIEKSHKTV 700
Qy 695 VVVSQHFIOQRWCIFEEYEIAQWQFLSRAGIIFIVLOKVEKTLRQO-VELYRLSRNT 753
Db 701 FVLSNFVKSERCKEYLDPSHFRLPDENNDAILILLEPIEKKAIPOKFCUKRKIMNTKT 760
Qy 754 YLEWEDSVLGRHIFWRRLRKAL 775
Db 761 YLEWPMDEAQRGEGFWNLRAAI 782

RESULT 12
US-10-732-796A-4
; Sequence 4, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.


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QY 587 ---COMKTIIGVSLVSVVAVLYKPY--PHMLLAGCIKYG-----GENI-Y 634
DB 582 VSECHRTALVSGMCALFLLILTGVLCHRFHGLMYKMMWAMAOAKRPRKAPSRNICY 641
QY 635 DAFVYSSODEDWVNEVLVKNLEEGVPPFOLCLHYRDPFGVAIAANIHEGPHSKRYI 694
DB 642 DAFVYSERDAYWENLWQLENNPPFKLCHKRDPFGKMIIDNII-DSIEKSHKTIV 700
QY 695 VVVSQHFIOSRWCIFFEYELAQTWQFLSRAGIIFIVLQKVEKTLRQO-VELYRLLSRNT 753
DB 701 FVLSNFVSKWCKYELDFSHFRLPDENNDAAIILLEPIEKKAIPQRCFKLRKIMTKT 760
QY 754 YLEWEDSVLGRHITWRRLRKAL 775
DB 761 YLEWPMDEAQREGFWVNLRAAI 782

RESULT 14
US-10-741-600-1391
; Sequence 1391, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1391
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1391

Query Match 14.5%; Score 602.5; DB 17; Length 784;
Best Local Similarity 27.0%; Pred. No. 2.3e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

QY 8 IPDNLPSFTKNLDSLFPNPLRHGSGSPFPPELOVLDLSCRCIOTIEDGAVQSLSHLSTL 67
DB 46 IPSGLTEAVKSLDLSNNRITITYSNLDORCVNLQALVLTSGINTIEEDSPSLGLEHL 105
QY 68 ILTGNPIQSLALGAFSGLSLOKL-----VAVENTLASLENFPIGHLKT----- 111
DB 106 DLSYNYLSNLSGSKPLSLTFNLGNPKYKTLGETSLFSLTKLQILRVGNMDTFKI 165
QY 112 -----LKELVANHLIOSFKLPRYFSNLTNLEHLDSLSSNK-----IOST 150
DB 166 QKDFAGLTFLELEIDASDLSYE-PKSLKSIQWVSHLILMHKOHILLEIFVDVTSSV 224
QY 151 YCTDLRVLHQPMLNLDSLGNPNMF--IQGAKKEIRLHKLTLRN--NPDLS-NYMK 204
DB 225 ECLER-----DTDLDTFHFSLSLSTGETNSL-IKKEFTRNKKTIDESLFOVK 271
QY 205 TC--IOGLAGLEVRLV-----GEFNEGNLEKFKDSALEGLCNLTIEEFRLA--YLDTYL 257
DB 272 LLNQISGLELEFDDCTINGVGNFRASNDNRVIDRGKYE--TLTIRLHLHPRFTLYF-- 326
QY 268 DDIDLEFNCCLTNVSSFSVSVTIEVKOPSYNFGQHLVELVCKFGQFPPTLKLSKLRLT 317
DB 327 -DLSTLYSLTERVK-----RITVENSKYF-----LVPCILSQ----- 357
QY 318 FTSNKGNAFSEVDLPSLEFLDSRN-----GLSPKGCSSODPCTTSLKYLDSLFGNVI 372
DB 358 -----HKSLEYLDLSNLWVEYLKNSAC--EDAMPSLQTLILRQN-- 397
QY 373 TMSNFIQLBOLEHLDFQHSNLSKQMSFVSFLSLNLIYLDISHHTVAENGIFNGLS 432
DB 398 -----HL-----ASLEKTFE--TLTTLKNLNIIDSK----- 422
QY 433 LEVLMAGNSFOENLPDIFTELRLNLTPLDLSQCLBOLS--PTAENSLSLQVLNMSH 489
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DB 423 -----NSFHS--MPETCQWPEKMKYLNLSSTRHSVTCIP-----KTLBILDVSN 466
QY 490 N--NPFSLD-----TFP-YKCLNSLOVLDVSLNHMTSKQELQHPSSL 531
DB 467 NNILFSLNLPQLKELYISRNKMTLTPDASCLLPMILVAKTSRRAITTFPSKQLSF-HTL 525
QY 532 AFLNLTQNDFACTGESHOSFLOWIDKORQLVEV-----ERMECATPSPDKQMPVLSNIT 586
DB 526 KTLBAGGNFICSEBPSFTQ-----EQALAKVLIDMPANVLCOSPSHVRCQYQDVRLS 581
QY 587 ---COMKTIIGVSLVSVVAVLYKPY--PHMLLAGCIKYG-----GENI-Y 634
DB 582 VSECHRTALVSGMCALFLLILTGVLCHRFHGLMYKMMWAMAOAKRPRKAPSRNICY 641
QY 635 DAFVYSSODEDWVNEVLVKNLEEGVPPFOLCLHYRDPFGVAIAANIHEGPHSKRYI 694
DB 642 DAFVYSERDAYWENLWQLENNPPFKLCHKRDPFGKMIIDNII-DSIEKSHKTIV 700
QY 695 VVVSQHFIOSRWCIFFEYELAQTWQFLSRAGIIFIVLQKVEKTLRQO-VELYRLLSRNT 753
DB 701 FVLSNFVSKWCKYELDFSHFRLPDENNDAAIILLEPIEKKAIPQRCFKLRKIMTKT 760
QY 754 YLEWEDSVLGRHITWRRLRKAL 775
DB 761 YLEWPMDEAQREGFWVNLRAAI 782

RESULT 15
US-10-145-014-23
; Sequence 23, Application US/10145014
; Publication No. US20020168755A1
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Fan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tan, Jimmy C.
; APPLICANT: Zavadny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: J806010D
; CURRENT APPLICATION NUMBER: US/10/145,014
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/982,308
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,163
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-014-23

Query Match 14.5%; Score 599.5; DB 13; Length 784;
Best Local Similarity 27.0%; Pred. No. 4e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

QY 8 IPDNLPSFTKNLDSLFPNPLRHGSGSPFPPELOVLDLSCRCIOTIEDGAVQSLSHLSTL 67
DB 46 IPSGLTEAVKSLDLSNNRITITYSNLDORCVNLQALVLTSGINTIEEDSPSLGLEHL 105
QY 68 ILTGNPIQSLALGAFSGLSLOKL-----VAVENTLASLENFPIGHLKT----- 111
DB 106 DLSYNYLSNLSGSKPLSLTFNLGNPKYKTLGETSLFSLTKLQILRVGNMDTFKI 165
QY 112 -----LKELVANHLIOSFKLPRYFSNLTNLEHLDSLSSNK-----IOST 150
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Db 166 QKDPAGLTFFLELEIDASDLOSYE-PKSLKSIQUNVSHILHMKQHILILETFVDVTSSV 224
QY 151 YCTDLRVLHQWPLNLISDLISLPMNF--IQGAFKEIRLHKLTLRN---NPDSL-NVMK 204
Db 225 ECLERL-----DTRDITFHSLSTGERTNSL-IRKFTFRNVKITDESLFOVMK 271
QY 205 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFKSALEGLCNLTIEEFRLA--YLDYYL 257
Db 272 ILNQISGLLETFEDDCTLNGVGNFRASDNDRVIDPGKVE---TLFIRLRHIDPRFYLFY-- 326
QY 258 DIIILFNCLTNVSSFSVLVSTIERVKDSYVFGWQHLELVNCKFGQFPTLKSKAKRLT 317
Db 327 -DLSTLYSLTERVK---RITVENSKVE-----LVPCLLSQ----- 357
QY 318 FTSNKGNAFSEVDLPSELEFLDLSRN---GLSFKCCSQSDFGTTSKLYDLSEFNGVI 372
Db 358 -----HLKSLEYLDSENLWEEYLNKSAC---EDAMPSLQTLILRN--- 397
QY 373 TWSNPFLEGLQLEHLDFOHSNLKQWSEFSVFLSLRNLYLDISHTHTRVAFNGIFNGLS 432
Db 398 -----HL---ASLEKTGE--TLLTLKNLTNIDISK----- 422
QY 433 LEVLMAGNSPQENFLPOLFTELRNLTFLDLSQCOLEQLS---PTAFNSLSLOVLNMSH 489
Db 423 -----NSFHS--MPEYQWPERKMYLNLSTRHSVTGCI P-----KLEILDVSN 466
QY 490 N--NFFSLD-----TFP--YKCLNSLOVLDYSLNHMTSKQELQHPSSL 531
Db 467 NNLNLPSLNLPOLKELYISRNKLTMLTPDASLLPMLLVLKISRRAITTFSEKQDLSF-HTL 525
QY 532 AFLNLTQNDFACTCEHQSFLQWIKDQROLLEV-----ERMECATPSDKQMPVLSLNT 586
Db 526 KTLKAGNNFICSCEFLSFTQ---EQALAKVLLIDWPANYLCDSPSHVRGQOVQDVRLS 581
QY 587 ---COMNKTIIGVSVLTVVSVAVLVYKFY--FILMLAGCICKGR-----GENT-Y 634
Db 582 VSECHRIALVSGMCCALFLILLTGVLCRHFGLWYMKMMWMLQAKRKRPRAPSRNICY 641
QY 635 DAFVIYSSODEDMVRNELVKNLEEGVPPOLCLHYRDFIPGVAIANIIEGFFHKSRYI 694
Db 642 DAFVSYSEKDAYWERTLWQELLENRPFKLCILHKRDFIPGKIIDNII-DSIEKSHKTV 700
QY 695 VVVSQHFIQSRWCIFEYELIAQTWQFLSSRAGIIFIVLQVEKTLRLQO--VELYRLLSRNT 753
Db 701 FVLSNFVSEWCKEYELDFSHFRLFDENNDAIILLLEPIEKKAIPQRFCKLRKIMNTXT 760
QY 754 YLEWEDSVLGRHIFWRRLKAL 775
Db 761 YLEWPEDEAQREGFWNLRAAI 782

Search completed: March 12, 2005, 20:27:52
Job time : 74.7097 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:01 ; Search time 20.6156 Seconds
(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985B-4

RefSeq ID: [NM_001163261.1](#)
 RefSeq Score: 414.1
 RefSeq: [1](#) MELNFKIPDNLPFSTKLD.....SMNPEGTGTCGNQGEATSI 799
 Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%

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Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	625.5	15.1	661	2	I56258	RP105 - mouse
2	474	11.4	786	2	T08664	Toll protein-like
3	452	10.9	1097	2	A29943	Toll protein precu
4	421	10.5	1385	2	T13852	gene wheeler prote
5	433	10.2	1385	2	T13887	tlr protein - fruti
6	392	9.5	1066	2	T15864	hypothetical prote
7	333.5	8.1	1134	1	A29944	cholepin precursor
8	309	7.5	605	2	UC5239	insulin-like growt
9	302	7.3	853	2	T17461	disease resistance
10	297	7.2	605	2	A41915	insulin-like growt
11	296	7.1	1531	2	T42218	slit-1 protein hom
12	292	7.1	994	2	H96510	probable disease r
13	291	7.0	845	2	T07039	Hcr9-0 protein - t
14	290	7.0	603	2	UC1282	insulin-like growt
15	290	7.0	855	2	T07015	Ct-4A protein - t
16	289.5	7.0	603	2	T24313	hypothetical prote
17	289.5	7.0	1112	2	T10504	disease resistance
18	289	7.0	855	2	T17460	disease resistance
19	287.5	6.9	662	2	S42799	garp precursor - h
20	284.5	6.9	907	2	JE0176	orphan G protein-c
21	284	6.9	603	2	UC6178	insulin-like growt
22	284	6.9	907	2	UC0153	G protein-coupled
23	281.5	6.8	622	2	JC7973	syntleurin - human
24	281	6.8	1134	2	T04587	hypothetical prote
25	280	6.8	890	2	T00800	disease resistance
26	278.5	6.7	1019	2	C96519	probable disease r
27	276.5	6.7	768	2	T17462	disease resistance
28	276	6.7	983	2	684524	probable disease r
29	276	6.7	1027	2	H85089	receptor protein k

30	270.5	6.5	1523	2	T13955	2	MEGF8 protein - ra
31	270	6.5	1143	2	T10636	2	hypothetical prote
32	266.5	6.4	1091	2	A58532	2	glial cell membran
33	266.5	6.4	1784	2	C96615	2	hypothetical prote
34	265.5	6.4	863	2	A55173	2	cf-9 protein precu
35	265	6.4	910	2	G84648	1	probable disease r
36	264.5	6.4	766	2	T01817	2	hypothetical prote
37	264	6.4	1469	2	B36665	2	salt protein 2 pre
38	264	6.4	1480	2	A36665	5	salt protein 1 pre
39	262.5	6.3	967	2	T48210	2	hypothetical prote
40	261.5	6.3	1031	2	T13174	2	gpi50 protein - fr
41	260.5	6.3	1109	2	T18536	2	receptor-like prot
42	259	6.3	1029	2	T00712	2	protein kinase hom
43	257	6.2	738	2	T19398	8	hypothetical prote
44	254	6.1	771	2	T02565	2	disease resistance
45	253.5	6.1	991	2	T52400	2	receptor-like prot

· ALIGNMENTS

RESULT 1

RP105 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I56258
 R:Myake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
 J. Immunol. 154, 3333-3340, 1995
 A:Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a member of the TNF receptor superfamily
 A:Reference number: I56258; MUID:95204928; PMID:7897216
 A:Accession: I56258
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-661 <RSS>
 A:Cross-references: UNIPROT:Q62192; GB:D37797; NID:G761711; PIDN:BAA07043.1; PID:G761711

Query Match	15.1k	Score 625.5	DB 2	Length 661
Best Local Similarity	28.5k	Pred. NO. 9.6e-37		
Matches 186	Conservative 113	Mismatches 273	Indels 81	Gaps 15

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OY      3  LNFYKIPDNI,PESTXKNLD,SNFPLREHLGVSFFPELOVDLDSRCEIOTIEBDAVOSLS 62
Db      42  LGANEI,PGTL,PNSTBCELEFSFNVFLPTIONTTFSRILNLTPLDFLRCCOIYWIHEDTFQSH 1010
OY      63  HJLSTLITGNP,QISALALGAFGSLGQYVAVERNVLASLENFP,IGH,KTYL,KELVAN,NLI 1222
Db      102  RLDITVLITNPNP,II,MAEETALSGPKAL,KHLP,FIQGISIDFIPLHNOKTL,ESI,YLGSNNH 1611
OY      123  QSEKLEPEYSNLTNTEH,LDLSNKKIOSIYCTDLDVHLOMP,LT,NL,SLINPMNFI,PGCA 1820
Db      162  SSI,KLPKGPPT - EKUKVLDPFQNNAIHYLKSDEMSLQO - ATNLSLNLNGNDIAGIBGA 218
OY      183  FKRI,RLHK,TLTANNPDSLAVN,KTCI,QI,AGLE,VH,RLV,UGERFNGN,LEKDKSL,BELCN 242
Db      219  FDSAVFQSL---NFGGTOQLNLVIFPKGJKNSTIOSLWLGTFEDMD- EDISPAVFBELCE 273
OY      243  LTIIEERLALYLDYUDDIIDLFCNCLTNVSSFSI,SVTIERKDFSNYFNGOHL,VLNCKF 3020
Db      274  MVSFESINTL-QKHYPFNISNTFHCS-----GLQELDL,TATVHL 310
OY      303  GQPPPT--LTKSLKSLKULTPTSNKGN- AFSEVDLP,SLF----- 337
Db      311  SELPSGLVAGLSTLTKLVLISANKFENL,COI SASNPSP,LT,HL,SI IKONTYRLB,LTGCGLENLE 370
OY      338  ---LDLSRNGLSFKGQCSQSDPFTTSLDKYLDLSFNGVITMSSN- FLGLBQLEHLDFQHS 392
Db      371  NIRELDSLHDDIETSDCCNLQ,LRNLSHLOSNLT,SI,NEPL,SL,KTB,FAFCEPQLETLDLAFT 430
OY      393  NIKQMSBPVPLSL,NL,LYLDI,SHHTHVA,NG,ENG,LSL,VL,XMAGNSFOENFL--PD 450
Db      431  RLKVKDAQSPFOUHL,KLVYLNLSHSLDISEQ,LP,FDGL,PA,LO,ANTL,NGNHPKGN,IKOTXN 480

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Qy 451 IFTLRNLTFLDLSOCQEQSLPTFNSLSLQVLMNHNPFSLDTPPYKCLNSLQ--V 508
Db 491 SLQGTGRLEIVLWLSFCDLSSIDQHAFTSLKMNHNHDLNHRN---LTSSIEALSHKIGY 547
Qy 509 LDYSLNHNMTSKQGLQHPSSSLAFL-----NLQNPACTCEHOSFLOMKDROLLV 562
Db 548 LNLASNHNISIT-----LPSLLPILISOORTNLNQNPLDCTCSNYIFLEMVKNMOKLE 600
Qy 563 EVERMECATPSDKQMPVLSLNTIQNMKTTIIGVSVLSVSVVAVLVYKPY 615
Db 601 DTEDTLCENPILRGVRLSDVTLSCSMAVGIFPLVFLVAILLIFAVKXF 653

RESULT 2
T08664
Toll protein-like receptor DKFP54710610.1 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08664
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gaasenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, May 1999
A:Reference number: 216466
A:Accession: T08664
A:Molecule type: mRNA
A:Residues: 1-786 <PDB>
A:Cross-references: UNIPROT:Q15399; EMBL:AL050262
A:Experimental source: fetal brain; clone DKFP54710610
C:Genetics:
A>Note: DKFP54710610.1

Query Match 11.4%; Score 474; DB 2; Length 786;
Best Local Similarity 25.5%; Pred. No. 4.2e-22;
Matches 204; Conservative 130; Mismatches 303; Indels 162; Gaps 32;

Qy 83 SGLSLQKLVAVETMLASLENPFIQHLKT-----LKELVANLISQFLLPEYFENL 134
Db 34 NGLINHPKDLQSKTITLINSQVYISELMTSDLSLSKRLILISNRLOYLDISYFKRN- 92
Qy 135 TNLHLDLSSNKIQSIYCTDLRLVHQMPPLNLS-LDLSLNPMTI-----QPGAFKEIRLH 189
Db 93 QELVYLDLSHNKLVIKISC-----HPTVNLKHLDLSPNAPDALPICKEFGNMQLKPL 144
Qy 190 KLTLRNNPDSLNMVMTCTIQGLAGLEVHRLV-----GFRNKGULEKFDKSALEGLCNL 243
Db 145 GLS-----TTHLEKSVLPPLAHNLISKVLVGLGETYGEKEDPGGLQDFNTESLHIVPT 198
Qy 244 TIEEFLAVLDYLDIIDLFNCLTNVSSFSLVATIEKVDQFSYNFGQHLNCKRG 303
Db 199 NKE-----FHFILDVSVKTVANIELSNIKCVLEDSKCSYFLSLIAKIQ 241
Qy 304 QPPTLKLSLKRLLFTSNK-----GNAFSEVDLP-SLEFLDLSRNGLSFRG 349
Db 242 TNPKLSLTLNNIETTWNSFIRLLQVHTTWYSSISNVYKLGQGLDRDPDYSGLSLKA 301
Qy 350 CCSQ--SD-----FGTTSLK-----YLDISENGVI-- 372
Db 302 LSIHQVADVDFGFPQSYIYEIIFSNMNIKNFTVSGTRVMYMLCPSKISPEFLHIDFNNMLLT 361
Qy 373 -TMSNFGLEBQLEHLDPOHNSLKQMSERS-VFLSLRNLYLDISHHTHRAFN---GIF 427
Db 362 DTVEFNCGHLELELTLLIQMNQKLSKAEMTTQKSLQQLDIS--QNSVSYDEKKKDC 419
Qy 428 NGLSLEVLKMAKNSFOENF--LPDIFTELRLFLDLSOCQEQSLPTAFNSLSLQV 484
Db 420 SWTKSLLSLNNSSNLTDTIPRCLEP-----RIKVLDLHNSKIKSI-PKQVYVKEALQOE 472
Qy 485 LMSNHNPFSLDTPP---YKCLNSLQVLDVSLNHNMTSKQGLQHPSSSLAFLNLTOND 540
Db 473 LNVAVN---SLTDLFGCGSFSLSVLIIDHNSVSHPSADPFQSCQKMS---IKAGNP 525
Qy 541 FACTEHOSFLOMKDQRLIVEY-----ERMECATPSDKQ-----MPVLSLNTIQ 588
Db 526 FOCTELGEF---VKNIQVSSVLEGMFDSYKCPSSYRGTLTKLDFHMSLSLNTITL 582
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Qy 589 MNKTIIGVSVLSVSVAVLVYKFFPHMLLAGCIKRYGENI-----YDAEV 638
Db 583 IVTIVATMLVLAIVTSLICYLDLPWYLR--NVCMQTQRRRARNPILEELQRLQFHAFI 641
Qy 639 IYSSODEWVWNEVLNKLRE-GVPPFQCLHYRPFIFQVALAANIHEGFHRSKRVYV 697
Db 642 SYSGHDSFWVWNEVLNPLEKEGM--QICLERNFVPGKSIVENII-TCEIKSYKSLFVL 697
Qy 698 SQHFQSRWCIFEYEIAQTMQFLSSRAGIIFIVQKV-EKTLAQVELYLLSRNTYLE 756
Db 698 SPNFVQSMCHYELYPAHNHLFHEGSNSLILILEPFPQYSIPSSYKTKSLMARRTYLE 757
Qy 757 WEDSVLGHIFWRRLKRL 775
Db 758 WPKESKRGGLFWANLRAAI 776

RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A29943
R:Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A>Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, ap
A:Reference number: A29943; MUID:88135760; PMID:2449285
A:Accession: A29943
A:Molecule type: DNA
A:Residues: 1-1097 <HMS>
A:Cross-references: UNIPROT:P08953; GB:M19969; GB:J02682; NID:g158640; PIDN:AAA28941.1;
C:Genetics:
A:Gene: FlyBase:Tl
A:Cross-references: FlyBase:FBgn0003717
C:Keywords: transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-1097/Product: Toll protein #status predicted <MAT>

Query Match 10.9%; Score 452; DB 2; Length 1097;
Best Local Similarity 24.1%; Pred. No. 1.6e-20;
Matches 224; Conservative 140; Mismatches 329; Indels 238; Gaps 42;

Qy 8 IPDNLPESTKN--LDSEFNLRLHGSYSPFPELOVLDSRCEIQTEDGAYQSLSHL 64
Db 165 IPANLITDMRLSHLELRAN-IEEMPSHLFDLLENLSIEFGSNKLRQMPRGIFGKMPKL 223
Qy 65 STLLTNGPIQSLALGAFSGLSQKLVAVETNLASLENPFIQHLKTLELVANHLIOS 124
Db 224 KQLNLMNQQLNLTKHDFEGATSVLGIIDHNGIEQLPHDFAHLTVVTDINLSANLFRS 283
Qy 125 FKLPE-YFSNLTNLEHLDLSNKKIQSIYCTDLRLVHQMPPLNLSLDLSLNPMTIQPGAF 183
Db 284 -LFGQLEFDHKNHLEVRALMNKRVPPLATLPBRALRANQPELOIILRLAEQLS---PDDL 337
Qy 184 KEIRLKLTLNPNDSLNMVMTCTIQGLAGLEVHRLVGEFRNENLEKFDKSALEGLCNL 243
Db 338 FE--HSQTINISLIGNLKLTLPLATLEHQVNLSLDLSNN--RLTHLPDSLRAHTTNL 392
Qy 244 TIEEFLAVLDYLDIIDLFNCLTNVSS--FS---LVSTTIR-----VDFPSINF 290
Db 393 T-----DLRLD-----NLTLGISGDIFFSNLGNLVTLVMSRNLRTIDSRFAVSTN 438
Qy 291 GMDHLEL-----VNCKRGQRP---TLKLSLKLTLFTSNKGNAFVS 328
Db 439 GLRHLHLDHNDIDIQPLDIDMLQTOINSPFGVYHGLITLNLKR-NSIIFYNDMKKTML 497
Qy 329 EVDLPSEFLDLSRNGLSFKGCCSQSDFGTSLSKYLDLSFNGVITWMSNFGLEBQLEHLD 388
Db 498 Q-----LRELDLSYNNIS-----SLGYEDLAF-----LSQNRL-----HVN 528
Qy 389 FOHNSLKQMS-BEVSFVS--LRNLIVYDISHTH-----TRVAPNGIFNGL----- 430
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Db      529 MTHANKRIATLAEVDYHLEGVYNNLVHVDLNDNPLVCCTIIMFIQVGVGHKPOYSROF 588
Qy      431 -----SSLEV 435
Db      589 KLRTRLVYCSQPNVLEGFVROIEPTLICPLDFSDPRERKCPRCNCNCHVITYKALVI 648
Qy      436 LKMAQNSFOENFLPDIFTELRLVTFLLD-----SQOLEQLSPYAFNSLSLQVLMNSH 490
Db      649 NCHSGNLTHVPRLPNHL---KMQQLMELHLENNTLRLPSANTPGVESVTS---LHLAGN 702
Qy      491 NEFSLDT--FPYKCLNSLOVLDYSLNHMTSKKQELQHPSSLAFLN-----LTON 539
Db      703 NLTSLDVLDP-----TNLTHLDISWNL-----QMLN--ATVAGFLNRTMKRSVKLSGN 751
Qy      540 DFACCTEHSQFLQWIKDQRLVEVERMECATPSDKQMPVLSTNTCCOMNKTII-IGVSV 598
Db      752 PAMCCTCTAKPRLLFQDNPERIGDRNEMCVAAEMPTRVELSTNDICAEKGVFALAV 811
Qy      599 ---LSLVVSVAVLVYKF-----YHMLMLAGCIRYRGENT-----YDAFVIYSS 642
Db      812 VIALGLLGLAGFAALYYKQTEIKIWLVAHNL-----WFTVEBDLDKDKKFDATISYSH 867
Qy      643 QDEDMVRNELVKNLEEGVPPPOLCLHYRPIGVAAIANIHGFKSKRVIVVVSQHRT 702
Db      868 KDQSFIEDLVLPOLHEGPOKFCVHERDMLVGHIPENIM-RVADSRTIIVLSQNET 926
Qy      703 QSRWCIFEYELAQTFQFLSSRAIIFIV---LQYEKTLRQOVELYRLSHNTYLEMD 759
Db      927 KSEMARLEFRARHRAHNSNGRSRIIVIIYSDIGDVK--LDEELKAY--LKNATYLMKD 982
Qy      760 SVLGRHIFWRRLKALLDGKSNNEGTG 790
Db      983 P-----WFWDKLRFALPHRR---PVGNIING 1005

RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C.Accession: T13852
R.Eldon, E.; Kooyer, S.; D'aveyln, D.; Duman, M.; Lawinger, P.; Botas, J.; Bellen, H.
Development 120, 885-899, 1994
A.Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
A.Reference number: Z1796; MUID:95324375; PMID:7600965
A.Accession: T13852
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-1189 <EUD>
A.Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:G415682; PID:G1019104; PIDN:AAA7920
A.Genetics:
A:Gene: wheeler
A:Cross-references: FlyBase:FBgn0004364

Query Match      10.5%; Score 433; DB 2; Length 1389;
Best Local Similarity 24.4%; Pred. No. 3.4e-19;
Matches 217; Conservative 138; Mismatches 356; Indels 178; Gaps 34;

Qy      19 LDSLNPRLRHLSYSFSPPELOVDLSRCEIQTIEDGAYQSLSHSTLILGNPIQSLA 78
Db      338 LNLNNALTRISQKTFKELYFLQIIDMRNNSIGHIEGAFPLVYNLHTNLNENRLHTLD 397
Qy      79 LGAFGLSLQKLVAVETMLASL-ENFPIGHLKTLKELVAHNLIOFPLPEYFSULTVL 137
Db      398 NRIFGSLYVLTKL-TLNNLVSVESQARNCSDLKELDLSN--OLTEVPAVVDLSMTL 454
Qy      138 EHLDSLNRKIGIYCTDLVLTQMPLLN-----SLDLSLNPWF 177
Db      455 KTLIDGENDISEFKNTFRNLNQLTGLRIDNRIGNITVGMFODLPRLSVLNLAKRROS 514
Qy      178 IQPGAF-KEIRLHKLTLRNPFDSLNWKCIQGLABEVRHVLVGFRR----- 226
Db      515 IERGAPDKNTEIARLDRKF-----LTDINGIFATLASLMLNLSNHLVWFVDAFIP 568

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Qy      227 GNLEKFD--KSALGELCNL--TIEEFLAYLDYLDIIDLFNCLTNVSSFSLSVSTIER 282
Db      569 SNLKWLDIHGVYIALGVYKLOEIRVTLTDASHNRITEL-GAMSVPSIRSLLEFINNI 627
Qy      283 VQDFSYN--FGQHLIELYNCKRGQPTLKLSKLTFTSNK-----GNAFS----- 328
Db      628 IQQIQANTFVDKTRLARVDLVANVLSKLSNALRAVAPSAEKPVEPFYIGNPFECDCSM 687
Qy      329 -----EVDLPSELFL-----DLNRNGLSFK-----GC 350
Db      688 EWLQRIINLTTQHRHVVDLGNIECLMPSRSPAPRLASLSASDFVCKESHCPPTGC 747
Qy      351 CSQSDFGTSLKYLDLSFNGVITMSSNFL--GLEQLHLDFQHSNLKQNSFVSFLSLN 408
Db      748 CEYQCECEVICPGNCSCHDATMTATNIYDCGRQDLAAL-----PRIPQDVADLYLDGN 803
Qy      409 LIYLDISHTHTRVAANGIFNGLSLEVLKMAQNSQENFLPDIFTELRLVTLFDSQCL 468
Db      804 MPELEVGHVGRNRRLRALYLNASNMTLQNGS-----LAQLVNLRLVHLNENKL 852
Qy      469 EQLSPYAFNSLSLQVLMNSHNPFSLDTPPYKCLNSLOVLDYSLNHMTSKKQELQHP 528
Db      853 TALBGTBRSLGLBELYHNMMLTHISNATPELVSLDLNRRSLPHLQYRH-- 910
Qy      529 SSLAFNLTONDFACTCEH-QSFLQWIKDQRLVEVERMECATPSDKQMPVL----- 581
Db      911 SLQGLTIGRANWMSRCQQLRELQFVSDNMAVVDADHDIYCLDAGIKRELBIGMLANG 969
Qy      582 -----SLNTCCOMNKT-IIQ-----VSULVSVSVAVLVYKFYHMLMLAAC 624
Db      970 PDCSDLDLASNISQDLACIGPCMPALVILFVAVVLIIVFVESVRMMLFA-- 1027
Qy      625 IKYG-----RGEN---IYDAFVIYSODEDMVRNELVKNLEEGVPPOLCLHYRDFIG 675
Db      1028 -HYGVRCBPREDGKLYDAIILHSKDYREVCCNIAELHSGRPPLCTCQQRD-LTP 1085
Qy      676 VAAANIIHEGFHKSRYIVVVSQHFQSRWCIFEYELAQTFQFLSSRAIIFIVLQK-- 733
Db      1086 QASHQLV-EGARASRKIILVLTRLMLATEWRIFRMA-----FHSRLGL-----AQKLV 1136

Qy      734 -VEKTLRQOVELYRLSHNTYLEMDVYLGRHT-----FWRRLKAL 775
Db      1137 IIEFTSVSAEEDVALS--PLYK---SVPSNRLLTCDRYFEWELKRYAL 1180

RESULT 5
T13887
c1r protein - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C.Accession: T13887
R.Chiang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A.Title: Expression of a novel Toll-like gene spans the parasegment boundary and contri
A.Reference number: Z17805; MUID:95151581; PMID:7848870
A.Accession: T13887
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-1185 <CHI>
A.Cross-references: UNIPROT:Q24591; EMBL:576155; NID:G913247; PID:G913248; PIDN:AAB33883
A.Genetics:
A:Note: c1r
A:Cross-references: FlyBase:FBgn0004364

Query Match      10.2%; Score 421; DB 2; Length 1385;
Best Local Similarity 24.0%; Pred. No. 1.9e-18;
Matches 213; Conservative 139; Mismatches 359; Indels 178; Gaps 33;

Qy      19 LDSLNPRLRHLSYSFSPPELOVDLSRCEIQTIEDGAYQSLSHSTLILGNPIQSLA 78
Db      338 LNLNNALTRISQKTFKELYFLQIIDMRNNSIGHIEGAFPLVYNLHTNLNENRLHTLD 397

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C:\Genetics

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OY      79 LGAFEGSLSLQGLVAVENTINLST--ENPFIQHKLTKELNVAHNLQSRLDEYSNLTNL 137
Db      388 NRIENGVLVYLTL-LLNNLVSVBSQAAPRNCSDIKELDISSN-QLTVEEAAODLSML 454
OY      138 EHLDISSNKIGSITCYCTDLRVLHQMDLNL-----SDLSLNPNNF 177
Db      455 KTLIDGENQGISFPKNTFRNLNQTLGLRLIDNRIGNITVGMPQDLPRLSVLNLAKRLOS 514
OY      178 IQPGAP-KEIRLHKULTLRNPFDSLNVMTKCIOGLAGLEVHRILVIGEPRNE----- 226
Db      515 IERGAFFDKTTEIEAIRLDKKF-----LTDINGIPATLASILMNLSENHLWEPDYAIF 568
OY      227 GNLEKFD--KSMBEGCNLU--TIEEFRLAYDYDDIIDLFNCLTNVSISLYSYTER 282
Db      569 SNLKMLDIGHNGIAELGVNYKIQEBIRVTTLTADASHNRITETI-GAMSVENSITELLFINNI 627
OY      283 VMDFSYN--FGQHIELVNCKRGQPPTLKSLSKLTFTSNK-----GGNAFS----- 328
Db      628 IGQIQANTFVDKTRLARPLDVANULSKISSLALRAVPASAEKPPEPIFGNPFECCDSM 687
OY      329 -----EYDLPSELFL-----DLSRNGLSEFK-----GC 350
Db      688 EWLGRIINNLTTRQHPHVVDLGNIECLMDHSRAPLRPLASIASDPVCYSHSCPTCHC 747
OY      351 CSQSPFGTTSKYLDLSFNGVITYMSNFL--GLEDELHDQHSULKCMSEFSVPLSI RN 408
Db      748 CEYECECEVICPCGNSCFHDAIYAWTNTIVDCGRDPLAL---PWRIPQDVSDIYDGN 803
OY      409 LIYLDISHTHRTVAANGI-FNGLSSLEVLKMGANSQGFNPLDIPTELNLTFLLDSQCQL 468
Db      804 MPELEVGHLTGRRNLRALIYNASNLMTLONGS-----LAQLVNLVLIHENKXL 852
OY      469 EQLSPFAFNSLSLOVLNMSSHNNFSLDTFPYKCLNSLOVLDSLNHIIMTSKKOLAHFP 528
Db      853 TALBESTERSGLABELVLIHNMLIHISNAFPEPLVSJLEVRLDNRNRSLSLPHIQYRH-- 910
OY      529 SSLATLNTQNDFACTCH-QSFLOWIKDQROLVERMECAPPSDKQMPLV----- 581
Db      911 SLQGILTGTGRNWMSCRCOQLRELAQFVSDNAMVVARDADIYCDLAGIRBELIGNLANG 969
OY      582 -----SLNTICQN-----KTIIGSVLSVSVVAVLVYKFPHMLLAGC 624
Db      970 PDCSLLDNASNISSSODLAGGYRLPLAAVLVIPLDVALLIVFVRESVRMMLEPA-- 1027
OY      625 IKYG-----RGEN---IYDAFVIYSODEDMVRNELVKNLBEGVPPQLCIHYRDFPG 675
Db      1028 -HYGRVCEPREDEDGXLYDALILHSEKDYEVCNIAALEHGSGPPRLTIQGRD-LRP 1085
OY      676 VAIAANIHEGHFSKRKVIVVVSQHFIOSRCIFEYELAQTWOFISSPAGITFYLOK-- 733
Db      1086 QASHLLQV-EGARPARSKIIILVLTNRMLATEWNRIFRNA----FHESIRGL----- 1136
OY      734 -VEKTLMAQQVELVRYLLSRNTYLEMEDSVLGRHI-----FMRRRLRKLL 775
Db      1137 IIETSVALEDVAELS-PYLK--SVPSNRLLTCDRYFWEKLRUYAI 1180

RESULT 6
T15864
hypothetical protein C56E.6 - Caenorhabditis elegans
CSpecies: Caenorhabditis elegans
CDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
CAccession: T15864
R.Fulton, L.
submitted to the EMBL Data Library, November 1995
A>Description: The sequence of C. elegans coemid C56E.6.
A.Reference number: S69019
A.Accession: T15864
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-1066 <Full>
A.Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIDN:AAA81C
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A:Gene: CESP:CS566.6
A:Intron: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 9
Query Match 9.5%; Score 392; DB 2; Length 1066;
Best Local Similarity 27.2%; Pred. No. 9e-17;
Matches 150; Conservative 96; Mismatches 214; Indels 92; Gaps 22;
QY 24 NPLRLGYSFSPFPELQVLDLSRCEIQITEDGAYQSLSHLSTLLTNPISLALGAFS 83
DB 154 NKVRRLDKHSFRSFRKIRELIDISYNOIQIVEDSFEYGHQSDLSYRIAYLPRG--- 210
QY 84 GLSSLDKVAVENTNLASLENPIGLHKLTKELVANHLLIOSFKLPEYSSNLTNLEHLDLS 143
DB 211 -----MLKNF---AKTLTKLKAENNTH--TPREALRDLNLTNLTNIN 248
QY 144 SNKIQSI-----YCTDLRLVHQMPLNLNLSDLSLNPNNFIOPGAFKEIRLKLTLRNPF 197
DB 249 GKTKLRIDDDVLKGCIDTLY-----ELFIANNYLEHI PHGVLSGMK-----QL 291
QY 198 DSLNVMKTCIQGLAGLEVHRLVLGEFPEEGNLEKPKDSALEGLCNLTPEBPRLAYDLYL 257
DB 292 EHLIDSKNKMISL-----KKPISLISITKEETSTVRRLNLAGNRINNMSDYL 338
QY 258 DDILDFNCLTNVS-SFSLVSVTIERKQDSYNGMQLHELVNCKFGQEPPL-KLKSILR 315
DB 339 --IFEMPLLTYDVAFNRIKFTISPRVEKIKNL--ESLFIQNNQLAHFPSLFRIDKLRH 394
QY 316 LFTFSN---KGVNAPSEVDPLSELEFDLSRNGLSFKCCOSSDPTGTS---LKLYDLSFN 369
DB 395 LMLDNNQIQIKDN-FSLADLPKLOHLSLAGNQDI---ITENMGSSSSSELSKSLTNLAH 450
QY 370 GVITWSS-NFLGLEDEHLDFOHSNLMKQSEFVSFLSRLMLIYDISHTHTRVAFNGIFN 428
DB 451 KTHSISRSEFSDLDNLQQLRLSHNNIRITISMT-FSNILRLRYLDLSHNRITIKILPSALY 509
QY 429 GLSSLEVLKMAGNSFOENFPLDFTELRNLTFLDLSQCQLEQLSEPTAFNSSLQVLAWS 488
DB 510 QLPALDVLHLDDHNNLE-IDRDAFRSPSDQLSLKSHNAFRFCEPLGISIQVHQLDLS 568
QY 489 HNNFELDPFPYKCL-NSLDVDSLNMHTSKKQOHLHPSSLAFLNLTQN-----D 540
DB 569 SNOINIDIF---CIARGIKLSLANSVEKIRKRLQD-ATELTSIDISHNGIITDVSD 624
QY 541 FACTCEHQSFLQ 552
DB 625 AFCECKRLSHIK 636

RESULT 7
A29944
choplin precursor - fruit fly (*Drosophila melanogaster*)
N:Alternate names: photoreceptor cell-specific membrane protein
C:Species: *Drosophila melanogaster*
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29944; A21123
R:Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
Cell 52, 291-301, 1988
A:Title: Choplin, a cell surface glycoprotein required for *Drosophila* photoreceptor cell
A:Reference number: A29944; MUID:88135762; PMID:3124963
A:Accession: A29944
A:Molecule type: DNA
A:Residues: 1-1134 <REI>
A:Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M19012
R:Zipursky, S.L.; Venkatesh, T.R.; Teplow, D.B.; Benzer, S.
Cell 56, 15-26, 1984
A:Title: Neuronal development in the *Drosophila* retina: monoclonal antibodies as molecular
A:Accession: A21123
A:Molecule type: protein
A:Residues: 31-43, 'HX', 46-49, 'H' <ZIP>
C:Genetics:
A:Cross-references: FlyBase:FBgn0000313

A,Intons: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
 C,Superfamily: chaperlin; leucine-rich alpha-2-glycoprotein repeat homology
 C,Keywords: cell adhesion; glycoprotein; membrane protein
 F,1-29/Domain: signal sequence status predicted <SIG>
 F,30-1134/Product: chaperlin #status predicted <MAT>
 F,80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR>
 F,103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
 F,128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F,152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F,177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
 F,201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
 F,226-243/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
 F,250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
 F,279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
 F,303-325/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
 F,326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
 F,351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
 F,375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
 F,401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
 F,428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
 F,453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
 F,477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
 F,502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
 F,527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
 F,551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
 F,577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
 F,601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
 F,625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
 F,649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
 F,673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>
 F,708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
 F,733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
 F,757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>
 F,781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>
 F,805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
 F,828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
 F,854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
 F,879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
 F,903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
 F,928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR>
 F,949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR35>
 F,973-996/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
 F,996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
 F,1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
 F,1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Query Match 8.1%; Score 333.5; DB 1; Length 1134;
 Best Local Similarity 23.0%; Pred. No. 4.7e-13;
 Matches 177; Conservative 114; Mismatches 249; Indels 231; Gaps 30;

10 DNLPSTKRLDLPNPLRLHLSVSPFPELQV-----L 43
 346 DSLVNSLQILDLSGNNLTGLHKLRFNFVLYKISMKNKIKIQKPTTFNVAHTLKL 405
 44 DLS-----RCEIQIETEDGA---YOSLS-----HLSTLILTNPIQ 75
 406 DLSGRNDPTNQLTRNTRKMNMSLSLSRLSSSVGPEDPFCVELEDQITRASLS 465
 76 SLALGAFSLSLQKLVAVETNLASLEN--PPIGLKTLKELNVAHNLIQSFKPEYIS 132
 466 GLOSHAFKVRGKRLDFSENGISSTIENPAFHIGH--SLISLKMSHGSGALPAEPUR 523
 133 NLTNLEHDLSSNKIOSICTDLRLVHOMPLNLISLISLPMNFIOPGAFK---EIRH 189
 524 HTLSIQEIDFSNNHSSMSDTSFHLKNIURL-----LELDNRLEQVLKTFPGGDHSKLE 579
 190 KLTLRNN-----FDSLNVKTCIQGLAGLEVHRLVLFGEFNEGNLEKFDKSALEG- 239
 580 EISLRFNHLTISIQHTFFLEALRK-----LHLDNKIKIRBRAPMNDLEVLSTLRGN 634
 240 -LCNLITIEEF-----RLAYIDYLDL-----IDLNCLTNVSSFSLSVYTIKVKDSYNF 290
 635 KINNLADESFQNLPKLEILDMAFNQLPNNFYFDQVGLTSLNIN--VNVSHNOIRQLMYS 693

291 GWOHLELVNCKFGQFPTLKLSLKRLEFTSNKGNVASEVDLPSEFLDLSRNGLSF--K 348
 694 SW-----SGRNEHCGHMSNKKIDLSHNNISILHP 724
 349 GCCSOSDRCGT-----SLKYDLSNNGVITMSN--FLGLEOLEH 386
 725 GYFRPAELSLTHLHLYNSLMTTRDVGNNPHIQMDLSYMWIHELDFDAFKNTKOQL 784
 387 LDFOHNSIKOMSEFVFLSLNLYLIDISHYTR--VAENGIFNG-----429
 785 VPFGRNYLSDLPQ-DIFPVGRLRVDSHHNKLPLNLYNGMEKLDVSHNMMLKIP 843
 430 ---LSLEVLKMAGNSFOENFLP-----DIFTELNLTFDLISQCLFOLSPFANSLS 481
 844 SSSLISLAALMLCELHLSNNPFLSTHSDLSNKFSLSLYLDISYVYLIRIDAVFATWPK 903
 482 LQVLMNSN-----NFF-----SLDFPKCLNSLOVDYSLNHITS 519
 904 LAVIDLSHNRDLKWKDKSFMLENSLKLGLNLSLTVPEIRLKYLEFRLGYNE-LPS 962
 520 KKOELHPPSSLAFLNTQNDFACTCEHQSFLOWIKDQROLVEVERMECATPSDKQ--- 576
 963 IPELARNMSLRLMLDSNND-----LTNVPMTQALPHLRRLML 1002
 577 -GMPVLSNITCOMNKTIIGVSV-LSVLVSVAVLVYKFFHMLLAGCI 625
 1003 SGNPITSLN-----NSFQVNMEDLEMDISNFRLHYREY-----GCL 1040

RESULT 8
 J05239
 Insulin-like growth factor acid-labile chain - baboon
 C,Species: Papio sp. (baboon)
 C,Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
 C,Accession: J05239
 R,Delnany, P.; Baxter, R. C.
 Biochem. Biophys. Res. Commun. 227, 897-902, 1996
 A,Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
 A,Reference number: J05239; MUID:97040714; PMID:8886027
 A,Contents: liver
 A,Accession: J05239
 A,Molecule type: mRNA
 A,Residues: 1-605 <DE>
 C,Comment: This factor is structurally related to proinsulin and have insulin-like meta

Query Match 7.5%; Score 309; DB 2; Length 605;
 Best Local Similarity 24.5%; Pred. No. 7.2e-12;
 Matches 155; Conservative 92; Mismatches 235; Indels 150; Gaps 23;

4 NFYKIPDMLPSTKRLDLPNPLRLHLSVSPFPELQVLDLSRCEIQIETEDGAYOSLSH 63
 64 NUTRLPDLIPGTOALMDNSNLSITPPAARNLSSIAFLNQQGQSLSEFQALLGLEIN 123
 64 LSTLILTNPIQISALGAFS-----GLSLQKLVAVETNLA 99
 124 LCHLLENNQRLSLAVGFATPALALGLSNRRLSLREDEGLFEGILMIDNLGNMSIA 183
 100 SIENPPIGLKTLKELNVAHNLIQSFKPEYFNSNLTNLEHDLSSNKIOSICTDLRLVH 159
 184 VLPDAFRLGLGLRLVLVAGNKL--AYLDLPALFSGIAELRELDLSKNALRALI--KANFA 239
 160 QMPPLNLISLISLPMNFIOPGAFKEIR-LHKLTLRNNFDSLNVAKTCIQGLAGLEVHRL 218
 240 QLPRLQ-KLYIDRNLIAAVAPGAFGLKALRWLDSH--RVAGLLEDFPGLGLGRVURL 297
 219 VLGEFRNEGNLEKFDKSALEGLCNLTIEFRLAYIDYLDLIDLFNCLTNVSSFSLSV 278
 298 -----SHNLIASIRPRTFEDL-----HFLERL-----QLGHN 324
 279 TIERVKDSYNGWOHLELVNCKFGQFPTLKLSLKRLEFTSN--NKGANVASEVDLPSE 336
 325 RIRQLAERSFE-GIGQLLEVLTLDHNQLOEVKVGAFGLTNVAVNMLSGNCIR--NLPEOV 381

```

QY 337 LUDLSR-NGLSKGGC-----SQSDFGTTSLKYLDTLSNGYITMSNPL-GLEQLEHDF 389
Db 382 FRGLKJLHSLHBSGLCRIRPHYTAGLSGLRRLTLKONGVLVGBEESQJWGLAELELDL 441
QY 350 QHSNLKQMSSEFSVFLSNRLIYDLISHYTRAFNGIINGLSSEVLTMAGNSFOENLP 449
Db 442 TSNQJ-----THLP---HQLFGQJGKJLELYLLSHNRLE- LP 474
QY 450 -DIFELANLFTLDSOCQLEBOLPFAFNUSLSLOVAMSHNPFSLDTPPYKCLNSLOV 508
Db 475 ADALGPRLEAFPLDVSHNRLEALPGSLIASIGRLKYLWLRNN--SLRTFPQ----- 524
QY 509 LDYSLNHMTSKKQELQHPSSILAFLNTONDFACTCEHOS-----FLOWI 554
Db 525 -----PCLERLWLEGNPMWDCSTLXKLRLPALQNPASVAPRFYAI 565
QY 555 ---KQROQLVEVERMECATPSDKQGMFVLSL 583
Db 566 CEGDDCQPPVYTYNNITCASPEEVAGLDRDL 597

```

RESULT 9

disease resistance protein D - tomato
C.Species: Lycopersicon esculentum (tomato)
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T17461
R.Parniske, M.J. Jones, J.D.
Proc. Natl. Acad. Sci. U.S.A. 96, 5850-5855, 1999
A.Title: Recombination between diverged clusters of the tomato Cf-9 plant disease resistance gene
A.Reference number: Z18801; MUID:99254130; PMID:10318973
A.Accession: T17461
A.Statut: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-853 (#PAR>
A.Cross-references: UNIPROT:O9ZS82; EMBL:AF119040; NID:g4235640; PID:g4235641; PIDN:AA0119040
C.Genetics:
A.Gene: NLOD

Query Match	7.3%;	Score 302;	DB 2;	Length 853;
Best Local Similarity	24.6%;	Pred. No.3.1e-11;		
Match 185;	Conservative 102;	Mismatches 288;	Indels 184;	Gaps 33;
Qy	17	KNLDSFNF-----PLRHLSGYSFESFPELOVLDLSRCRCIQTIIDGAYQSLSHLTILITG	71	
Db	111	KRLDLSYNDPFGSPF-----SPKFGFSNLTJHLDLDSFPTGIIISGISHLSKLYLRKST	166	
Qy	72	NPIQSLAG-----AFSGLSLQKLVAVETNLASLENFPIGHLKTKELNVANHLLQSF	125	
Db	167	DYPGSLSGPHNFELLKNLTQLRRLNYDVNLSS--TIPENFSSHLTNLRLAAYTELRGI	224	
Qy	126	KLPEYFSNLTJLHEHLDLSNNKIQSIYCTDRLVLMQPLNTSLDLSLPMNFIOGAFKE	185	
Db	225	-LPEFEFHLNLSBEDLSFNPQLYRFPPTTKMSNASLIVNLV-AGVNIADRI-PESSSH	281	
Qy	186	IRLHKLTIRNNPDSLNVKTCIQGLAGLEVRLVYGEFRNEGNEKEFDKSLBGLCNLT	244	
Db	282	L-----TALHKLHMGYTNLSGPIPK-----PLMNLTTH	308	
Qy	245	IEEPRFLAYDY-YLDDITDLFNCLTNVSPFLVSYTIE-RVKDSSYNGQHLTELV----	298	
Db	309	IESL---FLDYNHLEGPISHTPIPEKLSLSLGNPNFGRLEFPISSFNKMWKLERLDPS	365	
Qy	299	NCKRGQAPFT--LKLKSLRLTFTSNK--GGAFAFEV-DLPSELEFLDSHNGLSFK-----	348	
Db	366	NFLTGPISNVSGIQNLQOLLISSNHNGTIPSWIFSLPSTLVNLSDNTLSGKIQEKS	425	
Qy	349	-----GCCSGSDPGTSSLKLYLDSFNGV--TMSNPLGLGEQLEHLDPFQHSN	393	
Db	426	KTLFVSLBQNKLEBPILPRSLNMQPFLQALLSHNNISGHSISAI CNKTFITLLNLKSN	485	
Qy	394	LK-----QMSSEVFLSLRNLTLYDLSHTHTRVAENGIPNGLSLSEVLKMAGNSFOE	445	

[illegible]

RESULT 10

Insulin-like growth factor-binding complex acid-labile chain precursor - human

C/Species: Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence
C/Accession: A41915
R/Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A/Title: Structure and functional expression of the acid-labile subunit of the insulin-1
A/Reference number: A41915, MUID:92357025, PMID:1379671
A/Accession: A41915
A/Status: preliminary
A/Molecule type: mRNA; protein
A/Residues: 1-605 <LEO>
A/Cross-references: UNIPROT:P35859; GB:M86826; NID:G148407; PIDN:AAA36047.1; PID:G148408
A/Experimental source: liver
A/Note: sequence extracted from NCBI backbone (NCBI:P110171)
F:95-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:123-142/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:219-244/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F:339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F:483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

[illegible]

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QY 100 SLENPIGHTKTLKEINVAHNLIOSEFKLPEYFSNLTNLEHLDSSNKIQSIYCTDLRVLH 159
DB 144 VLPDAAPFGLGSLRELVLVAGNRL-AVLQALFSGLAELRELDSSNARAI---KANVY 239
QY 160 QMPLNLSDLSLNPMPNFIQGAPEIR-LHKLTLRNPNFDSLNMTKTCIOGLAGLEVRL 218
DB 240 QLPRLQ-KLYLDRNLIAAVALPAGFLGKALRWLDLSHN-RVAGLLEDTFPGLLGLRVRL 297
QY 219 VLGEERNNGENLEKPKSALLEGCONLTIEEFLAYLDVYLDIIDLFNCLTNVSSFSIVS 278
DB 298 -----SHNATASLRPRYKOL-----HFLLEU-----QLGHN 324
QY 279 TIERVDSFSYNGWOHLBELVNCQFQFPYLKLSKRLFTFS--NKGNAFSEVDLPSE 336
DB 335 RIRQLAERSFE-GLQGLVLTLDHNOQLEVKAGAFGLGTVNAVMLSGCLAR-NLPEVY 381
QY 337 FLIDLR-NGLSFKGCC-----SQSDFGTTSLXYLDLSENGVITMGSNPL-GLEQLEHLD 389
DB 382 FGLGKLSHLEGSCLGRIRPHTFGLSGLRRLFLKONGLVGIEQSLMGALRELDL 441
QY 390 QHSNLKONSEFVFLSLRLIYLDISHHTTRVAFNGIEFNGLSLEVLKMGNSFOENPL 449
DB 442 TSNOL-----THLP-----HFLFQGLKLEVLISRLRLAE-LP 474
QY 450 -DIFTELRLTLFLDLSQCOLEQSPAFNSLSLQVLMNSHNNFSLDTPPYKCLNSIQV 508
DB 475 ADALPRLQAFWLDVSHNRLALPNSLAPLGRILRLSLRNN---SLRFTTQ----- 524
QY 509 LDYSLNHTWTSKKQELQHPSSLAFLNLTQNDPACTCEHOSPLQWTKD-----QRO 559
DB 525 -----PGLERLWLEGNFWDCCP-----LKALRDPALONPSAVPRF 561
QY 560 LLEVERMECATPSPDKQMPVLINLTQMNKTIIGVSU 598
DB 562 VOACEGDQCPPAYTN-----NITCASPEVVGDL 594

```

RESULT 11

T42218
 silt-1 protein homolog - rat
 N/Alternate names: MEGF4 protein
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T42218
 R/Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A/Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A/Reference number: Z14126; MUID:98360089; PMID:9693030
 A/Accession: T42218
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1531 <NKA>
 A/Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:G3449289; PIDN:BA32460.1; PID:G3
 A/Experimental source: strain Sprague-Dawley; brain
 C/Genetics:
 A:Gene: MEGF4
 C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

```

QY Query Match 7.1%; Score 296; DB 2; Length 1531;
DB Best Local Similarity 22.2%; Pred. No. 1.6e-10;
Matches 158; Conservative 94; Mismatches 241; Indels 218; Gaps 25;

QY 8 IPDNLPSTKNLDSLNPRLRHGYSFFSPFELQVLDLSRCRIQTEGDAGYSLSTL 67
DB 303 IPANLPETTERLRLEINGIKSIIPGAFSPYRKLRIDLSNNOIAETAPDAFQGLNSLNSL 362
QY 68 ILTGNPIOSIALGAFSGSLSLQKLVAVETNLASLENFPIGHUKTLKEINVAHNLIOSEFKL 127
DB 363 VLYGNKTTDLPGRVFGGLVTLQELL-----LNA--NKINCIR- 397
QY 128 PEYFSNLTNLEHLDSSNKIQSI---YCTDLRVLHOMPLNLSDLSLNMPNFIQGAPE 184

```

```

DB 398 PDAFODLONLSLYDNKIOSLAKGTTSLRAID-----THLAONP--FIDCNLK 448
QY 185 EIRLRLTLRNNFDSLNMTKTCIOGLAGLEVRLV---LGEERNNGENLEKPKSALLEG 241
DB 449 WLA-----DFLRNPIET--TGARCSRRRLANKRIGQKS---KKPSCAKE--- 491
QY 242 NLTIEEFLAYLDVYLD-----DIIDLFNCLTNVSSFSVLVSTLERRVDFSYNGWOHLE 296
DB 492 ---QYFIPTGEDYHIANSECTSDVACPACRCEASVEVSCGLKSKRIPE-RIPQSTTELR 546
QY 297 LVNCKP-----GQPTLKLSKRLUTFTSKMGNAFSEVDLPSEFLDLSNNGLSFKGC 350
DB 547 LNNEISILEATGPKR-KLSHLKKNLSNNK---VSEIDEGTE----- 586
QY 351 CSQSDFGTTSLXYLDLSENGVITMGSN-FLGLEQLEHLDFOHSNLKONSEFVFLSLRL 409
DB 587 -----GATSVSEHLTANOLESVAGSGFRGLDGLRTLMRLNNRISCHINDS-FGLGLRV 639
QY 410 IYLDISHHTTRVAFNGIEFNGLSLEVLKMGNSFOENF----- 447
DB 640 RLISLYDNHITTSIPGARDTLOALSTLNLINLPFNCQLAWLGDMLRKRTVTGNPRCQ 699
QY 448 -----L 448
DB 700 NPDFLRQIPLQDVAPDFRCRCEGQEEVCLPRPQCPQBCACLDIVVRCNKHQALPKGI 759
QY 449 PDIFTEL-----RLTLFLDLSQCOLEQSPAFNSLSLQVLMNSHNN 491
DB 760 PRNVTLELYDGNQFLVGEQSLTPKYLQVLQVLSNNKISLSNSSFTNNSQLTTLISVYA 819
QY 492 FFSLDTPPYKCLNSIQVLDYSLNHTWTSKKQELQHPSSLAFLNLTQNDPACTCEHOSPL 551
DB 820 LQCIPLPFAFGRLSRILSLIHGNDVSTLQEGIFADV-TLSLSHLAGANPLYCDCHLRWLS 878
QY 552 QMKRQRLVLEVERMECA-----TPSDK---QGMVPLSINITC 587
DB 879 SWVKTYR---EPGIARCAQPEMEGKLLTTPAKKFCQGPSPALVQAKC 926

```

RESULT 12

H96510
 probable disease resistance protein [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: H96510
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Hansen, N.F.; Hughes, B.; Hulzar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: H96510
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-994 <STO>
 A/Cross-references: UNIPROT:Q9C637; GB:AB005173; NID:g11321768; PIDN:AA634245.1; GSPDB:
 C/Genetics:
 A:Gene: F2G19.6
 A/Map position: 1

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QY Query Match 7.1%; Score 292; DB 2; Length 994;
DB Best Local Similarity 23.6%; Pred. No. 1.6e-10;
Matches 152; Conservative 92; Mismatches 241; Indels 158; Gaps 30;

QY 1 MEINLYKIPDNLPSTKNLDSLNPRLRHGYSFFSPFELQVLDLSRCRIQTEGDAGYOS 60
DB 281 LKLSIY---NTSFS-GTIPNISINLKHLTS-----LKLQQAFAFSGRIFSSLRSS 324

```


Db 64 NLTHTLPIVSTRALNLDGNNLSIPSAFQNLSDFLANLQGSWLRSLERQALLGLON 123
 Qy 64 LSTLITLGNPIQSLALGAFSGSLQKLVAVETNLASLENPFIQHLTKLKEINVA----- 118
 Db 124 LYVHLERNRLNLAVALGFTHTPPLASLSLSNLLGRLEEGFQGLSHLMDLNGNSLV 183
 Qy 119 -----NHLI-----QSFKLPEYPSNLTNLEHLDSSSNKIQSIYCTDLRYLHQ 160
 Db 184 VLPDVTFOGLNHLVLAGNKLTYLQPYLFCGLSELRDLSSRLARSV---KANVFA 240
 Qy 161 MFLNLSLDLSINPMNFIOPGAFKEIR-LHKLTLRNFPDLSNVMKTCIOGLAGEVRYLV 219
 Db 241 LPRLO-KLYLDNLTAAVAPGAFGLMKALRWLDLSIN-RVAGLMETTFGLGLVLR 298
 Qy 220 -----LGEFR-NEGNELEKFDKALBGLCNLTIEFRLAYLDYLDI- 260
 Db 299 HNAIALSRPRTEKDLHLEELQLGHNRIHQGERTFEGQLGEV---LTLDNDQITEVR 354
 Qy 261 IDLENCNTNVSSFSLSVYI---ERV---KDPSTNFGQHLVYNCKGQFPYTKLSL 313
 Db 355 VGAFSGLEFNVAWNLSGNCRLSRPFRVFOGLDKLSLHLSCLGHVRLHTE--AGLSGL 412
 Qy 314 KRLTFTSNKGNAFSEVD-----LPSLEFLDLSRNGLSFKGCCSQSDPGTTSKXLDLS 367
 Db 413 RRLFRD-----NSISIERQSLAGLSLELDELDTNRLLTH--LPRQLFOGLHLYLIS 466
 Qy 368 FNGVITWSSNFLGLELEHLDFOHSNLMKQSESVFLSLRNLIYDISHHTTRVAFNGIF 427
 Db 467 YNQLTTLTSAEVLG-----PLQRAFWLDISHNHLLETLAGELF 502
 Qy 428 NGLSLEVLKMAGNSFOENFLPDITELRNLTFLDLSQCLEQLSPFTAFNSLSLQVLMN 487
 Db 503 SSLGRVRLSLNNLSLQ--TFSP-----OGLERL----- 530
 Qy 488 SHNNEFSLDTPPYKCLNSLOVL-DYSLNHNMTSKQELQHPSSSLAFNLQNDPACTCE 546
 Db 531 -----WIDANPMDSCPLKALDPALQ-----PGVVPFRVQT-----VCE 566
 Qy 547 HOSFLQWIKDQRQLIVEVERMECATPSPDKQGNPVLISLNT 586
 Db 567 -----GDQCQPVYTYNNITCAGPANVSGLDLNDVSET 598

RESULT 15
 CF-4A protein - tomato
 C:Species: Lycopersicon esculentum (tomato)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T07015
 R:Takken, P.L.; Schipper, D.; Nijkamp, H.J.; Hill, J.
 Plant J. 14, 401-411, 1998
 A:Title: Identification and Ds-tagged isolation of a new gene at the Cf-4 locus of tomato
 A:Reference number: Z15863; MUID:98335213; PMID:9670557
 A:Accession: T07015
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-855 <TAK>
 A:CDS8-references: UNIPROT:O50024; EMBL:Y12640; NID:e1289424; PIDN:CAA73187.1; PID:e128
 C:Genetics:
 A:Experimental source: strain Cf-4; isolate MM-Cf-4
 A:Gene: Cf-4A
 A:Map position: 1

Query Match 7.0%; Score 290; DB 2; Length 855;
 Best Local Similarity 24.8%; Pred. No. 1.8e-10;
 Matches 187; Conservative 95; Mismatches 281; Indels 190; Gaps 36;

Qy 19 LDLSNPNR---HLCGYSPFSPBELQVLDLSRCETQTEBDGAYQSLSHLSTLITLGNPIQ 75
 Db 85 LDIGSQSQGKRFHNS-SLFOLSNKLRLDLSND-----FTGSP- 123
 Qy 76 SLALGAFSGSLQKLVAVETNLASLENPFIQHLTKLKEINVAHNLQSFKL---PEYF- 131

Db 124 SPKFEBSFDLTHLD---LSDSNFTGVIPSEISHLSKLHVLRLS---DOYKLSLGFHNE 176
 Qy 132 ---SNLTNLEHLDLSNNKIQ-----SIYCTDLRYLHQ-----MP-----LNLNS-LDL 170
 Db 177 LLLKXLTQLQREHLHLSVNISSITPBNFSPHLLNMLSLSTELNGVLPBRVFIHLSNELLD 236
 Qy 171 SLNPMNFIQ-----PGAFKEIRLHKLTLRNPF-DSLNVMKTCIOGLAGEVRYLV 221
 Db 237 SYNPLQTVRFPPTIWNSSASLVKYLISRVNLAGNIPDSFSYLTA-----LHLEDV 287
 Qy 222 EFRNENLEKFDKALBGLCNLT-IEEPRLAYLDYLDIIDLFNCLTNVSSPFSVSVYI 280
 Db 268 YTNLSGPIPK-----PLMNLTNIESLDLDY--NHLBGPQLPIPEFKLSLTLGNND 338
 Qy 261 ERVKDF-SYNFGQHLVY---NCKFGQFP--LKLKSLKRLTFTSNK-IGNAFSEV-D 331
 Db 339 DQGLEFLSPNRSWTQLEELDPSNSLTGP1PENVSGLRNLOSLYLSNNLNGSIPSWID 398
 Qy 332 LPSLEFLDLSRNGLS-----FKGCCSQSDPGTTSKXLDLSFNGV 371
 Db 399 LPSLSLDLSNNTFSGKIQEFKSKTSLIVTLKONQKGP1PNSLINOESLQFLLSHNNI 458
 Qy 372 I-TWSSNFLGLELEHLDFOHSNLMKQSESVFLSLRNLIYDISHHTTRVAFNGIFNGL 430
 Db 459 SGHISSICNLKILVNLVLDGSSNNEGTTPQCYVERNEYLSHLDLSNNRSLGTTINTTFSIG 518
 Qy 431 SLEVLKMAGNSFOENFLPDITELRNLTFLDLSQCLEQLSPFTAFNSLSLQVLMNSH 490
 Db 519 NSFRAISLHGNKLTGK-VPRSLINCKYLTLLDIGNNQLNDTPRNLGYLSQKILSLRN 577
 Qy 491 NFFSLDTPPYKCLNS-----LQVLDY-----LNHNMTSK-QELQHPSSL 531
 Db 578 KLHG-----PIKSSGNTNLFMRQLIIDLSSNGPSGMLPERILGNLTQTMKKFDENTRFPBYI 633
 Qy 532 A-----FINLQNDPACTCEHOSFLQWIKDQRQL 562
 Db 634 SDRIYYVYLTITTTKGQDYDSVR1FTFRMNLINLSKNRFBGRI--PSIIIGDVGKRTLNL 691
 Qy 563 EVERMECATPSPDKQGNPVL-----SLNITCOMNKTIIIGSVLSVAVSVAVLVYKPYF 616
 Db 692 SHNVLEGHIPVSLQNLVLSLESLDSSNKISGAIPOQLASLFLFLEVLNLS-----HN 742
 Qy 617 HMLLAGCITKYGGENITYDAFYISSQDEDMWR 649
 Db 743 HLV---GCIPKQKQ---FDSFGNTSYQQNDGIR 769

Search completed: March 12, 2005, 19:57:00
 Job time : 28.6156 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:15:31 / Search time 86.9834 Seconds
(without alignments)
3712.721 Million cell updates/sec

Title: US-09-396-985B-6

Perfect score: 4335

Sequence: 1 NMPPLHAGTLMALFLSCL.....GRALNPDETSEEQEATTLT 835

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_15Dec04:*

1: geneseqp19808:*\n2: geneseqp19908:*\n3: geneseqp20008:*\n4: geneseqp20018:*\n5: geneseqp20028:*\n6: geneseqp20038:*\n7: geneseqp20048:*\n8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2860.5	66.0	839	6	ABU04773 Human exp
2	2860.5	66.0	839	6	ABU04774 Human exp
3	2860.5	66.0	839	6	ABU04775 Human exp
4	2860.5	66.0	839	7	AD078785 Human PRO
5	2860.5	66.0	839	7	AD088826 Human PRO
6	2864	65.6	837	2	AAW86361 Human DNA
7	2844	65.6	837	2	AAE16102 Human DNA
8	2844	65.6	837	6	ABU04776 Human exp
9	2837	65.4	837	5	AAE16116 Human exp
10	2796.5	64.5	801	8	AD057797 Squirrel
11	2782.5	64.2	795	8	AD057791 Rhesus mo
12	2781.5	64.2	795	8	AD057800 Hamadryas
13	2777	64.1	808	8	AD057803 Chimpanze
14	2773	63.7	808	8	AD057782 Chimpanze
15	2761	63.5	801	8	AD057785 Gorilla t
16	2751.5	62.9	799	2	AAW86352 Human DNA
17	2726	62.9	799	5	AAE16093 Human DNA
18	2726	62.9	799	5	ABE83162 Human DNA
19	2726	62.9	799	6	ABR42963 Human Tol
20	2726	62.9	799	7	AD0839121 Human Tol
21	2726	62.9	799	7	ADP56656 Human Tol
22	2726	62.9	799	8	ADP48597 Human Tol
23	2558.5	59.0	745	8	ADP57799 White-fac
24	2440	56.3	738	8	ADP29455 Human sec

26	898.5	20.7	208	3	AAW88059 Human Tol
27	883	20.4	179	7	AD042707 Murine To
28	761.5	17.6	178	8	ADN12270 IL-1R/TLR
29	602.5	13.9	661	2	AAW28510 Product o
30	602.5	13.9	661	2	AAW87556 B cell su
31	602.5	13.9	661	7	AD038652 Human sec
32	602.5	13.9	661	7	AD069098 Human MP5
33	595	13.7	650	3	AAW82527 Human RPL
34	588.5	13.6	632	2	AAW47274 Human B-C
35	575	13.3	1032	5	AAO21588 Murine To
36	575	13.3	1032	7	AD085953 Mouse Tol
37	575	13.3	1032	7	ABW01559 Murine To
38	559	12.9	1050	5	AAO21579 Murine To
39	559	12.9	1050	7	AD085947 Mouse Tol
40	559	12.9	1050	7	ABW01556 Murine To
41	546	12.6	1059	5	AAO21587 Murine To
42	546	12.6	1059	7	AD085951 Human Tol
43	546	12.6	1059	8	AD088188 Human 122
44	541.5	12.5	859	6	AAE33341 Mouse Tol
45	541	12.5	1041	2	AAW41768 Human PRO

ALIGNMENTS

RESULT 1
ABU04773 standard; protein; 839 AA.
ID ABU04773
AC ABU04773;
DT 29-JAN-2003 (first entry)
DE Human expressed protein tag (EPT) #1439.
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
KW Homo sapiens.
OS WO200278524-A2.
PN 10-OCT-2002.
PD 28-MAR-2002; 2002WO-US009671.
PE 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PT 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
PA (ZYCO-) ZYCO INC.
PI Chicx RM, Tomlinson AJ, Urban RG;
DR WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.
XX Example 2; SEQ ID NO 1439; 134p; English.
XX The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a

```
CC mammal an immunogenic response directed against any of the purified
CC polypeptide, the purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for transnational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 839 AA;
XX
Query Match      66.0%; Score 2860.5; DB 6; Length 839;
Best Local Similarity 66.5%; Pred. No. 4.1e-244;
Matches 559; Conservative 115; Mismatches 159; Indels 7; Gaps 5;
QY 1 MMPLHLAAGTLIMAL-FLSCLRPGSLNPCIEVLPNITYQCMQDNLSKIPHDIPYSTKNLD 59
DB 1 MMSASLALAGTLIPAMAFSLCVRPESWPCVEVPNITYQCMELNFKIDPNLPSTKNLD 60
QY 60 LSFNPKILRSYSFTNPSQQLWDLSCREIETIEDKAMHGLANGLTVLTGNPIKSPSG 119
DB 61 LSFNPKILRSYSFTNPSQQLWDLSCREIETIEDKAMHGLANGLTVLTGNPIKSPSG 120
QY 120 SFSGLTNLENVAVERKMTSLSEFHIGQLSLKLVANVNLHSLFCLPEYFSLTNLEHY 179
DB 121 AFSGLSSLOKLVAVETNLASLEFPIGHKTLKELNVAHNLQSFCLPEYFSLTNLEHY 180
QY 180 DLSYNIQTISYVDLOFLRENPOVNLDSLNLNPIDISOAQAQFQIRLHELTLSRPNSS 239
DB 181 DLSNNKIQITCTDLRAVLHQMPLNLSLNLNPNMFIQPGAKELRHKTLRNPNFSL 240
QY 240 NVLKMCLQWMTGLVHRLILGEFKNERNLSEFDRSVMEGLCNVSIIDEFRILYINHESDI 299
DB 241 NVMKTCIOGLAGLEVRLVGEFRNENLEKFDKSLLEGICMLTIEFRILYADYLDI 300
QY 300 NVL-NCLANISAMSPFGVHIIKHADVPRHKQOSLIIRCHLKRPKLSLPLKSLTLT 358
DB 301 IDLFCNLTVSSSLVSVTIERKQDSYNGWGHLELVNCKRQFPLKLSKRLTPTS 360
QY 359 NNEDISFGQLALPSLRYLDSLRYNAMSFRGCCSYSDGTNNLKYLDLSPNGVILMSANFNG 418
DB 361 NKGGMASFVDLPJLEFLDSLNRGLSFKGCCSDGTTSIKYLDLSPNGVILMSNFI 420
QY 419 LSELEYLDLPOHSTLTKVTERSVFLSEKLLYLDISTNTKIDPFGILGILSLNTLKMAG 478
DB 421 LEQLHELDFOHSLNKKOMSEFSVFLSLRNLIYLDISHTHRAVFNGLISLEVLKMG 480
QY 479 NSFKQNTLSNVFNNTNLFTLDSLKQGLISGVDPDLYRLQLMNSNNLLFLDPSTY 538
DB 481 NSFOENFLPDILFELRNLTFLDLSQQLSLSTANSSLSQVLNMSNNFESLDTPEY 540
QY 539 KOLYSRLTDCSFNRIS-EGILQHPKSLAVFNLTNNSVACICEYONFLQWQXQKMF 597
DB 541 KCLNSLOVDYSLNHTMTSKQELQHPSSIAFLNLTQMDFACTCHGQFLQWIKQRL 600
QY 598 LVNVEQMKASPIDKASLVDFTNSTCYIKTISVSVSVLVAVTAFILYHFYHLI 657
DB 601 LVEVERMECATPSDKQMPVLSL-NITQMNKTIIGSVYLSVLVAVVAVLVYKFFHLM 659
QY 658 LTAGCKKYSRGSBIYAPVITISQONEDWYRNLVKNLREGVRRFQCLATYRPIPVAA 717
DB 660 LTAGCKIKYRGENVYDAFVYISQDEDWARNELVKNLREGVRRFQCLATYRPIPVAA 719
QY 718 ANIIQGFHKSRIYVVRHFIQSRMCIFFEYELIAQTQWFLSRSRGIPIVLEKYVSKLL 777
DB 720 ANIIHGFIHKSRIYVVSQHFIQSRMCIFFEYELIAQTQWFLSRSRGIPIVLEKYVSKLL 779
QY 778 ROQVELYRLLSRNTYLEWEDNALGRHIFWRRLKALLDQKALNP--ETSEEOBATTLL 834
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DB 780 ROQVELYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDQKSWNPBGVTCGMQBEATSI 839
|||||
RESULT 2
ABU04774
ID ABU04774 standard; protein; 839 AA.
ABU04774;
29-JAN-2003 (first entry)
Human expressed protein tag (EPT) #1440.
Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
kinase; protease inhibitor; transporter; cytoskeletal protein;
receptor; transcription factor; cancer; MHC;
major histocompatibility complex; myeloma; colon cancer; gastric cancer;
adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX Homo sapiens.
XX OS
XX WO200278524-A2.
XX PN
XX 10-OCT-2002.
XX PD
XX 28-MAR-2002; 2002WO-US009671.
XX PF
XX 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0356855P.
XX PA
XX (ZYCO-) ZYCOS INC.
XX PI
XX Chicz RM, Tomlinson AJ, Urban RG;
XX DR MPI; 2003-040607/03.
XX PT
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 1440; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for transnational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 839 AA;
XX
Query Match      66.0%; Score 2860.5; DB 6; Length 839;
Best Local Similarity 66.5%; Pred. No. 4.1e-244;
Matches 559; Conservative 115; Mismatches 159; Indels 7; Gaps 5;
QY 1 MMPLHLAAGTLIMAL-FLSCLRPGSLNPCIEVLPNITYQCMQDNLSKIPHDIPYSTKNLD 59
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Db      1 MMSASRLAGTLLPAAAFSLCVBPESWPCVEVVPNTTYOCMEINFKYKIDNLPSTKND 60
Oy      60 LSFNPLKIRSYSFNTFSQLOWLDLSRCEIETIEDKAMGMLNSTLVLTGNPIKSFSPG 119
Db      61 LSFNPLRHLGYSFSPFPELOVLDLSRCEIQTIEDAYOSLSHSLTLITGNPIQSLAG 120
Oy      120 SFGSLTNLENLVAVETKMTSLBGFHIGQISLKKLVANANLHSPKLPYFSNLTNLEHV 179
Db      121 AFSGLSLQKLVAVETNLASLENFPIGHLKTLKELVANANLQSFCLPEYFSNLTNLEHL 180
Oy      180 DLSYNTIQTISVKDLOFLRENPOVNLSDLSNPIDSIOAQAQFQIRLHELTLSRNFNS 239
Db      181 DLSNNTIOSIYCTDLRVLHQMPLNLSDLSNPMPFIOPGAFKEIRLKLTLRNPNFSL 240
Oy      240 NYLKMCLQMMTGIAVHRLLIGEFKNERNLESFDRSVMGLCNVSIDEFRLTYINHSDDI 299
Db      241 NVMKTCIOGLAGLEVRLVGEFRNGNLEKPDKALBGLCLNLTIEFRLAYLDYLDI 300
Oy      300 YNL-NCLANISAMSTGVHAKHADVPRHFKWQSLIIRCHLKPFPKSLPFLKSWTLTT 358
Db      301 IDLFNCLTNVSSFLSVSTIERKDPSPYNGQHLVNCQFQPTLTKLSKRLTFT 360
Oy      358 NREDSFQGLAPSLRYLDLSRANSPFCSSYSDGTNNLKTLDLSNGVILMSANFNG 418
Db      361 NKGNAFSEVDLPSEFLDLISRNGLSFKGCCSDPTTSLKXLDLSFNGVITMSNFDG 420
Oy      419 LRELEFLDFQHSITLKVTEFSVFLSEKLYLDISTNTKIDPDGIFLGISLNTKMG 478
Db      421 LROLEHLDPQHSNLMKQMSFVFLSRNLITLDISTHTRVAFNGIFNGLSLEVLKMG 480
Oy      479 NSFCKDLSNVFNTNTNLFLDLSKCOLBQISRGVDTLYRLQLMNSHNNLFLDPHY 538
Db      481 NSFQENFLPDIETELNLTFLDLSQCLQSLSTANSLSLQVAMSHNNFSLDTPFY 540
Oy      539 KQIYSIRTDSCFNRIETS-KGILQHPKSLAVENLTNNSVACTCYQNFQWQDKMF 597
Db      541 KCLNLSQVLDYSINHTSKOELQHPPSLAFLNTQNDPACTCHOSFLQWIKQOROL 600
Oy      598 LVNVEQMKASPIDMKASLVLDFTNSTCYIKTIVSVSVSVVAVTVAFLYHFEFHL 657
Db      601 LVEVERMECATPSDKQMPVLSI-NITQMNKTIIGVSVLSVAVVAVLKYKFFHLM 659
Oy      658 LTAGCKKYSRGSIDYDAFYISSQNEQWYRNELVKNLESGVPRFOLCHYRDFIPGVA 717
Db      660 LLAGCIXKRGEMIVDAFYISSQDEQWYRNELVKNLESGVPRFOLCHYRDFIPGVA 719
Oy      718 ANIIOGFHKSRKVVVSRHPTQSRWCIFEYHIAQTWQPLSSRSIIFIVLEKVKSL 777
Db      720 ANIIEGFHKSRKVVVSRHPTQSRWCIFEYHIAQTWQPLSSRSIIFIVLEKVKSL 779
Oy      778 RQOVELYRLSRNTYLEMEDNLGRHIFMRRLKALLDDKALNPD--ETSEBEOATLL 834
Db      780 RQOVELYRLSRNTYLEMEDSVLGRHIFMRRLKALLDDKSNPBGTGTGICNMQEATSI 839

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XX      XX WO200278524-A2.
PN      XX
PD      XX 105OCT-2002.
PF      XX 28-MAR-2002; 2002WO-US009671.
XX      XX
PR      XX 28-MAR-2001; 2001US-0279495P.
PR      XX 21-MAY-2001; 2001US-0292544P.
PR      XX 08-AUG-2001; 2001US-0310801P.
PR      XX 01-OCT-2001; 2001US-0326370P.
PR      XX 04-DEC-2001; 2001US-0336780P.
PR      XX 20-FEB-2002; 2002US-0358985P.
XX      XX
PA      (ZYCO-) ZYCOS INC.
PI      Chicz RM, Tomlinson AJ, Urban RG;
DR      WPI; 2003-040607/03.
XX      XX
PT      New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT      cytoskeletal proteins, receptors or transcription factors), useful for
PT      treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT      leukemia.
XX      XX
PS      Example 2; SEQ ID NO 1441; 134pp; English.
XX      XX
CC      The invention describes a purified polypeptide, which comprises a
CC      fragment of a kinase, phosphatase, protease, protease inhibitor,
CC      transporter, cytoskeletal protein, receptor or transcription factor. The
CC      polypeptide is useful as an immunogenic composition for eliciting in a
CC      mammal an immunogenic response directed against any of the purified
CC      polypeptide. The purified polypeptide, or the antibody that binds to this
CC      polypeptide, is useful for treating cancer. The polypeptide is also
CC      useful for identifying compounds that binds to a naturally processed
CC      class I or class II MHC-binding polypeptide. The polypeptides and
CC      polynucleotides are particularly useful for treating or preventing
CC      myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC      lymphoma or leukemia. These are also useful for screening agents for
CC      treating the above mentioned diseases. This sequence represents an
CC      expressed protein tag (EPT) isolated from human tissue for translational
CC      profiling. Note: This sequence does not appear in the printed
CC      specification but was obtained in electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX      XX
SQ      Sequence 839 AA;
XX      XX
Query Match 66.0%; Score 2860.5; DB 6; Length 839;
Best Local Similarity 66.5%; Pred. No. 4.1e-244;
Matches 559; Conservative 115; Mismatches 159; Indels 7; Gaps 5;

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Oy      1 MWPLHLIAGTLLMAL-FLSCLRGSLNPCIETLPNITQOCMDONLSKIPHDIPYSTKND 59
Db      1 MMSASRLAGTLLPAAAFSLCVBPESWPCVEVVPNTTYOCMEINFKYKIDNLPSTKND 60
Oy      60 LSFNPLKIRSYSFNTFSQLOWLDLSRCEIETIEDKAMGMLNSTLVLTGNPIKSFSPG 119
Db      61 LSFNPLRHLGYSFSPFPELOVLDLSRCEIQTIEDAYOSLSHSLTLITGNPIQSLAG 120
Oy      120 SFGSLTNLENLVAVETKMTSLBGFHIGQISLKKLVANANLHSPKLPYFSNLTNLEHV 179
Db      121 AFSGLSLQKLVAVETNLASLENFPIGHLKTLKELVANANLQSFCLPEYFSNLTNLEHL 180
Oy      180 DLSYNTIQTISVKDLOFLRENPOVNLSDLSNPIDSIOAQAQFQIRLHELTLSRNFNS 239
Db      181 DLSNNTIOSIYCTDLRVLHQMPLNLSDLSNPMPFIOPGAFKEIRLKLTLRNPNFSL 240
Oy      240 NYLKMCLQMMTGIAVHRLLIGEFKNERNLESFDRSVMGLCNVSIDEFRLTYINHSDDI 299
Db      241 NVMKTCIOGLAGLEVRLVGEFRNGNLEKPDKALBGLCLNLTIEFRLAYLDYLDI 300
Oy      300 YNL-NCLANISAMSTGVHAKHADVPRHFKWQSLIIRCHLKPFPKSLPFLKSWTLTT 358

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Oy      59
Db      60
Oy      119
Db      120
Oy      179
Db      180
Oy      239
Db      240
Oy      299
Db      300

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Db 301 IDLNFCLINVSBSLVSTIERVKDFSYNFGQHLVNVCKFGQFPTLKSLKRLTPTS 360
Qy 359 NREDISFGQALPSLRAYDLDSRNAMSFRCSCSYDPGTNNLKYLDLSPNGVILMSANFNG 418
Db 361 NKGNAFSEVDLPSEFLDLSRNGLSFKCCSQSDPGTTLSTKYLDSFNGVITMSNFI 420
Qy 419 LEELEYLDPQHSSTLKKVTEFSVFLSEKLLYLDISTYNTKIDPDGIFGLISLNTLKMAG 478
Db 421 LEQLEHLDPOHSNLKQMSSESVFLSLRNLIYLDISHHTTRVAFNGIFNGLSLEVLKMAG 480
Qy 479 NSFQNTLSNVFTNTNTNLFEFLDSKQLEQISRGVDTLYRLQLNMSHNNLLFLDPESHY 538
Db 481 NSFQENFLPDIFTELRLNTFLDLSCQQLSPPTANSLSSQLVLMNSHNNFSLDTPPY 540
Qy 539 KQVSLRLTDCSPNRLET-SKGLQHPKSLAVFNLTNNSVACICEYONFLQWYDQKF 597
Db 541 KCLNSLOVLVDSLHNTMTSKQELQHPSSLFLNLTONDFACTCHQSFLQWIDQRL 600
Qy 558 LVNVEQMKCASPIDMKASLVDPFTNSTCYIYKTIISVSVSVLVVATVAFLYHFFPHLI 657
Db 601 LVEVERMECATPSPDKQMPVLSL-NITCOMNKTIIIGSVLSVLVSVAVLVYKFFPHLM 659
Qy 658 LIAGCKTSRGSIVDAFVIYSSQNEDEWVRNELVKNLEBGPFRFOLCLHYRDPFGVAIA 717
Db 660 LIAGCIKTYGRGENIYDAFVIYSSQDEDEWVRNELVKNLEBGPFRFOLCLHYRDPFGVAIA 719
Qy 718 ANIOEGFHKSRYIVVVSRRHFIQSRWCIFEYEIAQTMQFLSSRSGIIFIVLEKYEKSL 777
Db 720 ANIHGPHKSRKVIIVVVSQHFIQSRWCIFEYEIAQTMQFLSSRSGIIFIVLQYKYEKTL 779
Qy 778 RQVVELYRLSRNTYLEMEDNALGRHIFWRRLKALLDGKALNDP---ETSEEDPATTL 834
Db 780 RQVVELYRLSRNTYLEMEDSVLGRHIFWRRLKALLDGKSWNPBGTVGTGCMQGEATSI 839

RESULT 4
ADCT8785
ID ADCT8785 standard; protein; 839 AA.
AC ADCT8785;
XX
DT 01-JAN-2004 (first entry)
DE Human PRO protein #7.
XX
KM human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
XX Crohn's disease.
OS Homo sapiens.
XX
PN WO2003034984-A2.
XX
PD 01-MAY-2003.
XX
PF 15-OCT-2002; 2002WO-US033070.
XX
PR 19-OCT-2001; 2001US-0340083P.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL;
XX
DR WPI; 2003-481990/45.
XX
DR N-PSDB; ADCT8784.
XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
XX disorder e.g., ulcerative colitis or Crohn's disease.
XX
PS Claim 12; SEQ ID NO 14; 327bp; English.
CC The invention comprises the amino acid and coding sequences of human PRO
XX proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
CC sequence represents a human PRO protein of the invention.
SQ Sequence 839 AA;
Query Match 66.0%; Score 2860.5; DB 7; Length 839;
Best Local Similarity 66.5%; Pred. No. 4.1e-244;
Matches 559; Conservative 115; Mismatches 159; Indels 7; Gaps 5;
Qy 1 MNPFLHAGTLMAL-FLSCIRPGSLNPCIIVLPITTCQMDONLSKIPHDIPYSTKLD 59
Db 1 MMSARLGLTLPAAAFSLSCVRSPSWEPCVEVPPIYQCMELNFKLPDLNLPSTKND 60
Qy 60 LSFNPLKILRSYSFTNFSQLOMLDLSCREITIEDKAMHGANOUSTVLVTCNPIKSPSPG 119
Db 61 LSFNPLRLHLSGYSFSPSPFELQVLDLSREIGITIEDGAQSHLSTLTLTGNPIQSLAG 120
Qy 120 SPSGLTNLENIVAVETKNTSLGPHIGQLISLKLINVAHNLISHFKLPEYFSNLTNLEHV 179
Db 121 AFSGLISLQKLVAAVETNLIASLENFPIGHLTKLELNVAHNLIOGFKLPEYFSNLTNLEHL 180
Qy 180 DLSVNYIOTISVQLOFLRENPQVNLSDLSLNPIDSTQAFQCIIRLHELTIASNPSS 239
Db 181 DLSNKTQSIYCTDLRVLHQPMLNLSDLSLNPNFQPAFKIRLKLTLRNPNDSI 240
Qy 240 NVLKMCLQMTGLVHVRLLIEGFKNERLLEFSDRSVMEGLCNVSIDEBRLTYINHFSDDI 299
Db 241 NVMTKCIQGLAGLVEHRLVLOEFPNENGLERKFDLSALEGLCNLTIEERLAVLDYVDDI 300
Qy 300 YNL-NCLANISAMSFYGVHIIHADVPRIHPMQSLSITRCHLKPPLKSLPPLKSWTLTT 358
Db 301 IDLNFCLINVSBSFISVSTIERVKDFSYNFGQHLVNVCKFGQFPTLKSLKRLTPTS 360
Qy 359 NREDISFGQALPSLRAYDLDSRNAMSFRCSCSYDPGTNNLKYLDLSPNGVILMSANFNG 418
Db 361 NKGNAFSEVDLPSEFLDLSRNGLSFKCCSQSDPGTTLSTKYLDSFNGVITMSNFI 420
Qy 419 LEELEYLDPQHSSTLKKVTEFSVFLSEKLLYLDISTYNTKIDPDGIFGLISLNTLKMAG 478
Db 421 LEQLEHLDPOHSNLKQMSSESVFLSLRNLIYLDISHHTTRVAFNGIFNGLSLEVLKMAG 480
Qy 479 NSFQNTLSNVFTNTNTNLFEFLDSKQLEQISRGVDTLYRLQLNMSHNNLLFLDPESHY 538
Db 481 NSFQENFLPDIFTELRLNTFLDLSCQQLSPPTANSLSSQLVLMNSHNNFSLDTPPY 540
Qy 539 KQVSLRLTDCSPNRLET-SKGLQHPKSLAVFNLTNNSVACICEYONFLQWYDQKF 597
Db 541 KCLNSLOVLVDSLHNTMTSKQELQHPSSLFLNLTONDFACTCHQSFLQWIDQRL 600
Qy 558 LVNVEQMKCASPIDMKASLVDPFTNSTCYIYKTIISVSVSVLVVATVAFLYHFFPHLI 657
Db 601 LVEVERMECATPSPDKQMPVLSL-NITCOMNKTIIIGSVLSVLVSVAVLVYKFFPHLM 659
Qy 658 LIAGCKTSRGSIVDAFVIYSSQNEDEWVRNELVKNLEBGPFRFOLCLHYRDPFGVAIA 717
Db 660 LIAGCIKTYGRGENIYDAFVIYSSQDEDEWVRNELVKNLEBGPFRFOLCLHYRDPFGVAIA 719
Qy 718 ANIOEGFHKSRYIVVVSRRHFIQSRWCIFEYEIAQTMQFLSSRSGIIFIVLEKYEKSL 777
Db 720 ANIHGPHKSRKVIIVVVSQHFIQSRWCIFEYEIAQTMQFLSSRSGIIFIVLQYKYEKTL 779
Qy 778 RQVVELYRLSRNTYLEMEDNALGRHIFWRRLKALLDGKALNDP---ETSEEDPATTL 834
Db 780 RQVVELYRLSRNTYLEMEDSVLGRHIFWRRLKALLDGKSWNPBGTVGTGCMQGEATSI 839

RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
AC ADD48826;
XX

DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
DE Human Protein AAF05316, SEQ ID NO 14536.
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
OS Homo sapiens.
OS Unidentified.
PN MO2003016475-A2.
PD 27-FEB-2003.
PF 14-AUG-2002; 2002WO-US025765.
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PI Woolf C, D'urso D, Befort K, Costigan M;
PI MPI; 2003-268312/26.
DR GENBANK; AAF05316.
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PS Example 1; Page: 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPD at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 839 AA;

Query Match 66.0%; Score 2860.5; DB 7; Length 839;
Best Local Similarity 66.5%; Pred. No. 4.1e-244;
Matches 559; Conservative 115; Mismatches 159; Indels 7; Gaps 5;

QY 1 MPELHLAAGTIAL-FLSGLRGSLNPECEVLPNTYQOMDNLSKIPHDIVYSTRKND 59
DB 1 MMSASRLAGTLIPAAKFLSCVPSWBPCEVVEVNPITYQCEMLNPFYKIPDLPSTKND 60

QY 60 LSFNPLKIRSYSEFTNFSQLQMLDLSRCEIETIEDKAMHGLNQSTLVITGNPIKFSFG 119
DB 61 LSFNPLRHIGSYSEFSPPELQVLDLSRCEIQTEBGAAYOSLSHSTLLITGNPIOSLAG 120
QY 120 SFGSLTNLENLVAVETKMTSLGEPHIGOLISLKKLVANHLJHSPLPEYFNSLTLREHY 179
DB 121 AFSGSLSLQKLAVERNLASLNFPLGHKTLKELVANLQSFELPEYFNSLTLREHY 180
QY 180 DLSYNYIQTSVKDLOFLENPOVNLSDLSINPIDSIOQAPOGIRHLEHLTRSNFNS 239
DB 181 DLSNKKIGSIYCTDLRYHLQWPLNLSDLSINPNNFIOPGAFKEIRLHKTLRNPFSL 240
QY 240 NVLRKCLQMTGLYHRLILGFEKNERNLBSDRSYMBGLCVSDEPFLTYINHSDDI 299
DB 241 NVMKTCIQGLAGLEVHRLVGEFRNENKEPKSALBELCNLTIEEPFLAYLDYLDI 300
QY 300 NVL-NCLANISAMSTGVCHIKILAVPHRKKOSIIRCHLKPPPKSLPFLKSTLTPT 358
DB 301 IDLFNCLTNVSSFSLSVSTIERVKDPSYNGQHLBELVCKFGQFPTLKLKSLKRLTFS 360
QY 359 NREDISFGQALPSIRYLDLSRNAMSFRGCCSYDFGTNNLKYLDLSPNGVILMSANFNG 418
DB 361 MKGNAFSEVDLPSEFLDLSRNGLSFKGCCQSDPGTSLKXLDLSPNGVILMSANFNG 420
QY 419 LEELEYLDFOHSTLKKVTEFSVLSLEKLLYLDISYNTKIDPDGIFGLISLNTLKMG 478
DB 421 LEQLEHLDFOHNLKOMSEFVFLSLRLNIYLDISHTHTRVAFNGIFNGLSLEVLKMG 480
QY 479 NSFKNLTLSNVTNTNTNLFLDLSKQLEQIRGVFDITXRQLNMSNNLLFLDPSHY 538
DB 481 NSFQENFLPDITELRLNLTFLDLSQCLEQLSPFLAFNSLSSLOVLMNSHNNFSLDTPY 540
QY 539 KQYSLRTDSCSFNLETS-KGILQHPKSLAVPLTNNSVACICEYQFLQWVKQKMF 597
DB 541 KCLNSIQVLDYDLNHLNIMSKQELQHPSSLAFLNLQNDPACTCEHGFQWIKQDRL 600
QY 598 LVNVEQMKCASPIDMKASILDVFTNSTCYIYTIISVSVSYLVAATVAFLIHYFPHLI 657
DB 601 LVEVERMECATPSDKQGMVLSL-NITQMNKTIIGVSIVSLVSVVAVLYKXFPHLM 659
QY 658 LTAGCKYRGSGSIYDAFVYSQNEBWRNLNLERGVRFOLCHYRDPFIPVATA 717
DB 660 LTAGCKYRGSGSIYDAFVYSQNEBWRNLNLERGVRFOLCHYRDPFIPVATA 719
QY 718 ANIIOGFPKSRKIVVWSRHPFIOGRWCIFEYELIAQTMQFLSSRSGLIPIVLEKYEKSL 777
DB 720 ANIIRGFPKSRKIVVWSRHPFIOGRWCIFEYELIAQTMQFLSSRSGLIPIVLEKYEKSL 779
QY 778 RQVVELYRLSLNNTYLEWEDNALGRHIFWRLLKALLDQKALNP---ETSEEDQATTL 834
DB 780 RQVVELYRLSLNNTYLEWEDSVLGRHIFWRLLKALLDQKALNPDEGTGCMQDEATSI 839

RESULT 6
AAW86361
ID AAW86361 standard; protein; 837 AA.
XX
XX AAW86361;

XX 15-MAR-1999 (first entry)
XX
XX Human DNAX toll-like receptor DTLR4.

KW DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW interleukin 1 receptor; phosphate metabolism; innate immunity response;
KW modulate inflammatory function; morphological effect;
KW immunological disorder.

OS Homo sapiens.
XX
XX
PN WO980547-A2.
XX
PD 12-NOV-1998.

XX 07-MAY-1998; 98WO-US008979.
PF 07-MAY-1997; 97US-0044293P.
XX 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
XX (SCHE) SCHERING CORP.
PA Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
PI MPI: 1999-059670/05.
XX N-PSDB; AAV80675.
DR Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
PT metabolism, modulate inflammatory function or innate immunity responses.
XX Claim 3; Page 147-149; 171pp; English.
PS
XX The present invention specifically describes human DNAX toll-like
CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC in the present invention. Also described are: (1) a fusion protein
CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC an antibody or antibody fragment which specifically binds to a DTLR
CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC host cell comprising the vector of (4). The host cell of (5) can be used
CC to produce the DTLR proteins. The DTLR proteins can be used to alter
CC phosphate metabolism, to modulate inflammatory function, innate immunity
CC responses or morphological effects. The DTLR proteins can be used in the
CC treatment of conditions exhibiting abnormal expression of the receptors
CC of their ligands. These abnormalities are typically manifested by
CC immunological disorders
XX
SQ Sequence 837 AA;
Query Match 65.6%; Score 2844; DB 2; Length 837;
Best Local Similarity 66.5%; Pred. No. 1.2e-242;
Matches 558; Conservative 114; Mismatches 159; Indels 8; Gaps 6;
QY 2 MFLHAGTLIMAL-FLSCLRPGLNPTCEVLNPTTYOQMDNLKIPHDISTKNDL 60
DB 1 MSASRLAGTLIPAMAFSCVPESWEPCEV-PNTTYQCEMLNPFYKIPNLFPSTKNDL 59
QY 61 SFNPLKILRSYSFTNFSQQLMDLSRCEIETIEDKAMGMLNQLSTLVLTGNPIKSFPSGS 120
DB 60 SFNPLRHIGSYFFSPPELQVLDLSRCEIQIETIEDGAYOSLSLSTLILGNLQSLALGA 119
QY 121 FSGLTNLENLVAVETKMTSLSGFHIGQLISLKKLVANHLISFKLPEYFSMLNLEHYD 180
DB 120 FSGLTSLQCLVAVETNLASLENFPIGHLKTLELVANHLIQLSFKLPEYFSMLNLEHYD 179
QY 181 LSYNYIQTISVKDLQFLRENPOVNLSDLSLNPDISIQAGQGRHETLTARSFNNSN 240
DB 180 LSSNKIQSTICTDLRFLQHPMLNLSLSDLSLNPMPNIOGAKERLKLTLTRNNFDSLN 239
QY 241 VLKMLQONTGLAHVRLILGEFKNERNLSPDRSWEGLCNYSIDEFRLTYINHRSDYI 300
DB 240 VKTKICIQGLAGLEVRLVYGEFRNGNLEKPKFKSALGECNLTIEFRALVADYLDI 299
QY 301 NL-NCLANISAMSFTGVHAKIADVPRRHKWQSLIIRCHLKPFPKLSLPLKSWTLTTN 359
DB 300 DLFNCLTNVSSFSFLSVLTERVDFSYNGWHLRLVNCFKQFPFLKLSKRLTFISN 359
QY 360 REDISFGOLALPSLRYLDSRNAMSPGSCSYSDPGTNLKLTLDSFNVITMSANPGL 419
DB 360 KGGNAFSEVDLPSLEFLDSRNGLSFKGCSQSDPGTSLKTLDSFNVITMSANPGL 419
QY 420 BELLEVLPQHSSTLKVTESVFLSEKLILYLDISYNTKIDPDGIFLGLISINTLKMAN 479
DB 420 BELLEHDPQHSNLMKQMSERSVFLSLRNLYLDISHTHFRVANNGFNGLSSEVLAKMGN 479
QY 480 SFKDNLTLSNVFTNTNLTFLDLSSKCOLBOISRGVDPDTLYRLQLLNASHNLLFLDP SHYK 539

DB 480 SFQENFLPDIPTERLNLFLDLSCQLEQLSPTRAFNSLSIQVLMNSNNFSLDTPFYK 539
QY 540 QVSLRTDSCSFNRLET-SKILQHPKSLAVPNLTNNNSVACICEYQNFLOMVKDQKML 598
DB 540 CLNSIQVLDYSLNHNIMSKQELQHPBSLAFMLTQNDPACTEHSQFLQWIDQRL 599
QY 599 VNVQMKCASPIDMKASLVDFTNSTCYIYKTIISVSVSVLVAVATVAFLLYHFFHLIL 658
DB 600 VEVERMECATSDSKQGMVLSL-NITCOMNTIIGSVLSVLSVAVLVYKFFHML 658
QY 659 IAGCKYRSGSIYDAPIYSSQNEQWNRNLVKNLEGVRRFQCLHYRPFIGVALAA 718
DB 659 IAGCKYRGENIYDAPIYSSQDEWNRNLVKNLEGVRRFQCLHYRPFIGVALAA 718
QY 719 NIIOGFKSRKVIVVSRHFIQSRWCIFEEYIAQTMQFSSRSGIIPYVEKYKSLLR 778
DB 719 NIIEGFKSRKVIVVVSQHFIOQRWCIFEEYIAQTMQFSSRSGIIPYVEKYKSLLR 778
QY 779 QVVELYRLLSNNTYLEWEDNALGRHIFWRRLKALLDQKALNPD---ETSEBQBATTL 834
DB 779 QVVELYRLLSNNTYLEWEDSVLGRHIFWRRLKALLDQKSNPNRGVGTGCMQDEATSI 837
RESULT 7
ID AAE16102 standard; protein; 837 AA.
XX AAE16102;
AC 26-MAR-2002 (first entry)
XX Human DNAX Toll like receptor (DTLR) 4 #2.
DE Human DNAX Toll like receptor; DTLR; therapy; immunological disorder;
XX Human; DNAX Toll like receptor; DTLR; screening; immunomodulator; chromosome 9q32-33.
XX Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX Homo sapiens.
XX WO200190151-A2.
XX 29-NOV-2001.
XX 23-MAY-2001; 2001WO-US016766.
XX 25-MAY-2000; 2000US-0207558P.
XX (SCHE) SCHERING CORP.
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
DB MPI: 2002-083085/11.
XX N-PSDB; AAD26292.
PT New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
PS Claim 3; Page 41; 297pp; English.
XX The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression

CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTR or cells that express it. The present sequence is
CC human DTR4 protein. The DTR4 gene is located on chromosome 9q32-33.
CC
CC NOTE: The present sequence SEQ ID NO 26 is related to the
CC sequence shown in page 240-243 (AA016116). However these sequences differ
CC at several locations

SQ Sequence 837 AA;

Query Match	65.6%;	Score 2844;	DB 5;	Length 837;
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Best Local Similarity 66.5%; Pred. No. 1.2e-24;
Matches 558; Conservative 114; Mismatches 159; Indels 8; Gaps 6

[illegible]

RESULT 8
ABU04776

ID ABU04776 standard; protein; 837 AA.

AC ABU04776;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1442.

KM Translational profiling; expressed protein tag; ERT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 08-AUG-2001; 2001US-0310801P.
A1 00M 2001 2001US-0326370D
PR 08-AUG-2001; 2001US-0310801P.
A1 00M 2001 2001US-0326370D

PR 04-DEC-2001; 2001US-0336780P.
PR 04-FEB-2003; 2003US-035008EP

XX
XX
(ZYGO) ZYGO TNG

XX
XX

Ch... PM ...
New ... AT ...
T...

XX WPT 3003-040607/03

XX Nov 2013

PT cytoskeletal proteins, receptors on

PT leukemia.

PS Example 2; SEQ ID NO 1442; 134pp; English

The invention describes a purified polypeptide which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (BPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at http://wipo.int/pub/published_pct_sequences

Sequence 837 AA;

Query Match	Score	DB	Length
65.6%	2844	6	837

Best Local Similarity 66.5%; Pred. No. 1.2e-242;
Matches 558; Conservative 114; Mismatches 159; Indels 8; Gaps 6

QY 2 MWLLHAGTATL - FLSCTRPGSLNCPCEVNTPTTCOMDONLSKIPHDIPSTKNLDL 60
| | | | | : | | | | | : | | | | : | | : | |
Db 1 MSASRIAGTLIAPAMAFISCVRPSEMEPCVEV- PNTTCOMEALNFYKI PMNLPESTQNLDL 59

QY 61 SFNPILIKRSYSFTNSQLQMIDLSRCIEITEDXAMHGINSULTVLGNPKFSRPSGS 120
| | | | | : | | | | | : | | | | : | | : | |
Db 60 SNNPLRHIGSYSEFSPPELOVDLSRCIEITLEDAYOSLSHSUTILLGNPQSIALGA 119

QY 121 FSGLTNLENVAVETKMTSLSEGFHIGQLISLKKLVANHLHSFPLPEYFSNLTNLEHVD 180
 DB 120 FSGLSLQKQVAVETNLASLENFPIGHLKTLKELVANANHLIOSFYLPEYFSNLTNLEHVD 179
 QY 181 LSYNYIQTISVNDLOFLRENPOVNLSDLSLNPIDSIOAOFOGIRLHETLRSPFNSSN 240
 DB 180 LSSNKIOSIYCTDLRVHOMPLNLSDLSLNPMNFIOGAFKEIRLHKLTLTRNPFDSLN 239
 QY 241 VLKMLQNMGTGLHVRHLILGEFKNERNLSEFDRSVMEGLCNVSIDEFRLTYINHSDDIY 300
 DB 240 VMKTCIOGLAGLEVHRLVLFGEFRNEGNELEKFKSALLEGICNLTIEFRLAYIDYLDI 299
 QY 301 NL-NCLANISAMSTGVHAKIADVPRHFKWQSLSIRCHLKPPKLSLPLKSWTLTTN 359
 DB 300 DLFNCLTNVSSFSLSVSTIERVKDPSYNGWQHLELVNCKFOFPTLKLKSLKRLTFTSN 359
 QY 360 REDISFGOLALPSLRVLDLSRNAMSFRGCCSYSDGTNNLKYLDLSPNGVILMSANPGL 419
 DB 360 KGNNAFSEVDLPSEFLDLSRNGLSFKGCCSDGTSLKYLDSLPGNVITMSSNPLGL 419
 QY 420 BELEYLDFQHSSTLKKVTESEVFLSEKLYLDISYNTKIDPDGIFLAGISLNTLKMAGN 479
 DB 420 EQLHLDFQHSVNLKQMSSESVFLSLRNLIYLDISHTRVAVANGIFNGLSLSEVLKMAGN 479
 QY 480 SPKNTLSNVPTNTNLTFLDLISKQLEQISRGVDTLYRLQLMSSHNNLLFLDP SHYK 539
 DB 480 SFOENFLPDIFTELNNLTFLDLISQCLBQLESPFAENSLSSLOVLAMSHNNPFLDTPPYK 539
 QY 540 QUSRTDSCFNRIETS-KGILGHPKSLAVFNLTNNSVNCICEYONFLOVVKQKMF 598
 DB 540 CLNSIQVLDYLSNHTMTSKQELQHPSSLARLNTQNDPACTQHOSLOIKQOROL 599
 QY 599 VNVQMKCASPIDMKASIVLDFTNSTCYIKTIIISVSVSVLVAVTAVFLIYHFPHIL 658
 DB 600 VEVEEMECATPBDKQGMPLSL-NITCQMNKTIIGVSLVSVLVAVIYKFFHML 658
 QY 659 IAGCKKYSRGSIIYAFVIYSSQNDWTRNELVKNLESGVPRPOLCHYRDFPGVATAA 718
 DB 659 LAGCKYRGGENIYDAFIYSSQDEDMWVRELKVLKLEGVPEFQCLHYRDFPGVATAA 718
 QY 719 NIIQGFHKSRIYVVSRRHFIOSRKCFEYEAQTQWFLSSRGIIFLYLEKVKSLR 778
 DB 719 NIIHGFHKSRIYVVSQHFIOSRKCFEYEAQTQWFLSSRGIIFLYLEKVKSLR 778
 QY 779 QOVELYRLLSRNTYLEMEDNALGRHIFWRRLKALLDGKALNPD--ETSEBEQEAATL 834
 DB 779 QOVELYRLLSRNTYLEMEDSVLGRHIFWRRLKALLDGKSNMPEGTGTCGCMWQATSI 837

RESULT 9
 AAE16116 standard; protein; 837 AA.
 AC AAE16116;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.
 XX
 KW Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
 XX interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 211 /label= unknown
 FT /note= "Encoded by AAY"
 XX
 XX W0200190151-A2.
 XX
 PD 29-NOV-2001.

XX 23-MAY-2001; 2001WO-US016766.
 PF 25-MAY-2000; 2000US-0207558P.
 PR (SCHE) SCHERING CORP.
 PA Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
 PI WPI; 2002-083085/11.
 DR N-PESDB; AAD26306.
 PT New DNAX Toll like receptor (DTLR) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 XX
 PS Claim 3; Page 240-243; 297pp; English.
 XX
 CC The invention relates to mammalian receptor proteins, e.g., primate,
 CC human DNAX Toll like receptor (DTLR) protein and their corresponding
 CC nucleic acids. The DTLR is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTLR is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTLR is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
 CC receptor family members, for the DTLR or its various fragments. The
 CC purified DTLR can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression
 CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTLR or cells that express it. The present sequence is
 CC human DTLR4 protein, alternative version. The DTLR4 gene is located on
 CC chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
 CC be similar to the sequence shown in page 41 (AAE16102). However these
 CC sequences differ at several locations
 XX
 SQ Sequence 837 AA;
 Query Match 65.4%; Score 2837; DB 5; Length 837;
 Best Local Similarity 66.4%; Pred. No. 5e-242;
 Matches 557; Conservative 114; Mismatches 160; Indels 8; Gaps 6;
 QY 2 MPLHLAAGTLIMAL-FLSCLRPQSLNPCIYELPNITYQCMDQNLKIPHDIPYSTKNLDL 60
 DB 1 MSARLACTILIPMAFLSCRPSEMEPCVEY-PNITYQCMELNYYKIPDNIPSTKNLDL 59
 QY 61 SFNPLKIRSYSTNFSQLOMLDLSRCEIETIEDKANGLNQSLTVLYTGNPIKSFSPGS 120
 DB 60 SFNPLRHIGSYSPFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLITGNPISLALGA 119
 QY 121 FSGLTNLENVAVETKMTSLSEGFHIGQLISLKKLVANHLHSFPLPEYFSNLTNLEHVD 180
 DB 120 FSGLSLQKQVAVETNLASLENFPIGHLKTLKELVANANHLIOSFYLPEYFSNLTNLEHVD 179
 QY 181 LSYNYIQTISVNDLOFLRENPOVNLSDLSLNPIDSIOAOFOGIRLHETLRSPFNSSN 240
 DB 180 LSSNKIOSIYCTDLRVHOMPLNLSDLSLNPMNFIOGAFKEIRLHKLTLTRNPFDSLN 239
 QY 241 VLKMLQNMGTGLHVRHLILGEFKNERNLSEFDRSVMEGLCNVSIDEFRLTYINHSDDIY 300
 DB 240 VMKTCIOGLAGLEVHRLVLFGEFRNEGNELEKFKSALLEGICNLTIEFRLAYIDYLDI 299
 QY 301 NL-NCLANISAMSTGVHAKIADVPRHFKWQSLSIRCHLKPPKLSLPLKSWTLTTN 359
 DB 300 DLFNCLTNVSSFSLSVSTIERVKDPSYNGWQHLELVNCKFOFPTLKLKSLKRLTFTSN 359
 QY 360 REDISFGOLALPSLRVLDLSRNAMSFRGCCSYSDGTNNLKYLDLSPNGVILMSANPGL 419
 DB 360 KGNNAFSEVDLPSEFLDLSRNGLSFKGCCSDGTSLKYLDSLPGNVITMSSNPLGL 419

QY 420 EELEVLDPQSHSTLTKVTERSVFLSLKLLYLDISTYNTKIDDPGIFLGISLNTLMAGN 479
 Db 420 EELEHLDPQSHSTLTKVTERSVFLSLKLLYLDISTYNTKIDDPGIFLGISLNTLMAGN 479
 QY 480 SEKDNLTSLVNTNTNLTFDLDSKQLEJOISRGVPTLRLQLLNMSSHNNLLFLDPSSHXK 539
 Db 480 SEQENFLPDTFELNLTLDLSQCLEQUSPTAFNSLSLQVLMNSHNNFLSLDPFXYK 539
 QY 540 QLYSLRTLDSCFNRIETS-KGILQHPKSLAVENLTNNSVACICEYONFLQWVKQKML 598
 Db 540 CLNSLQVLDYSLNHIMTSSKQELQHPSPSLAFNLQNDFACTCEHQSLQWIKQGRQL 599
 QY 559 VVVEQMKASPIDMKASLVLDFNTSGTCYTKTISVSVSUVAVATVAFLIHFPHIL 658
 Db 600 VEEVMECATPSPDKQMPVLSL-NITCQNKTKIIGSVLSVAVAVLYKFFPHML 658
 QY 659 IAGCKYSRGESIDYAFVYSSQNDWVNEVLKQLEBGPFCOLAHYRDPGVATIA 718
 Db 659 IAGCTKRGENTYAFVYSSQDEWVNEVLKQLEBGPFCOLAHYRDPGVATIA 718
 QY 719 NIIOGFHKSRKVIYVVSQHPFIOQRWCIPEYEAQOTWQPLSSRSGIIFVLEKVEKSLR 778
 Db 719 NIIEGFHKSRKVIYVVSQHPFIOQRWCIPEYEAQOTWQPLSSRSGIIFVLEKVEKSLR 778
 QY 779 QOVELYRLSRTYLEWEDNALGRHIFWRRLKALLDQKALPD--ETSEBQATTL 834
 Db 779 QOVELYRLSRTYLEWEDSVLGRHIFWRRLKALLDQKSNBEGVTGCMQOATSI 837

RESULT 10

ADOS7797 standard; protein; 801 AA.

ADOS7797;

12-AUG-2004 (first entry)

Squirrel monkey toll-like receptor 4 SEQ ID NO:18.

XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KW sepsis; severe sepsis; septic shock; asthma; squirrel monkey.

Salimiri sciturs.

Key Location/Qualifiers

FT Misc-difference 14

FT label= Leu, Phe

XX WO2004042365-A2.

XX 21-MAY-2004.

XX 03-NOV-2003; 2003WO-US036247.

XX 01-NOV-2002; 2002US-0423113P.

XX (EVOL-) EVOLUTIONARY GENOMICS LLC.

XX Messier W;

XX WPI; 2004-400726/37.

XX N-PSDB; ADOS7795, ADOS7796.

XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful

XX in treating sepsis and asthma, by comparing the TLR4 polynucleotide

XX sequence of the Old World monkey with that of a human.

XX Disclosure; SEQ ID NO 18; 111pp; English.

XX The invention relates to a novel method for identifying a nucleotide

XX change in a TLR4 polynucleotide sequence of an old world monkey

XX comprising comparing the TLR4 polynucleotide sequence of the Old World

CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents squirrel monkey TLR4.

SQ Sequence 801 AA;

Query Match 64.5%; Score 2796.5; DB 8; Length 801;

Best Local Similarity 67.7%; Pred. No. 1.8e-238;

Matches 539; Conservative 105; Mismatches 149; Indels 3; Gaps 3;

QY 31 VLENTTYQCDNDQNSKIPHDIPYSTKNDLSFNPPLKIRSYPTNFSQLQWMDLSRCIE 90
 Db 1 VLENTTYQCDNDQNSKIPHDIPYSTKNDLSFNPPLKIRSYPTNFSQLQWMDLSRCIE 90
 QY 91 TIEDKAMHGLNQLSTLVLTGNPIKSPSPGSGLTNLENLVAETKMTSLGEGHIGOLIS 150
 Db 61 TIEDGAYQSLSTLITLGNPIQNALGARGSLQKLVAVETHLSLENFPIGHLKT 120
 QY 151 LKLVANANLHSPFLPEYFENLTLEHVDLSYNTYQITSYKDLQFLEENPOVNLSDIS 210
 Db 121 LKDLVAVANLHSPFLPEYFENLTLEHVDLSYNTYQITSYKDLQFLEENPOVNLSDIS 180
 QY 211 LNPIDSIQAOAFQGRRLHELTLSNFNSNVLKQMLQMTGHLVHRLTIGEEKNERNES 270
 Db 181 LNPIDSIQAOAFQGRRLHELTLSNFNSNVLKQMLQMTGHLVHRLTIGEEKNERNES 240
 QY 271 FDRSVMEGLCNVSDIDEFLTYINHFSDIYNI-NCLANISAMSFTGVHIIKHADYPRHFX 329
 Db 241 FDRSVMEGLCNVSDIDEFLTYINHFSDIYNI-NCLANISAMSFTGVHIIKHADYPRHFX 300
 QY 330 WQSLSTIRCHLKPYPKLSLPLFKSWTLTTNRBDISFGQLAPSLRYLDLSRANSPFRGCC 389
 Db 301 WQSLSTIRCHLKPYPKLSLPLFKSWTLTTNRBDISFGQLAPSLRYLDLSRANSPFRGCC 360
 QY 390 SYSDGTNNLKYLDLSFNGVILMSANFMGLBELEYLDQHSSTLTKVTEFSVFLSEKLY 449
 Db 361 SYSDGTNNLKYLDLSFNGVILMSANFMGLBELEYLDQHSSTLTKVTEFSVFLSEKLY 420
 QY 450 LDISTYNTKIDDPGIFLGISLNTLKVAGNSPKONTLSNVEFTNTNLTFDLSSKQLEJOI 509
 Db 421 LDISTYNTKIDDPGIFLGISLNTLKVAGNSPKONTLSNVEFTNTNLTFDLSSKQLEJOI 480
 QY 510 SRGVPTDITRLQLNMSHNNLLFLDPSTYKOLYSRTIDCSFNRIETSKG-ILQHPKSL 568
 Db 481 SRGVPTDITRLQLNMSHNNLLFLDPSTYKOLYSRTIDCSFNRIETSKG-ILQHPKSL 540
 QY 569 AVFNLNNSVACICEYONFLQWVNDQKMLFVNVQMKCASPIDMKASLVLPFTSTCYIY 628
 Db 541 AVFNLNNSVACICEYONFLQWVNDQKMLFVNVQMKCASPIDMKASLVLPFTSTCYIY 600
 QY 629 KTIISVSYSVAVATVAFLIHYEFHLLIAGCKYSRGESIDAFYIYSSQNDWVNRN 688
 Db 600 KTIISVSYSVAVATVAFLIHYEFHLLIAGCKYSRGESIDAFYIYSSQNDWVNRN 659
 QY 689 ELVKNLEBGPVPPFCOLCHYRDPFIPGVAIAANIIOBGFHKSRKVIYVVSQHPFIO 748
 Db 660 ELVKNLEBGPVPPFCOLCHYRDPFIPGVAIAANIIOBGFHKSRKVIYVVSQHPFIO 719
 QY 749 YEIAQWQPLSSRSGIIFVLEKVEKSLLRQOVELYRLSNTYLEWEDNALGRHIFWR 808
 Db 720 YEIAQWQPLSSRSGIIFVLEKVEKSLLRQOVELYRLSNTYLEWEDNALGRHIFWR 779
 QY 809 LKALLDQKALNPDPT 824
 Db 780 LKALLDQKALNPDPT 795

RESULT 11

AD057791
ID AD057791 standard; protein; 795 AA.
XX
AC AD057791;
XX
DT 12-AUG-2004 (first entry)
XX
DE Rhesus monkey toll-like receptor 4 SEQ ID NO:12.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; rhesus monkey.
XX
OS Macaca mulatta.
XX
FH Key Location/Qualifiers
FT Misc-difference 635
FT /label= lys, Asn
XX
FN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOl-) EVOLUTIONARY GENOMICS LLC.
XX
PL Messier W;
XX
DR WPI: 2004-400726/37.
DR N-PSDB; AD057789, AD057790.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Disclosure; SEQ ID NO 12; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiaesthetic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents rhesus monkey TLR4.
XX
SQ Sequence 795 AA;
Query Match 64.2%; Score 2782.5; DB 8; Length 795;
Best Local Similarity 67.5%; Pred. No. 3.1e-237;
Matches 537; Conservative 109; Mismatches 146; Indels 3; Gaps 3;
QY 31 VLPNTTYQCMQDNLSKIPHDIPYSTKNLDSFNPILKILRSYSPYPSOLQWLDSCREIS 90
DB 1 VVPNTTYQCMQDNLPKIPNDLPSTKNDLSFNPILRHLSISYFPSPPLQVUDLSRCEIQ 60
QY 91 TIEDKAMHGLNQLSTVLVTGNPIKSPSPGSGLTNLENLVAETKMTSLSGFHIQGLIS 150
DB 61 TIEDGAYGSLSHLSTLITLGNPIQSLALGAFSGLSLQGLVAVENTNLASLENFPIGHLKT 120
QY 151 LKKLVAVANHLIHSFLDPEYFSNLTLNLEHDLSTNYITQITSVLDQFLKRNPOVNLSDLS 210
DB 121 LKELVAVANHLIOSFLDPEYFSNLTLNLEHDLSSNKIQNYTCKDLQVLHQMPLSNLSDLS 180
QY 211 LNPIDISIQAOFGRIHLHETLRSNPNSGNVLKMGCLQNNNTGLAHVRLIIGEFKRNLES 270
DB 181 LNPINPIQGAFTKRIHLKULTRSNFDLNVKTCIQGLAGLSEVRHLVIGEFRRERULEE 240

QY 271 FDRSVMGLCNVSIIDEPRLTYINHPSDDIYNL-NCLANISAMSTGVHIIADVPRHFK 329
DB 241 FDKSLBGLCNLTIEERFLTYLDYLDNIIDLFCNLANVSSFSIVSISKREVEDFSYVFR 300
QY 330 WOSLSIRCHLKAPPKSLSPFLKSMWLTLTNEDISFQGLAPSLRYLIDLSRNNASPRCC 389
DB 301 WQHLLEVNCKEQPPTELESBLKRLTFPANGNASFSVDPSLFEFLDTNGLSGFKCC 360
QY 390 SYSPFGTNLKYLDLSPNGVILMSANFMGLBELELDPOHSTLKVKTEFSYFLSLKELY 449
DB 361 SQSDPGTSLKXLDLSPNDVITMSNPLGLEKLEHIDPOHNLQMSQFSYFLSLRNL 420
QY 450 LDISYTNKIDPDGIFGLISLNTLKVAGNSFKONTLSNVFTNTNLTFLDLSKQLEOI 509
DB 421 LDISHTHRAVAFNGIFDGLSLKYLKVAGNSFOENFLPDIPTDLKNLTFLLDSQOLEOL 480
QY 510 SRGVPTLYRLQULNMSNNLLPLDPSHYKOLYSILRTDCFPNLERSKG-ILQHPFSL 568
DB 481 SPFAEDTLNKLQVLNMSNNPFSIDTPEYKCLPSLQVLDYSLNHIMTSSNNOELQHPSSL 540
QY 569 AVFNLTNNSVACICEYQNFQWVKQKFLVNVBOMKCAPIDMKASLVLDPNSTCYIY 628
DB 541 AFLNLTQNDPACTCHGQSLQWIKDQRLVYBAERMEGATPSDQGMVLSL-NITQGM 599
QY 629 KTIISVSYSVLYVATVAFELIYHFYFHLILIAQCKKTSRGESITDAPVITYSSQNEDEV 688
DB 600 KTIIGSVYSVLYVAVVAVLYKFEYFHLIMLAGCIXYGRGENIYDAFYIYSSQDEDEV 659
QY 689 ELVKNLESGVRPQLCHYRDFIPGVAAANIIOEGFHSKRVVWVSRHFIQSRWCFE 748
DB 660 ELVKNLESGVPPFQCLHYRDFIPGVAAANIHEGFHSKRVVWVSOHFIQSRWCFE 719
QY 749 YEIAQTWQFLSSRSGIIFIVLEKYEKSLRQOVELYRLSHNTYLEWEDNALGHIEMWR 808
DB 720 YEIAQTWQFLSSRSGIIFIVLQYKTEKTLRQVELYRLSHNTYLEWEDSVLGCHIFWR 779
QY 809 LKKALLDGKALNPDE 823
DB 780 LKKALLDGRSWNPDE 794
RESULT 12
AD057800
ID AD057800 standard; protein; 795 AA.
XX
AC AD057800;
XX
DT 12-AUG-2004 (first entry)
XX
DE Hamadryas baboon toll-like receptor 4 SEQ ID NO:21.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; Hamadryas baboon.
XX
OS Papio hamadryas.
XX
FN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOl-) EVOLUTIONARY GENOMICS LLC.
XX
PL Messier W;
XX
DR WPI: 2004-400726/37.
DR N-PSDB; AD057798, AD057799.
XX

PT Identifying a nucleotide change in a TUR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TUR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX
 PS Disclosure; SEQ ID NO 21; 11bp; English.
 CC
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TUR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TUR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TUR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TUR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents hamadryas baboon TUR4.
 XX
 SQ Sequence 795 AA;
 Query Match 64.2%; Score 2781.5; DB 8; Length 795;
 Best Local Similarity 67.7%; Pred. No. 3.9e-237;
 Matches 538; Conservative 106; Mismatches 148; Indels 3; Gaps 3;
 QY 31 VLPNITTCQMDONLSKIPHDIPYSTKNLDSFNPDKIRSYSTFNFSQOLWLDLSRCIE 90
 DB 1 VVPNITTCQMDLNFKYKIPDNIPFSTKNLDSFNPDKIRSYSTFNFSQOLWLDLSRCIE 60
 QY 91 TIEBKAMHGLNQLSTLVLTGNPIKSFSPGSGLTNLENVAVEVKMTSLSEFHIQOLIS 150
 DB 61 TIEBGAVSLSLTLITGNPIQSLGAFSGLSLQKLVAVETNLASLENFPIGHLKT 120
 QY 151 LKLNVAHNLHSPFLPEYFENLTNLEHVDSLNYNYIQTISVYDLOFLRENQVNLSDLS 210
 DB 121 LKELNVANLQSFLEPFYFENLTNLEHDLSSNNQIYCKDQVLTQMPLNLSLDS 180
 QY 211 LNPIDSLQAQAPQGRHLELIRSNFSSNVLKMLQNMGTGLHVRLLIGEFKERNIES 270
 DB 181 LNPINFIQPGAFKEIRHKLTLRSNFDLNVWKTICQGLAGLEVRLVGEFRNERNIEE 240
 QY 271 FDRSMEGLCNVSDIEPFLTYINHSDDIYNL-NCLANISMSFVGHIKIHADVPRHK 329
 DB 241 FDKALBGLCNLTLEEFRLTYLDYLDNIIDLFCNLAASSFLSVANIKREDPSYFR 300
 QY 330 WQSLIIRCHLKPEPKLSLPLKSWTLTTNREDISFGQALPSLRKYLDSRNAMSFRCGC 389
 DB 301 WQHELVAVCKEFGPPTLESLKRLTFANKGNAFSEVDLPSEFLDSRNGLSFKGCC 360
 QY 390 SYSDFGTNNLKYLDLSPNGVILMSANFNGLEBEYLDFOHSTLKKVTEFSVFLSEKLLY 449
 DB 361 SOSDFGTTSLKYLDLSPNDVITMGSNFIQLBQLEHLDFOHSLVKMQSGFSVFLSRNLTY 420
 QY 450 LDISTYTNKIDPDGFLGLISINTLKMGNSFKNTLSNVPTNTNLFPLDSKQLFOI 509
 DB 421 LDISHHTTVAFNGITFDLISLKVLMKMGNSFOENFLDIFDLNKLFLDLSQQLBQL 480
 QY 510 SRGVEDTLYRQLNLSHNNLLFLDPSHYKOLYSRTDSCFNRIETSKG-ILQHPKSL 568
 DB 481 SPTAFEDTLANKQVLNMSHNNFSLDVPYKCLPSIQVLDYSLNHTMTSKNGEPGFPSSL 540
 QY 569 AVFNLTNNSVACICEYQNFQWVQDKMFLVNVEMQKCAPIDMKASLVLDFTNSTCYIY 628
 DB 541 AFLNLTQDFACTECHQSFQWIKQDQRLVLEABREMCATPSDKGMFVLG-VNITTCQMN 599
 QY 629 KTIISVSVSIVLVATVAFLYHFEHLILAGCKKRGESINYAPVITYSSQNDWVRN 688
 DB 600 KTIIGVSFVSIVLVAVLAKYFPHMLLAGCKIKYRGENTYDAFYIYSSQDDWVRN 659
 QY 689 ELVKNLEBGPVFCIHYRDFIPGVAIAANIIOGFHKSRYIVVVRSHFIQSWMCFE 748
 DB 660 ELVKNLEBGPVFCIHYRDFIPGVAIAANIHHGFHKSRYIVVVOHFIQSWMCFE 719
 QY 749 YEIAQTWQFLSSRSGIIFIVLEKVKSLRQOVELYRLLSRNTYLEMEDNALGRHIFWR 808

DB 720 YEIAQTWQFLSSRSGIIFIVLEKVKSLRQOVELYRLLSRNTYLEMEDSVLGOHIFWR 779
 QY 809 LKALDQKALNPDE 823
 DB 780 LKALDQKALNPDE 794
 RESULT 13
 ID ADO57803 standard; protein; 808 AA.
 AC ADO57803;
 DT 12-AUG-2004 (first entry)
 DE Chimpanzee toll-like receptor 4 SEQ ID NO:24.
 XX toll-like receptor 4; TUR4; old world monkey; antibacterial;
 XX immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 XX sepsis; severe sepsis; septic shock; asthma; chimpanzee.
 OS Pan troglodytes.
 EN WO2004042365-A2.
 PD 21-MAY-2004.
 PE 03-NOV-2003; 2003WO-US036247.
 PR 01-NOV-2002; 2002US-0423113P.
 PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
 PI Messier W;
 DR WPI; 2004-400726/37.
 DR N-PSDB; ADO57801, ADO57802.
 PT Identifying a nucleotide change in a TUR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TUR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX
 PS Disclosure; SEQ ID NO 24; 11bp; English.
 CC
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TUR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TUR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TUR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TUR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents chimpanzee TUR4.
 XX
 SQ Sequence 808 AA;
 Query Match 64.1%; Score 2777; DB 8; Length 808;
 Best Local Similarity 66.7%; Pred. No. 9.9e-237;
 Matches 540; Conservative 113; Mismatches 150; Indels 6; Gaps 4;
 QY 31 VLPNITTCQMDONLSKIPHDIPYSTKNLDSFNPDKIRSYSTFNFSQOLWLDLSRCIE 90
 DB 1 VVPNITTCQMDLNFKYKIPDNIPFSTKNLDSFNPDKIRSYSTFNFSQOLWLDLSRCIE 60
 QY 91 TIEBKAMHGLNQLSTLVLTGNPIKSFSPGSGLTNLENVAVEVKMTSLSEFHIQOLIS 150
 DB 61 TIEBGAVSLSLTLITGNPIQSLGAFSGLSLQKLVAVETNLASLENFPIGHLKT 120
 QY 151 LKLNVAHNLHSPFLPEYFENLTNLEHVDSLNYNYIQTISVYDLOFLRENQVNLSDLS 210

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Db 121 LKELNVANHNLQSFGLPEYFNSLNLNLEHLDLSSNKIQSIYCTDLRVLHOMPLNLSDLS 180
Qy 211 LNPIDSIOAOPQGIIRLHELTLRSNPNSSNVLKMCLOMMTGIAVHRLILGEFKNERNIES 270
Db 181 LNPMPFIOPGAFKEIRLHKLTLRNNPDSLNVMTKICIOGLAGLEVHRLVGEFRNENIEK 240
Qy 271 FDRSMVEGLCNVSIDEFRLTYINHSDDIYNL-NCLANISAMSGTGVHIKHIAVPRHPK 329
Db 241 FDKSALBGLCNLTIEFRLAYLDYLDIIDLFCNCLTNVSSFSFLSVTIKSVKDSYNFG 300
Qy 330 WQSLSIIRCHLKPPKLSLPFLKSWTLTTNRDISFQGLAPSLRYLDSRNAMFRGCC 389
Db 301 WQHLVAVCKRQGFPTLKLSKRLTFTSNKGNAPSEVDLPSEFLDSNGSLFGCC 360
Qy 390 SYSDFGNNLKYLDLSPNGVILMSANFMGLBELEYLDFOHSTLKKTVEFSVLSLEKLY 449
Db 361 SOSDFGTTSLKXYLDLSPNGVILMSANFMGLBELEYLDFOHSTLKKTVEFSVLSLEKLY 420
Qy 450 LDISYTNKIDPDGIFLGLISLNTLTKMAGNSFKONTLSNVPTNTNLTFPLDLSKQLEQI 509
Db 421 LDISHHTRAVAFNGIFNGLSLEVLKMGANSFOENFLPDIFTELRLTFPLDLSQCLEQL 480
Qy 510 SRGVDTLYRLQOLNMSHNNLLFLDPHYKOLYSLRTLDCSPNRLETS-KGILQHPKSL 568
Db 481 SPTAFNSLSLQVLNMSHNNPFSLDTPPYKCLNSLQVLDSLNHMTSKQELQHPSSL 540
Qy 569 AVFNLTNNSVACICEYONFLOVMDQKMFVNVBQMKCASPIDMKASVLDPFTNSCTYIY 628
Db 541 AFLNLTONDFACCTGHOSFLOMKIQROLIVEVERMECATPSDKGMVLSL-NITCOMN 599
Qy 629 KTIISVSVSVLVVATVAFLIYHFFHLILLAGCKKTSRGSISYDAFVIYSSQEDWVRN 688
Db 600 KTIIGSVLSVSVLVVAVLVYKFYFHLMLLAGCIKRGENIYDAFVIYSSQEDWVRN 659
Qy 689 ELVKNLEBVGVRFOCLHYRDPFPGVAIAANTIOSGFKRSKRVTVVNSRHFIQSWCIFE 748
Db 660 ELVKNLEBVGVRFOCLHYRDPFPGVAIAANTIOGFKRSKRVTVVNSQHFQSWCIFE 719
Qy 749 YEIAQWOLFSSRSRGIIFVLEKYEKSLRQOVELYRLSRVTYLEWEDNALGRHIFWR 808
Db 720 YEIAQWOLFSSRAGIIFIVLQVKEKTLRQVELYRLSRVTYLEWEDSVLGRHIFWR 779
Qy 809 LKKALLDGRKALNPD---ETSEBEOATTL 834
Db 780 LRKALLDGRKSWNPBEGTVGTCNMGCATSI 808

RESULT 14
AD057782
ID AD057782 standard; protein; 808 AA.
XX
AC AD057782;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimpanzee toll-like receptor 4 SEQ ID NO:3.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS Pan troglodytes.
XX
PN M02004042365-A2.
XX
PD 21-MAY-2004.
XX
PE 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVL- ) EVOLUTIONARY GENOMICS LLC.

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PT Messier W;
XX WPI; 2004-400726/37.
DR N-PSDB; AD057780, AD057781.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Example 1; SEQ ID NO 3; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiaesthetic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents chimpanzee TLR4.
XX
SQ Sequence 808 AA:
XX
Query Match 64.0%; Score 2773; DB 8; Length 808;
Best Local Similarity 66.7%; Pred. No. 2,2e-236;
Matches 540; Conservative 112; Mismatches 151; Indels 6; Gaps 4;

Qy 31 VLNPITYQCDQNDLSKIPHDIPYSTKNLDSFNPCLKILRSYFTNFSQOLQMLDSRCEIE 90
Db 1 VVNPITYQCDQNLNLYKIPDNPFTSTKNLDSFNPCLRHSYFSPFELQVLDLSRCEIQ 60
Qy 91 TIEBKAMHGNQSLTVLQNGPIKSPGSGGLTNLENVAVETKMTSLGEGHIGOLIS 150
Db 61 TIEBGAQOSLSHTLTLTGNPDSLADGASGSLSQKLVAVETNLASLENFPIGHKT 120
Qy 151 LKELNVANHNLHSEKLEPEYFNSLNLNLEHVDLSYNYIOTISYKDLQPLRENQVNLSDLS 210
Db 121 LKELNVANHNLQSFGLPEYFNSLNLNLEHLDLSSNKIQSIYCTDLRVLHOMPLNLSDLS 180
Qy 211 LNPIDSIOAOPQGIIRLHELTLRSNPNSSNVLKMCLOMMTGIAVHRLILGEFKNERNIES 270
Db 181 LNPMPFIOPGAFKEIRLHKLTLRNNPDSLNVMTKICIOGLAGLEVHRLVGEFRNENIEK 240
Qy 271 FDRSMVEGLCNVSIDEFRLTYINHSDDIYNL-NCLANISAMSGTGVHIKHIAVPRHPK 329
Db 241 FDKSALBGLCNLTIEFRLAYLDYLDIIDLFCNCLTNVSSFSFLSVTIKSVKDSYNFG 300
Qy 330 WQSLSIIRCHLKPPKLSLPFLKSWTLTTNRDISFQGLAPSLRYLDSRNAMFRGCC 389
Db 301 WQHLVAVCKRQGFPTLKLSKRLTFTSNKGNAPSEVDLPSEFLDSNGSLFGCC 360
Qy 390 SYSDFGNNLKYLDLSPNGVILMSANFMGLBELEYLDFOHSTLKKTVEFSVLSLEKLY 449
Db 361 SOSDFGTTSLKXYLDLSPNGVILMSANFMGLBELEYLDFOHSTLKKTVEFSVLSLEKLY 420
Qy 450 LDISYTNKIDPDGIFLGLISLNTLTKMAGNSFKONTLSNVPTNTNLTFPLDLSKQLEQI 509
Db 421 LDISHHTRAVAFNGIFNGLSLEVLKMGANSFOENFLPDIFTELRLTFPLDLSQCLEQL 480
Qy 510 SRGVDTLYRLQOLNMSHNNLLFLDPHYKOLYSLRTLDCSPNRLETS-KGILQHPKSL 568
Db 481 SPTAFNSLSLQVLNMSHNNPFSLDTPPYKCLNSLQVLDSLNHMTSKQELQHPSSL 540
Qy 569 AVFNLTNNSVACICEYONFLOVMDQKMFVNVBQMKCASPIDMKASVLDPFTNSCTYIY 628
Db 541 AFLNLTONDFACCTGHOSFLOMKIQROLIVEVERMECATPSDKGMVLSL-NITCOMN 599
Qy 629 KTIISVSVSVLVVATVAFLIYHFFHLILLAGCKKTSRGSISYDAFVIYSSQEDWVRN 688
Db 600 KTIIGSVLSVSVLVVAVLVYKFYFHLMLLAGCIKRGENIYDAFVIYSSQEDWVRN 659

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QY 689 ELVKULEEVPFQCLHFRDPIPGVAIAANIIOGEGHKSRYIVVSRHFIOSRWCIFE 748
 DB 660 ELVKULEEVPFQCLHFRDPIPGVAIAANIIEGEGHKSRYIVVSRHFIOSRWCIFE 719
 QY 749 YEIAQTWQFLSSRSAGIIFIVLEKVEKSLRQVELYRLLSRNTYLEWEDNALGRHIFWRR 808
 DB 720 YEIAQTWQFLSSRSAGIIFIVLEKVEKSLRQVELYRLLSRNTYLEWEDSVLGRHIFWRR 779
 QY 809 LKKALLDGKALNPD--ETSEBEOEATTL 834
 DB 780 LKKALLDGKSWNPEGTVGTGCMWQBATSI 808

RESULT 15
 ID ADO57785
 ADOS7785 standard; protein; 808 AA.
 AC ADO57785;
 DT 12-AUG-2004 (first entry)
 DE Gorilla toll-like receptor 4 SEQ ID NO:6.
 XX
 XX toll-like receptor 4; TLR4; Old world monkey; antibacterial;
 KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KM sepsis; severe sepsis; septic shock; asthma; gorilla.
 XX
 OS Gorilla gorilla.
 XX
 PN MO2004042365-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 03-NOV-2003; 2003WO-US036247.
 XX
 PR 01-NOV-2002; 2002US-0423113P.
 XX
 PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
 XX
 PI Messier W;
 DR WPI; 2004-400726/37.
 DR N-PSDB; ADO57783; ADO57784.
 PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX
 PS Example 1; SEQ ID NO 6; 11bp; English.
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents gorilla TLR4.
 XX
 SQ Sequence 808 AA;

Query Match 63.7%; Score 2761; DB 8; Length 808;
 Best Local Similarity 66.5%; Pred. No. 2.6e-235;
 Matches 538; Conservative 112; Mismatches 153; Indels 6; Gaps 4;

QY 31 VLPNTTYQCMQDNLSKIPHDIPYSTKNDLSFNPLKILRSYGFNPSQLOMLDSRCEIE 90
 DB 1 VLPNTTYQCMQDNLSKIPHDIPYSTKNDLSFNPLKILRSYGFNPSQLOMLDSRCEIE 60
 QY 91 TIEDKAMHGLNLSLTVLTGNPIKSPSPGSGLTNLENLVAVETKMTSLGEGHIGQLIS 150

DB 61 TIEDAYOSLSHLSLTLITGNPIQSLALGAFGSLSSLOQLVAVETNLSLENFPIGHILKT 120
 QY 151 LKKLVANHLISFPLPEYFSNL/TNLEHVDLSYNTIQTISVVDLOFLRENPOVNLSDLS 210
 DB 121 LKELVANHLISFPLPEYFSNL/TNLEHVDLSYNTIQTISVVDLOFLRENPOVNLSDLS 180
 QY 211 INPIDIOAOFQIRLHELTLRSNPNNSNVLKMCLONNVTGLHVRHLJIGEFKERNLBS 270
 DB 181 INPMFIIOPGAFKEIRLHKLTLRNNPDSLNVMKTCIOGLAGLEVRRLVGEFRNEGNLEK 240
 QY 271 PDRSYMEGICNVSIDEFRLTYINHSDDIYNL-NCLANI SAMSFGVAHKHIAADVPBRK 329
 DB 241 PDKSALBGLCNLTIEFRLAYLDYIDIIIDFNCLTNVSSPSLVSVTIERKDSYNG 300
 QY 330 WOSLSIIRCHLKPPLKSLPFLKSWTLTNRNDSFGOLALSLRLDLSRVNAMSPRGCC 389
 DB 301 WQLELVNCKRGQPFPLKLSLKLRLTFNSKGNAPSEVDLPSEFLDSRNGLSFKGCC 360
 QY 390 SYSDFGTNNLKYLDLSPNGVILMSANFMGLEBELYLDFOHSTLTKKVTBPSVFLSLEKLY 449
 DB 361 SOSDFGTSLKYLDSLSPNGVITMSSNPLGLBQLBHLDPQHSNLKQMSFVSFLSLNLY 420
 QY 450 LDIYSTNTKIDPDGIFLGLISLNTLKAAGNSFKDNLNVFTNTNLTLFLDLSKQLEOI 509
 DB 421 LDISSHTRVAFNGIFNGISLSEVLKMGNSFOENFLPDIFTELNLTLFLDLSQCLEOL 480
 QY 510 SRGVFDTLRYLOLMSHNNLLFLDPSSHXYKOLYSRTLDSCSNRIETS-KGIIOPPKSL 568
 DB 481 SPTAFNSLSLOLVLMSSHNNFLSPTFPFKCLNSRLVDYSLNHIMTSSKQELQHPBSL 540
 QY 569 AVFNLTNNSVACICEYQNFQWQKDFLVNVEQMKCASPIDMKASVLDLDTNSTCYLY 628
 DB 541 AFLNLTONDFACTGHQSFQWIKDQROLVEVERMECATPEDKQMPVLSL-NITQCKN 599
 QY 629 KTIISVSVSVLVATVAFLIYHFFHLLIAGCKKYSBGESIYAPFVYSSQNDWVN 688
 DB 600 KTIIGVSVSVLVAVLVYKFFHMLLAGCTKYGGENVYDAFVYSSQDEBWMVN 659
 QY 689 ELVKULEEVPFQCLHFRDPIPGVAIAANIIOGEGHKSRYIVVSRHFIOSRWCIFE 748
 DB 660 ELVKULEEVPFQCLHFRDPIPGVAIAANIIEGEGHKSRYIVVSRHFIOSRWCIFE 719
 QY 749 YEIAQTWQFLSSRSAGIIFIVLEKVEKSLRQVELYRLLSRNTYLEWEDNALGRHIFWRR 808
 DB 720 YEIAQTWQFLSSRSAGIIFIVLEKVEKSLRQVELYRLLSRNTYLEWEDSVLGRHIFWRR 779
 QY 809 LKKALLDGKALNPD--ETSEBEOEATTL 834
 DB 780 LKKALLDGKSWNPEGTVGTGCMWQBATSI 808

Search completed: March 12, 2005, 19:55:04
 Job time : 90.9834 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:46 ; Search time 22.9539 Seconds

(without alignments)
2715.523 Million cell updates/sec

Title: US-09-396-985B-6

Perfect score: 4335

Sequence: 1 MNPPLHLACTLIMALFLSCL.....GRALNDETSEBQKATTLT 835

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/prodata/1/iaa/pctus_COMB.pep:*

6: /cgn2_6/prodata/1/iaa/backfillset.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2779.5	64.1	844	4	US-09-949-016-9438
2	602.5	13.9	661	1	US-08-514-014-4
3	602.5	13.9	661	2	US-08-833-823-4
4	502	11.6	784	4	US-09-982-308B-23
5	439.5	10.1	775	4	US-09-949-016-8799
6	300.5	6.9	605	3	US-09-063-950-5
7	290.5	6.7	603	1	US-08-190-802A-50
8	290.5	6.7	603	3	US-08-473-346-50
9	290.5	6.7	603	4	US-08-473-089-50
10	290.5	6.7	603	4	US-08-487-072A-50
11	288.5	6.7	1112	3	US-09-353-585-2
12	288.5	6.7	1112	3	US-09-353-585-3
13	281.5	6.5	605	1	US-08-190-802A-49
14	281.5	6.5	605	3	US-08-473-346-49
15	281.5	6.5	605	3	US-08-473-089-49
16	281.5	6.5	605	4	US-08-487-072A-49
17	281.5	6.5	605	4	US-09-538-092-1087
18	281.5	6.5	623	4	US-09-949-016-10995
19	279	6.4	1480	3	US-09-540-245A-7
20	279	6.4	1480	3	US-09-540-153-7
21	279	6.4	1480	5	PCT-US91-09055-2
22	279	6.4	1480	5	US-09-182-024A-5
23	274.5	6.3	1119	4	US-09-907-794A-294
24	274.5	6.3	1119	4	US-09-905-125A-294
25	274.5	6.3	1119	4	US-09-902-775A-294
26	274.5	6.3	1119	4	US-09-906-700-294
27	274.5	6.3	1119	4	US-09-906-700-294

28	274.5	6.3	1119	4	US-09-903-603A-294	Sequence 294, App
29	274.5	6.3	1119	4	US-09-904-920A-294	Sequence 294, App
30	274.5	6.3	1119	4	US-09-909-064-294	Sequence 294, App
31	274.5	6.3	1119	4	US-09-905-381A-294	Sequence 294, App
32	274.5	6.3	1119	4	US-09-906-618-294	Sequence 294, App
33	272.5	6.3	958	4	US-09-706-594-5	Sequence 5, App1
34	265.5	6.1	1016	3	US-09-180-439-8	Sequence 8, App1
35	264.5	6.1	968	3	US-09-180-439-3	Sequence 3, App1
36	264.5	6.0	1525	3	US-09-191-647-2	Sequence 2, App1
37	259	6.0	1525	3	US-09-540-245A-2	Sequence 2, App1
38	259	6.0	1525	3	US-09-512-283C-396	Sequence 396, App
39	259	6.0	1529	4	US-08-195-006-2	Sequence 2, App1
40	256	5.9	560	3	US-08-195-006-2	Sequence 2, App1
41	256	5.9	560	3	US-09-063-950-4	Sequence 4, App1
42	256	5.9	560	3	PCT-US94-07644A-2	Sequence 2, App1
43	256	5.9	560	3	US-09-182-024A-2	Sequence 2, App1
44	256	5.9	560	3	US-09-182-024A-2	Sequence 2, App1
45	255.5	5.9	1523	3	US-09-182-024A-2	Sequence 2, App1

ALIGNMENTS

RESULT 1	US-09-949-016-9438	Application US/0949016
Sequence 9438, App1	Patent No. 6812339	GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.	TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED	FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14	PRIOR FILING DATE: 2000-10-20	PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20	PRIOR FILING DATE: 2000-10-03	PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012	SOFTWARE: FASTSEQ for Windows Version 4.0	SEQ ID NO 9438
LENGTH: 844	TYPE: PRT	ORGANISM: Human
US-09-949-016-9438	Query Match	64.1%; Score 2779.5; DB 4; Length 844;
Best Local Similarity	65.8%; Pred. No. 76-246;	Matches 546; Conservative 112; Mismatches 161; Indels 11; Gaps 5;
10	TLIMAFSLCPGSLNPEVLTITTYOCMDONLSKIPHDIPYSTKNDLSFNPILKIR	69
21	TIPIPLANCR-----FTBEVAVPNITVOCMLNPKIPDNIPFSKNDLSFNPILRHG	75
70	SSFTNFSOLMDLSRCIEITEDKAWGNQLSTLVYTGMPKSPSGSSGLTNLEN	129
76	STSPFSFPLQVLDLSRCITQTEBQVSLSTLITGNPISLILAGASGLSSLOK	135
130	LVAETKMTSLBGFHIGQLISLKLNVANLTHSFKLPEYFSGNTNLLEHVDLSYNYQIT	189
136	LVAETNLSLBNPFIHGLKTLKEIVANHLISFPLPEYFSGNTNLLEHVDLSYNYQIT	195
190	SYKDIQFLRENPQVNLSDLSNPIDSTIOAQFQGRILHETLRSPNSNVLMKQLQM	249
196	YCTDLRVHQLMNLNLSLSDLSNPNFIOPGAFKIRLKLTLRNPNFSLNWKTCIOQL	255
250	TGLHVRLLIGFKERNLSEFDRSVMESGLCVSIDEFRLTYNHSFDIYNL-NCLANI	308
256	AGLEHVRVLGSPRNEGNIKEKPKDLSLCLNLTBEERLAVLDYLDIDILFNCLTNV	315
309	SAMSFYGVHIXIADVPRRHFKWQSLIIRCHLKPPKLSLPPLKSWTLTTNEDISFGOL	368

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Db 316 SSFSLVSVTEREVKPSYNGWQHLELVNCKFGQFPTLTKSLKLTFTSNKGNAFSKV 375
Qy 369 ALPSLRVYDLSRNAMSPRCGCSYDPGTTNNLKYLDSLFGNGVILMSANFMGLBELEYLDQ 428
Db 376 DLPSLEFLDLSNGSLFKGCCSQSDPGTSTSLKYLDSLFGNGVILMSANFMGLBELEYLDQ 435
Qy 423 HSTLKKVTEFSVPLSLKLYLDISYNTKIDPDGIFGLISLNTLKMAGNSFKONTLSN 488
Db 436 HSNLKQMSSEFSVPLSLRNLILYLDISHTHRAVFNGLFNGLSLEVLKMGAGNSFQENFLPD 495
Qy 489 VFTNTNLTFLDLSKQLEISRGVDDTXYRLQNLMSNNLLFLDPHYKOLYSRTLD 548
Db 496 IFTLRNLTFLDLSQCLEQLSPFANSLSSQLVLMNSHNNFSLDTFPYKCLNLSQVLD 555
Qy 549 CSFNRLET-SGILQHPKSLAVFNLTNNSVACICEYQFLQWVKQKQKFLVNEQMKCA 607
Db 556 YSLNHIHMSKQELQHPSSLAFLNLTDNPACTCEHQSFLQWIDQRLQVLEVERMECA 615
Qy 608 SPIDMKASIVLDPFTNSTCYIYKTIISVSYSVLVAVTAFLIYHFFHLILJAGCKYSR 667
Db 616 TFSDKQGMVLSL-NITCQMKTIIGVSVLSVLVAVVAVLYKFFHMLLAGCIKYGR 674
Qy 668 GSIYDAPYIYSSONEDWNRNLYKLEGVPRPOLCLHYRDPFGVAILAANIQGGFK 727
Db 675 GNIDAFYIYSSODEDWNRNLYKLEGVPRPOLCLHYRDPFGVAILAANIHEGFK 734
Qy 728 SRKIVVVSRRHFIQSRWCIFEYEIAQTMQFLSSRGGIPIYLEKYSKLROOVELYRL 787
Db 735 SRKIVVVSQHRFIQSRWCIFEYEIAQTMQFLSSRGGIPIYLEKYSKLROOVELYRL 794
Qy 788 SNTYLEWEDNALGRHIFWRRLKALLDQKALNP---ETSEEOEATTL 834
Db 795 SNTYLEWEDSVLGRHIFWRRLKALLDQKSNMPEGTGTCNMQBATSI 844

RESULT 2
US-08-514-014-4
; Sequence 4, Application US/08514014
; Patent No. 5707829
; GENERAL INFORMATION:
; APPLICANT: Jacoby, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,014
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A. 724
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI6000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-514-014-4
Query Match 13.9%; Score 602.5; DB 1; Length 661;
Best Local Similarity 28.2%; Pred. No. 3e-46;
Matches 185; Conservative 127; Mismatches 296; Indels 47; Gaps 18;

Qy 28 CIEVLPNTYQCMQDNLSKIPHDIPYSKTNLDSNPLKILRSYFTNFQQLQWDLRSR 87
Db 28 CIEKANTYCNENGLSEIPDLPNTPELFESFNPLPTNKRSLKMLNLTFFDLTRC 87
Qy 88 ELETEDKAMGMLNSTLVLTGNPIKFSGSGFGLTNLENLVAETKMTSLSEGFHIQ 147
Db 88 QINWHEPTFQSHQSLSTLVLTGNPLIMATSLANGPSLKLFLIQGIGNLEPIPHN 147
Qy 148 LISLKKLVNAINLHSPFLPEYFSNLINLEHVDLSYNTIQTISVKDQLFLBNPQVLSL 207
Db 148 LENLESILYSGNSHISIKFPDPF-ARMLKYLDPQNNAIHYISREDMSRLQ--AINDSL 204
Qy 208 DLSNLPDISIAQAFQGRHHELTIRSNFNSNVLKCLQWMTGLHVRLLIGFKERN 267
Db 205 NFNGNNVAGIELGAFDSTVFQSL---NFGTNPMLSVLFGNLQNSTQSLMTGFEDID 260
Qy 268 LESFDRSVMGLCNVSIDEFRLTYINHPD-DIYNLCLANISAMSFTGVHIKHADVPR 326
Db 261 -EDISSAMLKDLCEMSVSALQF-HRFSDISSTTFCQFQLOELDLATHLK---GLPS 315
Qy 327 HFKWQSLSIIR-----CHLKP-FPKLSLPLKSWTLTTNREDISFQQL-ALP 371
Db 316 GMK--GLNLKLKLYLVSNHFPQLCQISANPPSLTHLYIRG---NVKKLHGVGCLFKLG 370
Qy 372 SLRVLSRNAMSPRCGCSYDPGTTNNLKYLDSLFGNGVILMSANFMGLBELEYLDQHS 430
Db 371 NLQTDLSHNDIEASDCCSLQKLNLSHQTNLSNEPLGLQSQAFKPCQLELDLAF 430
Qy 431 TLKVTESVPLSLKLYLDISYNTKIDPDGIFGLISLNTLKMAGNSFKONTLSN 488
Db 431 RLHINAPSPFQNLHFLQVNLTYCFDLSNQHLLAGPVLRLNLTKNHHQDGTITKTN 490
Qy 489 VFTNTNLTFLDLSKQLEISRGVDDTXYRLQNLMSNNLLFLDPHYKOLYSRL 545
Db 491 LQQTGSLKLVILSLSCGLSIDQAFHSLGKSHVDLSHNSLTCDISLSHLKGIY--- 547
Qy 546 TLDSFNRLETSGILQHPKSLAVFNLTNNSVACICEYQFLQWVKQKQKFLVNEQMK 605
Db 548 -LNLANSINITISPRLLPLISQOSTINLSHPDCTCSNHPFLTWYKKNLHKLKESSEET 606
Qy 606 CASPIDMKASIVLDPFTNS---TCIYKTIISVSYSVLVAVTAFLIYHFFHL 656
Db 607 CANPESLRGVSLDVKLSGITAIGIFPLIYFLLAILLFPAYKYLKRWYQGH 661

RESULT 3
US-08-833-823-4
; Sequence 4, Application US/08833823
; Patent No. 5969093
; GENERAL INFORMATION:
; APPLICANT: Jacoby, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
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ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,823
FILING DATE: 10-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-823-4

Query Match 13.9%; Score 602.5; DB 2; Length 661;
Best Local Similarity 28.2%; Pred. No. 3e-46;
Matches 185; Conservative 127; Mismatches 296; Indels 47; Gaps 18;

28 CTEVLPNTYQCGDDQLSKIPHDIPYSTKNLDSFNPFLKILRSYFTNSQOLQWLDLSDRC 87
28 CLEKANKYKNCENGLSEIPDTLPTTELEFSFNPFLTIHNRISRLMNTFLDLTLC 87
88 BIETIEDKAMHGLNQLSTLVLTGNPIKSPSGSLTNLENLVAETKNTSLGPHIQ 147
88 QINMIHEDTFQSHQSTLVLTGNPLIFMAETSLNPKSKILHFLIQTGINSNEFPVNH 147
148 LISLKLVAHNLHSHFKLPEYFSNLTNLEHVDLSNYIQTISVKQLQFLRENPQVNL 207
148 LNLLESLYGSNHSISIKKPKQFP-ARNKVLDPQNNALHYSIREDMRSLEQ--AINL 204
208 DLSLNPIDISIQAFQIRLHELTLRSNPNSSNVLKMCCLQNMGTGHHVHLILGEFKN 267
205 NNGNNVKGIEGAFSTVQSL---NFGGTPNLSVIRNGLQNSTTQSLIMLSTGFEDID 260
268 LESFDRSVMGGLCNVSIDEFRLTYINHPSD-DIYNLNCIANISAMSGTGVHIGIADVR 326
261 -EDISSAMKGLCEMSVESLNLOE-HRFDISSTFQCFQIQEHLDTATHLK---GLPS 315
327 HRKWSLSLIR-----CHLKP--FPKLSLPFLKSWTLTNRNEDISFGQI-ALP 371
316 GNR--GLNLKLVLSVNHFDQLCOISANFSLTHLYIRG--NVKYLHLGVGCLKELG 370
372 SLRYLDSNNAMSGCCSYSDGCTNNLKYLDLSPNGVI-LSMANFMGLEEVLDPQHS 430
371 NQITLDSNNDIEMSCCLQLKNLSHLDTLNLSHEPGLQSOAQKCEPCQELDLAFT 430
431 TLKKTVEFVFLSEKLKLYLDISYNTKIDFDGIFGLISLNTLKMAGNSFKDNTL--SN 488
431 RHHINAPQSPQNLHFLQVNLNLYCFLDLSNQHLLAGLPVLRHLNKGHHFDGTTTKN 490
489 VETNTNTLTFDLSCQLEQISRGVDTLYRLQLMNSNNLI--FLDP-SHYKOLYSIR 545
491 LQQTWSLEVLILISCGSLISQQAQFHSIGKMSHVDLSHNSLTCDSIDLSHLKGIY-- 547
546 TLDCSNRIETSKGILQHPKSLAVFNLTNNSVACICEYONFLQWKQDKMFLVNEQMK 605
548 -LMLANSINIISPRLLPLISQOSTLNLSNPLDCTCSNIHFLTWKKNLHKLGSEETT 606
606 CASPIDMKASLVLDFTNS---TCYIYKTIISVSVLVAVATFLIHFYFHL 656

DB 607 CANPSSLRGVLSLVKLSGCIYTAIGFFLIVLALLAILFPFAVKYLLMKYQHI 661

RESULT 4
US-09-982-308B-23
Sequence 23, Application US/09982308B
Patent No. 6531290
GENERAL INFORMATION:
APPLICANT: Dalié, Barbara
APPLICANT: Fan, Xuedong
APPLICANT: Lundell, Daniel
APPLICANT: Lunn, Charles A.
APPLICANT: Tan, Jimmy C.
APPLICANT: Zavadny, Paul J.
TITLE OF INVENTION: Mammalian TNF-alpha Convertases
FILE REFERENCE: J06010C
CURRENT APPLICATION NUMBER: US/09/982,308B
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/156,163
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 08/889,909
PRIOR FILING DATE: 1997-07-10
PRIOR APPLICATION NUMBER: 60/021,710
PRIOR FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 784
TYPE: PRT
ORGANISM: Homo sapiens
US-09-982-308B-23

Query Match 11.6%; Score 502; DB 4; Length 784;
Best Local Similarity 24.9%; Pred. No. 6.5e-37;
Matches 210; Conservative 136; Mismatches 324; Indels 172; Gaps 32;

43 NLSKIPHDIPYSTKNLDSFNPFLKILRSYFTNSQOLQWLDLSDRCIETIEDKAMHGLNQ 102
42 SLNLSIPSGTEAVKSLDLSNNRIYISN-----SDIQRCV-----N 77
103 ISTLVLTGNPIKSPSGSLTNLENLVAETKNTSLGPHIGOLISLKLVAHNLH 162
78 LQALVLTSGNLTIEDSPSSLSGLLEHLDLSYNISSSWFKPLSLTFLNLGNPKY 137
163 SPKLPEYFSNLTNLEHVDL---SYNYIQTISVKQLQFLRENPQVNLSDLSNPIDSIQ 218
138 TLGETSLFSLHLYKQILRVGNMDTFTKIQKDFAGLTFLE-----LEIDASDQSYE 190
219 AQAFOGIR-----LH---ELTLRSNPNSSNVLKMCCLQ---NMTGLVHRLILGEFKY- 264
191 PKSLKSLQVSHLILHMKHILLLEIPVDYSSVECELEKRDLDLTFHSELSGTETNL 250
265 -----ERNLESFDRSVM-----GLCNVSIDEFRLTYINH-SDDIYNLNCIANIS 309
251 IKKTFIRNVKTI DESLFGVMKLLNQISGLLELPDDCTLNGVGNFRASDNDRVDPGKVE 310
310 AMSFTGVHIGIADVRHFKWSLSIRCHLKPFPKLSLP---FLKSWTLTNRNEDISF 365
311 TLTIRRLH-----PREFLYDLSLTVSLTERVARKITVENSKVLPCLLSQH----- 358
366 GQALPSLRYLDSNNAMSGCCSYSDGCTNNLKYLDLSPNGVI-LSMANFMGLEEVL 425
359 -----LKSLEYLDSNLNV-----EYLKNS-----ACEBAMSLQTLIR 395
426 DFQSTLTKKVEFVFLSEKLKLYLDISYNTKIDFDGIFGLISLNTLKMAGNSFKDNT 485
396 QNHSLASLEKTEG--TLTLTKNLTNIDIS-----KNSF--HS 427
486 LSNVETNTNTLTFDLSCQLEQISRGVDTLYRLQLMNSNNLI--LP-LDPSHYKOLY- 542
428 MPETCWEEKMKYKYLSSIRHISVTCIPKT---LEILDVSNNNLPSLNLPOLEKELY 484

QY 543 -----SLRTDGSFNRIFT-SKGILOHPKSLAVENLTNNSVACICEYON 586
DB 485 SRNKMLTLPDASLLPMLVLKISRVAITTFSEKQDLSF-HTLKTLEAGNNFTLCSECFIS 543
QY 587 FLOWVKDQKMFVNVVE---QMKCASPIDMKASLYLD-FTNSTCYIKTIISVSVSLVA 641
DB 544 FTQ--EQQALAKVLDIMPAANYLCDSPSHVGGQOVQVRLSVSBCHIALVSGMCALFTL 601
QY 642 VATVALYHYF-----YFHLI--LIAGCKYKSRGES---YDAFVIYSQNMEDVNRLELYK 692
DB 602 ILTGLVLCRPHGLWYMKMMWAMLOAKRPRKAPSNICYDAFVYSERDAYVENVLMWQ 661
QY 693 NIEBQVPRPOLCLHTRDFIPGVALAANITIOEGFHMSRKVIYVVRHFIOISRCIFEYETIA 752
DB 662 ELENRPFPKLCIHRKDFIPGKMIIDNII-DSIEKSHKTVPVLSNFVSEKCKEYELDFS 720
QY 753 QFWOFLSSGIIIFYLVEKESLLRQO-VELYRLSRVYLEWENALGRHIFWRKXK 811
DB 721 HFRLPDENDDAAILILEPIEKKAIPORPCUKIKMTKTYLEWPMDEAKOREGFWNLRA 780
QY 812 AL 813
DB 781 AL 782

RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRF
; ORGANISM: Human
US-09-949-016-8799

Query Match 10.1%; Score 439.5; DB 4; Length 775;
Best Local Similarity 24.7%; Pred. No. 3.5e-31;
Matches 201; Conservative 122; Mismatches 292; Indels 199; Gaps 32;
QY 43 NLSKTPHPIPYSTKNDLSFNPFLKILRSYFTNFSOLOMLDLSRCIEITIEDKAMHGLNQ 102
DB 77 SLNISPISGTEAVKSDLSNNRITYISN-----SDIQRCV-----N 112
QY 103 LSTVLGTGNPIKSPGSGFSGLTNLENLVAVETKMTSLEGFHHIGQLISLKIIVANHLIH 162
DB 113 LQALVLISNGVITTEBDSFSLGSLHLDLSYNYLSSSSWPKPSSLTFTPLNLGNPYK 172
QY 163 SFKLREYFSNLTNLEHVDL---SYNYIQTISVKDLOFLRENPOVNLSDLSLNPIDSTQ 218
DB 173 TLGERSLPSHLTKQLIRVGNNDTFTKIQKDPAGITPFE-----LEIASDLQSYE 225
QY 219 AQAFCGIR-----LH---ELTIRSNENSSNVLYKNCLO---NMTGLHVRHLLILEFKN- 264
DB 226 PKSLKSIQVNSHLIIMKHQHILLLEIFVNVTSVECTELRDYDLDLTFHSESLSTGETNSL 285
QY 265 -----ERNLESFDRSYME-----GLCNVSIDEFRLTYINHF-SDDIYNLANCLANIS 309
DB 286 IKKFTFRNVKITTDESLFQWVKLLNQISGLLELEFDDCTLNGVGNFRASNDNRVIDPGKVE 345

QY 310 AMSFTGVHIIKHADVPRHFKQSIISIRCHLKPPPKSLP-----FLKSWTLTNNEDISF 365
DB 346 TLTIIRRLHI-----PRFYLPYDSTLVSLEHVARIRIVENSKVPLVPCILSQH----- 393
QY 366 GQALPISRLYLDLSNANSPFGCCSYSPDFTNNLKIYLDLSFNGVILMSANFMGLEBEYL 425
DB 394 ----LKSLEYLDLSHNLAV-----BEYLKNS-----ACEDAMPSTLOTLILR 430
QY 466 DQHSHTLKKVTEFSVFLSEKLYLDISYTWTKIDPOGIPGLISLNTLKMAAGSFKONT 485
DB 431 QNHLSLEKTEG--TLTFLTKMLTNIDIS-----KNSF--HS 462
QY 486 LSNVFTNTNTNLTFLDLSKCOLQEOISRGVFDLYRLQLMLMSHNL-LF-LDPSSHXYOY- 542
DB 463 MPETCQWPEKMKYINLSSTRISHSVYGCIPKT---LEILDVSNNNLNLPSLNPOLKEXLYI 519
QY 543 -----SLRTDGSFNRIFT-SKGILOHPKSLAVENLTNNSVACICEYON 586
DB 520 SRNKMLTLPDASLLPMLVLKISRVAITTFSEKQDLSF-HTLKTLEAGNNFTLCSECFIS 578
QY 587 FLOWVKDQKMFVNVVE---QMKCASPIDMKASLYLDFTNSTCYIKTIISVSVSLVA 643
DB 579 FTQ--EQQALAKVLDIMPAANYLCDSPSHVGGQOVQVRLSVSECHRT---ALVSGMCCA 632
QY 644 TVAFLIHYFYFHLIILIAG--CKKY-----SRGESIYDAFYIY 678
DB 693 -----LFLILLTGLVLCRPHGLWYMKMMWAMLOAKRPRKAPSR-NICYDAFVSY 682
QY 679 SQONEDWRNELVKNLEBQVPRPOLCLHTRDFIPGVALAANITIOEGFHMSRKVIYVVRH 738
DB 683 SERDAYVVENIMVOLEENPNPFPKLCIHRKDFIPGKMIIDNII-DSIEKSHKTVPVLSN 741
QY 739 FIOSRCIFEYEIAQTWQFLSRSGIIFYVEKY 772
DB 742 FVKSBEWKYEIDFSHFRLPDENDDAAILILEPI 775

RESULT 6
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRGG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRF
; ORGANISM: Papio hamadryas
US-09-063-950-5

Query Match 6.9%; Score 300.5; DB 3; Length 605;
Best Local Similarity 23.9%; Pred. No. 1.3e-18;
Matches 155; Conservative 81; Mismatches 236; Indels 175; Gaps 20;
QY 39 CMDONLSKIPHDIPYSTKNDLSFNPFLKILRSYFTNFSOLOMLDLSRCIEITIEDKAMH 98
DB 60 CSSRNLTRLPGDIGGTGATLMDNUNSSISIPPAFRNLSLAFNLQGGQGLSLEPQALL 119
QY 99 GLNQLSTVLGTGNPIKSPGSGFSGLTNLENLVAVETKMTSLEGFHHIGQLISLKKLVANAH 158
DB 120 GLENCHILHLEBRNQLRSILAIVGTTPATALLGSHNNRLSRLEBGLFEFGCLNLMDLNIGW 179
QY 159 NLHSFKLPE-YFNSLNTNLEHVDLSYN---YIQTISVVDLOFLRENPOVNLSDLSLPI 214
DB 180 NSL--AVLPDAFAGLGLRELVLAGNRLAVLPALPSGLAEKRB-----LDLSRNAL 230


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QY 123 -----GLTNLENLVAETKMTSLGEGFHIQGLISLKKLVANHLIHSFYLPEYF 170
DB 180 NSLVVLPDPTVFGGLGNLHELVLGAKNKLTYLQPALFCGELRELDLSRNALRSVK-ANVF 238
QY 171 SNLTNLEHVDLSYNYIQTIS-----VVDLOFLRENPOVNLSDLSINLPIDSIQAQAFQ 224
DB 239 VHLPELQGLYLDRLNLITAVAPGAFMGKALRW-----LDLSHRVAGIMEDTPEG 288
QY 225 -IRLHELTLRSNFSNVLMKCLQNMGTGL-VHRLILGEFK-----NERNLSEFDSVMEG 278
DB 289 LLGHLVLAHLAN-----ALASLRPRFTKOLHLEBEIQLGHNRIQGEFTFEGLEGLEVLT 344
QY 279 LCNVSIDEFRL-TYINHFSDIYNL--NCLANISAMSTGVHIKILADVPRHFKMQSLSI 335
DB 345 LINDNITFVRVGAFFSGLFNVAVMNLGNCRLSPRVFGDLKLA-----SLHLSCLGH 400
QY 336 IRCHLKPPPKLS---LPLKSWTLTTNREDISFGQALPSLYLDSRNAMS-----FR 386
DB 401 VRLH--TFAGLSGLRRLFLRDNSSISIEQSLAG--LSELELDLTTNRLTHLPRQLFQ 455
QY 387 GCCSYDFGTNNLKYLDLSPNGVILMSANFMGLEBELEYLDFOHSTLKKVTERSVLSLEK 446
DB 456 -----GLGHELEVLISYNQLTLSAEVLG-----PLQR 483
QY 447 LLYLDISYNTKIDPDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTNLTFLDLSKQL 506
DB 484 AFWLDISLNH-----L 494
QY 507 EQLSGVVDTLVRLQLLMSHNL-----LFLDPSHYKOLYSLRTLDGCFNNIE 555
DB 495 ETLAEGFLSSIGRVRVYLSLRNNSLOTFSPQGLERLMDLPW-----DCS----- 540
QY 556 TSKGILGHFP-KSLAVFULTNNSVACICEYQNFLOWVD---QKMFVNVQMKCASPI 610
DB 541 -----CPKALRDFALQNGVV---PRFVQVCEGDGDCQVYTYN--NITCAGPA 585
QY 611 DMKASLVLDFTNSTCYIY 628
DB 586 NV-SGLDRDVSETHFVH 602

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RESULT 10
US-08-487-072A-50
; Sequence 50, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500

```

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; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
; INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
; US-08-487-072A-50

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Query Match          6.7%; Score 290.5; DB 4; Length 603;
Best Local Similarity 22.4%; Pred. No. 1,1e-17;
Matches 152; Conservative 99; Mismatches 204; Indels 223; Gaps 26;

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QY 39 CMDQNLKIPHDIPYSTKNDLSFNPILKRSYFTNFSQLOMDLSRCEIETIEDKAWH 98
DB 60 CSSKRLTLHPDIPVSTRALMDGNLSSIPSAFQNLSDIFNLQGSWLRSLPEQALL 119
QY 99 GLNQSLTVLGNPKSPSPGSPS----- 122
DB 120 GLQNLVYHLBRNRRLNLAVALFTFTPSLASLSLSSNLGLREBGLFQGLSHLMDNLG 179
QY 123 -----GLTNLENLVAETKMTSLGEGFHIQGLISLKKLVANHLIHSFYLPEYF 170
DB 180 NSLVVLPDPTVFGGLGNLHELVLGAKNKLTYLQPALFCGELRELDLSRNALRSVK-ANVF 238
QY 171 SNLTNLEHVDLSYNYIQTIS-----VVDLOFLRENPOVNLSDLSINLPIDSIQAQAFQ 224
DB 239 VHLPELQGLYLDRLNLITAVAPGAFMGKALRW-----LDLSHRVAGIMEDTPEG 288
QY 225 -IRLHELTLRSNFSNVLMKCLQNMGTGL-VHRLILGEFK-----NERNLSEFDSVMEG 278
DB 289 LLGHLVLAHLAN-----ALASLRPRFTKOLHLEBEIQLGHNRIQGEFTFEGLEGLEVLT 344
QY 279 LCNVSIDEFRL-TYINHFSDIYNL--NCLANISAMSTGVHIKILADVPRHFKMQSLSI 335
DB 345 LINDNITFVRVGAFFSGLFNVAVMNLGNCRLSPRVFGDLKLA-----SLHLSCLGH 400
QY 336 IRCHLKPPPKLS---LPLKSWTLTTNREDISFGQALPSLYLDSRNAMS-----FR 386
DB 401 VRLH--TFAGLSGLRRLFLRDNSSISIEQSLAG--LSELELDLTTNRLTHLPRQLFQ 455
QY 387 GCCSYDFGTNNLKYLDLSPNGVILMSANFMGLEBELEYLDFOHSTLKKVTERSVLSLEK 446
DB 456 -----GLGHELEVLISYNQLTLSAEVLG-----PLQR 483
QY 447 LLYLDISYNTKIDPDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTNLTFLDLSKQL 506
DB 484 AFWLDISLNH-----L 494
QY 507 EQLSGVVDTLVRLQLLMSHNL-----LFLDPSHYKOLYSLRTLDGCFNNIE 555
DB 495 ETLAEGFLSSIGRVRVYLSLRNNSLOTFSPQGLERLMDLPW-----DCS----- 540
QY 556 TSKGILGHFP-KSLAVFULTNNSVACICEYQNFLOWVD---QKMFVNVQMKCASPI 610
DB 541 -----CPKALRDFALQNGVV---PRFVQVCEGDGDCQVYTYN--NITCAGPA 585
QY 611 DMKASLVLDFTNSTCYIY 628
DB 586 NV-SGLDRDVSETHFVH 602

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RESULT 11
US-09-353-585-2
; Sequence 2, Application US/09353585
; Patent No. 6287865
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S

```

Jones, David A
Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses
thereof
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: YES
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: Cf2
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-353-585-2
Query Match 6.7%; Score 288.5; DB 3; Length 1112;
Best Local Similarity 23.5%; Pred. No. 4.4e-17;
Matches 158; Conservative 93; Mismatches 243; Indels 179; Gaps 26;
QY 23 GSINCEIVLNIT--YOCMONLSKIPHDIPY--STKNLDSFPLKILSYSTNTNSQ 78
DB 397 GSIPASLNLNLSLYNNQSGSIEEGYSSLYTLDLSNNSINGFLIPASGNSN 456
QY 79 LQWDLISRCIEETEDKAMHGLNQSTVLTGNPIKSPSPSGSLTNLMLVAETQWT 138
DB 457 LAFLEVLNQGLASSVPEIGYIRSLNVLDLSENLNGSIPASFGNLNLSRLNVNNDLS 516
QY 139 SLEGHIGQLISLKKLVANHLIHSFKLPEYFSNITNLEHVDLSYNYIQTISVNDQLR 198
DB 517 GSIPBEIGYLSRLNVLDSENLNG-SIPASFGNLNLSRLNVNNGSGSIEBIGYLR 575
QY 199 ENPQVNS-----LDLSNLP 214
DB 576 SLNDGLSENLNGSIPASLGNLNLMLYNNQSGSIEEGYSSLYTLDLSGNSL 635
QY 215 DSIOAQAFQAIR-LHELTFRS-----NFNSSNVLMK-----CLQWMT 250
DB 636 NGLIPASFPANRNQLALILNDNNLIGELIPSSVCNLTSLVLYMPRNLIKGVPCLGNIS 695

QY 251 GLVHRLILGEFKNE-----RNLES-----FDRSVMEGL-----C--NVSIDFRLTYINH 295
DB 696 NLQVLSMNSNFSGSELPSSIGNLTSLOQLDGRNNLBGAIPQCGNISLSLEVPWQNNKL 755
QY 296 SDDI---YNLNCILNISMSTGVHIXHIAVPRHF-----KQOGLSTRCHLK-PFPL- 346
DB 756 SGTLPNTSIC--SLISLNDHGNLEBD--BIPSLDNCCKLOVLDLGDNDLNLTDPWML 811
QY 347 -SLPFLKSWTLTTNRED-----ISFGQALPFLRYLDSRNAMSFRGCCSYDFTNNLKY 401
DB 812 GTLPFLRYLRLTSKLNHPRISSRAEIMFPDLRIIDSRNFS-----QDLPLSLEH 864
QY 402 LDLSFNGVILMSANFMGLELELYLDFQHSITKKVTSVFLSEKLYLDISYNTKIDF 461
DB 865 L-----KGMRTVDKT---MEEPSYESYDDSVVVVTK----- 893
QY 462 DGIFGLISLNTLKMAGNSFKDNTLSNVFTNTTLTFLDLSKQQLQVLSRGVFTLYRLQ 521
DB 894 -GLELEIVRIJLST-----YTVIDLSNNFEGHIPSLVDLALIR 931
QY 522 LLNMSHNNLFLDPSHYKQLYSLRTLDCSFNRIETSKGILQHPKSLA-----VFNLTN 575
DB 932 ILNVSHNALOGYIYSSLSGLSILSLDSFVQLS-----GEIPQQLASLTFLEFINLSH 985
QY 576 NSV-ACICEYONF 587
DB 986 NYLOGCIPQGPQF 998
RESULT 12
US-09-353-585-3
Sequence 3, Application US/09353585
Patent No. 6287865
GENERAL INFORMATION:
APPLICANT: Dixon, Mark S
Jones, David A
Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses
thereof
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 3:

Db 274 S-----HNRVAGLLEDTFFGLI--GLRVRLSHNAIASLRP 307
QY 389 CSYSDPGTNNLKYLDSLFGV-ILMSANFMGLEEYLDFOHSTLKVTESVFLSEKL 447
Db 308 RFFKDL--HFLEELQGHNRIRQLARSPREGIGLEVLTLDHNOQEV-KAGAFGLTLNV 364
QY 448 LVLDISYNTKIDFDGIFGLISLNTLKAAGNS-----FKDNTLSN 488
Db 365 AVMNLSGNCLRNLPQGVFRGLGKLSHLEGSCLGRIRPHTFTGSLGRLLFLKONGLVG 424
QY 489 V-----FTTNTNLTFLDLSCQLEQISRGVPTLYRLQLNMSHNNLLFLDPSHYQLYSL 544
Db 425 IEEQSLMGIALELELDLTSNQLTHLPHRLFGIGLGLVLLSRNLAEILPADALGPLQRA 484
QY 545 RTLDSPFRLETSKGILOHFPKSLAVFNLTNNSVACICEYQNFLO--VWYDQKMFVNV 602
Db 485 FVLDSHNRLEALPNSLAPLGLRLYLSLRNNSLRTFTQPPGLERLWDEG-----N 536
QY 603 QMKCASPID-----MKASLVLDFTNSTC-----YIKTTIISVSVSVL 640
Db 537 PWDCCGPLKALRDFALQNPASAVPRFVOALCEGDDCQPPAYTYNNITCASPPREV 590

RESULT 14
US-08-477-346-49
Sequence 49, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-477-346-49
Query Match 6.5%; Score 281.5; DB 3; Length 605;

Best Local Similarity 23.5%; Pred. No. 7.4e-17;
Matches 154; Conservative 83; Mismatches 242; Indels 175; Gaps 20;
QY 39 CNDONLSKIPHOIPSTKNDLDSFNPILKILNSYSPFNSQLOMDLSRCEIETEDKMH 98
Db 60 CSSRNLTRPDGVPDGTQALMDGNLSSVPPAAQNLSSIGFLWQGGQSLSEPPALL 119
QY 99 GLNOLSTVLITGNPIKSPSPGSGTLNLEMLVAETKMTSLGPHIGQLISLKLNVAH 158
Db 120 GLENLCHLHBRNQRLSLALGTFAHTPALASIGLSNNRLSRLEDGLFGLGSLMDNLG 179
QY 159 NLIHSEFKLPE-YFSNLTULEHVDLSYN--YIQTISVQDLOFLRNPQVNLSDLSLPI 214
Db 180 NSL--AVLPDAFRLGSLRELVLVAGNRLAYLQPLFSGLAELRE-----LDSRRAL 230
QY 215 DSIOAOF--QGIHRELTLRSNFSNSVNLKMLQMTGTHVRLILGFEKNERNESFDR 273
Db 231 RAIKANVFQLPRLKLYL-----DRNL----- 253
QY 274 SYMEGLCNVSIDEFRLTYINHSDDIYNLNCIANISAMSFTGVHIIKH1ADYPRHFKMSL 333
Db 254 -----IAAVAQAFGL-----KALRWLDL 273
QY 334 SITRCHLKPPPKLSLPLKSWTLTTNR-----EDISFQALAPSLRYLDLSRNSMSPGC 388
Db 274 S-----HNRVAGLLEDTFFGLI--GLRVRLSHNAIASLRP 307
QY 389 CSYSDPGTNNLKYLDSLFGV-ILMSANFMGLEEYLDFOHSTLKVTESVFLSEKL 447
Db 308 RFFKDL--HFLEELQGHNRIRQLARSPREGIGLEVLTLDHNOQEV-KAGAFGLTLNV 364
QY 448 LVLDISYNTKIDFDGIFGLISLNTLKAAGNS-----FKDNTLSN 488
Db 365 AVMNLSGNCLRNLPQGVFRGLGKLSHLEGSCLGRIRPHTFTGSLGRLLFLKONGLVG 424
QY 489 V-----FTTNTNLTFLDLSCQLEQISRGVPTLYRLQLNMSHNNLLFLDPSHYQLYSL 544
Db 425 IEEQSLMGIALELELDLTSNQLTHLPHRLFGIGLGLVLLSRNLAEILPADALGPLQRA 484
QY 545 RTLDSPFRLETSKGILOHFPKSLAVFNLTNNSVACICEYQNFLO--VWYDQKMFVNV 602
Db 485 FVLDSHNRLEALPNSLAPLGLRLYLSLRNNSLRTFTQPPGLERLWDEG-----N 536
QY 603 QMKCASPID-----MKASLVLDFTNSTC-----YIKTTIISVSVSVL 640
Db 537 PWDCCGPLKALRDFALQNPASAVPRFVOALCEGDDCQPPAYTYNNITCASPPREV 590

RESULT 15
US-08-473-089-49
Sequence 49, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULAR TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-473-089-49

Query Match 6.5%; Score 281.5; DB 3; Length 605;

Best Local Similarity 23.5%; Pred. No. 7.4e-17;
Matches 154; Conservative 83; Mismatches 242; Indels 175; Gaps 20;

QY 39 CMDQNSKIPHDIPYSTKNLDSFNPDKILRSYSFTNFSQLOWLDISRCETIEDKAWH 98
DB 60 CSSRNLTPLDPGVPGGTQALWLDGNLSSVPPAFQNLSSLGFTNLQGGQLSLEPQALL 119
QY 99 GLNQSTLYLTGNPIKSFSPGSGSLTNLENLVAVETKMTSLGPHIGQLISLKKLVNAH 158
DB 120 GLENLCHLERNQKSLGTATPALASLGSNNRSLRLEDGLFEGISLMDNLGW 179
QY 159 NLHSFKLPE-YFSNLTNLEHVDLSYN--YIQTISVKDLOFLRENPOVNLSDLSLNP 214
DB 180 NGL--AVLPDAFPGGSLRELVLAGNRLAYLQPALFSGLAIRF-----LDLSRNL 230
QY 215 DSIQAQAF-QGIRLHELTLSNPNSSNVLKMCLONNMTGLVHRLILGFEKNERNLESFDR 273
DB 231 RAIKANVFQLPRLQKLYL-----DRNL----- 253
QY 274 SVMBGLCNVSIDEFRLTYINHSDDLYNINCLANISAMSGVGHITKHIDVPRHFKWQSL 333
DB 254 -----IAAVAPGAFGL-----KALRWLDL 273
QY 334 SIIRCHLKPPLSLPFLSKWTILTNR-----EDISFGQALPSLRYLDSRNAMSGRC 388
DB 274 S-----HNRVAGLLBDTPGILL--GLRVLRLSHNAIASLRP 307
QY 389 CSYSDFGTNMLKYLDLSFNGV-ILMSANFMGLBELEYLDFOHSTLKCTEFSVFLSEKL 447
DB 308 RTFKDL--HFLBELQGHNRIRQLARSPEGQGLEVLFLDHNQLOEV-KAGAFGLTNV 364
QY 448 LYLDISYNTKIDPDGIFLGLISLNTLKMAANS-----FKONTLSN 488
DB 365 AVMNLSGNCRLNLPQGVFRGLGKLSLHLEGCLGRIRPHTFTGLSGLRRLPLKONGIAG 424
QY 489 V-----FTVTTNLTFLDLSKCOLEQISRGVFTLYRLQLNMSGHNNLFLDPGSHYQLYSL 544
DB 425 IBEQSLMGIAELLEDDLTNSQLTHLPRLFOGLGKLEYLLLSRNRLAELPADALGFLQRA 484
QY 545 RTLDGSFNRIETSKIGLOHFPKSLAVFNLTNNSVACICEYONFLQ--WVKDQKMFVAVNE 602
DB 485 FWLDVSHRRLBALPNSILAPLGRRLRYLSLRNNSLRTFTPPQPGLERLWLEG-----N 536
QY 603 QMKKASPID-----MKASLYLDFTNSGC-----YIKTIISVSVSYL 640
DB 537 PMDCGCPALRALDFALQNPASAVPRFVQALCEGDDCQPPAYTYNNITCASPPREV 590

Search completed: March 12, 2005, 19:59:02
Job time : 25.9539 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compen Ltd.

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:55:29 ; Search time 73.8956 Seconds
(without alignments)
3727.157 Million cell updates/sec

Title: US-09-396-985B-6

Perfect score: 4335
Sequence: 1 MNPPLHLAGTLMALFLSL.....GKALNPDETSEREQATTLT 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Published_Applications_AA.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2844	65.6	837	10	US-09-950-041-26
2	2726	62.9	799	10	US-09-950-041-8
3	2726	62.9	799	14	US-10-128-166-7
4	2726	62.9	799	16	US-10-732-563-8
5	2726	62.9	799	16	US-10-732-796A-8
6	602.5	13.9	661	13	US-10-114-893-10
7	602.5	13.9	661	15	US-10-038-854-134
8	597.5	13.8	661	15	US-10-038-854-135
9	597.5	13.8	661	15	US-10-037-417-107
10	575	13.3	1032	10	US-09-954-987B-192
11	575	13.3	1032	14	US-10-272-502A-31
12	575	13.3	1032	15	US-10-407-952-32
13	559	12.9	1050	10	US-09-954-987B-175

14	559	12.9	1050	14	US-10-272-502A-22	Sequence 22, Appli
15	559	12.9	1050	15	US-10-407-952-26	Sequence 26, Appli
16	546	12.6	1059	10	US-09-954-987B-187	Sequence 187, App
17	546	12.6	1059	17	US-10-407-952-30	Sequence 30, Appli
18	546	12.6	1059	17	US-10-753-267-30	Sequence 30, Appli
19	541.5	12.5	859	14	US-10-125-692-6	Sequence 6, Appli
20	541	12.5	1041	9	US-09-168-978-3	Sequence 3, Appli
21	541	12.5	1041	9	US-09-978-295A-498	Sequence 498, App
22	541	12.5	1041	9	US-09-978-697-498	Sequence 498, App
23	541	12.5	1041	9	US-09-978-192A-498	Sequence 498, App
24	541	12.5	1041	9	US-09-999-832A-498	Sequence 498, App
25	541	12.5	1041	10	US-09-978-189-498	Sequence 498, App
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37	541	12.5	1041	10	US-09-978-193A-498	Sequence 498, App
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41	541	12.5	1041	10	US-09-978-643A-498	Sequence 498, App
42	541	12.5	1041	10	US-09-978-375A-498	Sequence 498, App
43	541	12.5	1041	10	US-09-978-288A-498	Sequence 498, App
44	541	12.5	1041	10	US-09-978-188A-498	Sequence 498, App
45	541	12.5	1041	10	US-09-978-681A-498	Sequence 498, App

ALIGNMENTS

RESULT 1

US-09-950-041-26
Sequence 26, Application US/09950041
Publication No. US20030032090A1

GENERAL INFORMATION:

APPLICANT: Hardiman, Gerard T.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
APPLICANT: Ho, Stephen W.K.
APPLICANT: Liu, Yong-Jun

TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REFERENCE: DX0724XK1
CURRENT APPLICATION NUMBER: US/09/950,041
CURRENT FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05

PRIOR APPLICATION NUMBER: 60/044,293
PRIOR FILING DATE: 1997-05-07

PRIOR APPLICATION NUMBER: 60/072,212
PRIOR FILING DATE: 1998-01-22

PRIOR APPLICATION NUMBER: 60/076,947
PRIOR FILING DATE: 1998-03-05

NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.1

SEQ ID NO 26

LENGTH: 837
TYPE: PRT

ORGANISM: Homo sapiens

US-09-950-041-26

Query Match 65.6%; Score 2844; DB 10; Length 837;

Best Local Similarity 66.5%; Pred. No. 1.3e-222;
Matches 558; Conservative 114; Mismatches 159; Indels 8; Gaps 6;

Qy 2 MPLHLAAGLWAL-FLSCLRPGSLNPCIENVLPNTTYOQMDNLSEKIPHDIPYSTRKNDL 60
Db 1 MSASLAGLILHAMAFLSCVRPESMEPCVEV-PNITTYQCEMLNPFKIPDNLFSTRKNDL 59
Qy 61 SPNPKILRSYSFTNFSQLOWLDSRCIEIETIEDKAMGLNQLSTVLVTGNPIKSPSGS 120
Db 60 SFNPLRHIGYSYFSPFELQVLDLSRCEIQTIEDGAYQSLSHLSTLITLGNPQSLALGA 119
Qy 121 FSGGLNLENLVAVERKMTSLSEGFHIGQLISLKLNVANHLHSFCLPEYFSULTNLEHYD 180
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Qy 181 LSYNYIQTISVQDLQFLRENPOVNLSDLSNPIDISIOAQFQIRLHELTLRSFNSN 240
Db 180 LSSNKIQSITCTDLDLVLHQMPLNLSDLSLNPNNFIOGAFKEIRLHKTLIRNPFDSL 239
Qy 241 VLKMCLOMTGLVHRLILGEFKNERNLSEFDRSVMEGLCNVSIDEFRLTYINHFSDIY 300
Db 240 VMKTCIQGLAGLEVHRLVYGEFRNEGKLEKFDKSALEGLCNLTIEFRPLAYLDYLDII 299
Qy 301 NL-NCLANISAMSFQVHIKHIAVPRHFKMQSLIIRCHLKPFPKLSLIPFKSTLITN 359
Db 300 DLNCLTNVSSFSLSVTLERVKDSYNFGWQHELVNCKFQFPITLKLKSLRITPISN 359
Qy 360 REDISFGQALPSELRYLDSLRNMSFRGCCSYSDGTNNLKYLDLSPNGVILMSANFGL 419
Db 360 KGGNMFSEVDLPSELFLDSRNGLSFKGCCSQSDGTTSIKLTDLSFNGVITMSNFPGL 419
Qy 420 EELEYLDFOHSTLTKVTEPSVFLSEKLKLYLDISYNTKIDPBGILPLGISLNTLRKMG 479
Db 420 EQLHLDFQHSNLKQMSSESVFLSLRNLIIYLDISHTRVAPNGIFNGLSLEVLKMG 479
Qy 480 SPKQNTLSNVPTNTNLTFLDLSKQLEQISRGVDTLYRLQLMSNNLFLDPSHYK 539
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Qy 540 QLYSLRTDCSFNRILETS-KGILQHPKSLAVFNLTNNSVACICEYONPLQWQKQML 598
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Qy 599 VNVQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVSVLVAVATVFLIYHFYHIL 658
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RESULT 2
US-09-950-041-8
; Sequence 8, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Ho, Stephen W. K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS, RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XKI

; CURRENT APPLICATION NUMBER: US/09/950, 041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-8

Query Match 62.9%; Score 2726; DB 10; Length 799;
Best Local Similarity 66.5%; Pred. No. 5e-213;
Matches 532; Conservative 111; Mismatches 151; Indels 6; Gaps 4;

Qy 40 MDONLSKIPHDIPYSTKNDLSPNPKILRSYSFTNFSQLOWLDSRCIEIETIEDKAMHG 99
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Qy 100 LNOJSTLVLTGNPIKSPSGSFGSLTNLENLVAVERKMTSLSEGFHIGQLISLKLNVAN 159
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Qy 160 LIHSEKLPSEYSNLTNLEHNDLSYNYIQTISVQDLQFLRENPOVNLSDLSNPIDISIO 219
Db 121 LIQSFKLPEYFSNLTNLEHNDLSNKKIQSITCTDRLVHQMPLNLSDLSLNPNNFIO 180
Qy 220 QAFQIRLHELTLRSNFSNVLMKMCLOMTGLVHRLILGEFKNERNLSEFDRSVMEGL 279
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Qy 280 CNVSIDEFRLTYINHFSDIYNL-NCLANISAMSFQVHIKHIAVPRHFKMQSLIIR 338
Db 241 CNLTIEFRPLAYLDYLDIIDLFNCLTNVSSFSLVSTLIERVDFSYNFGWQHELVN 300
Qy 339 HAKPFPKLSLIPFLSWTLTNREDISFGQALPSELRYLDSLRNMSFRGCCSYSDPGTNN 398
Db 301 KFGQFPITLKLKSLRLFTFSNKGNAFSEVDLPSELFLDSRNGLSFKGCCSQSDPFTTS 360
Qy 399 LKYLDLSENGVILMSANFMGLEBYLDFOHSTLTKVTEPSVFLSEKLKLYLDISYNTK 458
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Qy 459 IDPGCIFLGLISLNTLKAAGNSFKONTLSNFTNTLTLFLDLSKQLEQISRGVPTLY 518
Db 421 VAFNGIFNGJSLSEVLKKAAGNSFOENFLPDIETELRNLTFLDLSQCLQLEQSPJANSLS 480
Qy 519 RLQOLNMSHNNLFLDLSHYKQLYSLRTDCSFRIETS-KGILQHPKSLAVFNLTNNS 577
Db 481 SLQVLNMSHNNPFSLDLPFYKCLNSLDVDSLNLHMTSKKQELQHPSSIAFLANTQND 540
Qy 578 VACICEYONPLQWQKQMLVNVQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSV 637
Db 541 FACHCEHQSFLQWKQKQRLVVERMECATPSDKQMPVLSL-NITQCNKTIIGVSV 599
Qy 638 SVLVAVATVAFIYHFYHILIIAGCKKYSRGSITYDAFVIYSSQDEDWYNELVKNLSE 697
Db 600 SVLVSVVAVLVYKFYHMLLACCIKYRGENIYDAFVIYSSQDEDWYNELVKNLSE 659
Qy 698 VPRFQCLAHYRDPISGVALIANITIOGFHKSARKVIYVVRSHFIQSRMCIPEYELIAQT 757
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DQ **720** LSSRAGIIFVLQKVEXKTLLRQOVELYRLSNLTLEMEDWSVLGHIIHWRRLRALLDGK **779**

DQ **618** ALNPD---ETSEBEQEAATL **634**

DQ **780** SAMPBEGTGTGCNMQEATSI **799**

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RESULT 3
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US20030077279A1
; GENERAL INFORMATION:
; APPLICANT: ARDITI, MOSHE
; APPLICANT: RAOVASHISHI, TRIPATHI
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
; TITLE OF INVENTION: TOLL-LIKE RECEPTOR-4
; FILE REFERENCE: 81476-0255398
; CURRENT APPLICATION NUMBER: US/10/128,166
; NUMBER OF SEQ. ID NOS: 2002-04-23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO 7
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-128-166-7

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Query Match	62.9%	Score 2726	DB 14	Length 799
Best Local Similarity	66.5%	Pred. No. 5e-213		
Matches 532	Conservative 11	Mismatches 151	Indels 6	Gaps 4

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QY 40 MDONLSKLPHDIPYSIKRKLDSNPRLKLRSSPSFNFQLOMDLDSRCELEIFEDKAMG 99
Db 1 MEINFYKIPNLPFSTKKNLDSFNPLRHLGSGSFSPPELQVLDLRSCIEQITEDGAYQS 60
QY 100 LNOGLSTVLVGNRIKFSFGSPSGGLTNLENVAVENTKMTSLGEGHIGQLISLXKLANVAH 15
Db 61 LSHLSTLLTGNITQSLAIGAFSGSLSLCKLVAVENTLASLENFPIGLHKLTKLELNAHN 120
QY 160 LHSFKLPEYFSNLTMLJEHVDSYNYITQTSVKDQOFRENPQVLSLDSLNPIDSIOA 214
Db 121 LIGSFILPEYFSNLTMLJEHVDSYNYITQTSVKDQOFRENPQVLSLDSLNPIDSIOA 214
QY 220 QAFQIGIRLHELTLSRNFSSNVLKMCLOMNTGLVHRLILGEPKERNLLESFDRSVMEGL 279
Db 181 GAFKEIRLHLTKLRNPFDSILNWKTCIQSLAGLEVRHLVGEFRBEGNLEKFDKSALEGL 240
QY 280 CWSIDEPFLTYLNHSDDIYVNLCLANISAMSPGCHIKIADVPRHFMQSLSTIRC 333
Db 241 CNLTIEFRLAYDYLDIDITLFCNCLTNVSSFSLSVATIEKVKQFSYNFMQHLIELVNC 300
QY 339 HLKPFPLSLPFLKSWTLFTTNREDISFGQALPRLRYLDSRNASFGCCSYSDFGTNN 398
Db 301 KRQGFPLKLSKRLTFTSNKGNANFSEVDDPSLEFLDSRNGSLFPGCCSQSDPFGTS 366
QY 399 LKLYLDSFNGVILMSANFGLBELEYLDFQHSITLKRVTFESVFLSEKLKLYLIDISYNTK 458
Db 361 LKLYLDSFNGVILMSANFGLBELEYLDFQHSITLKRVTFESVFLSEKLKLYLIDISYNTK 458
QY 459 IDPDGFLGLISLNTLKMAGNSFKONTLSNVFNTNTNLTFPLDISCOLEOISRQVFDIY 518
Db 421 VARENGFNGSLSEVILKMAGNSQENFPLDITTELRNLTPLDLSOQLEOISRQVFDIY 518
QY 519 RLQILNMSHNLLFLDPESHYKOLYSRLTLDSCFNRLETSKGLIHPFKSLAVNLTNNS 577
Db 481 SLQVILNMSHNPFSLDTPPYKCLNSQVLYDYSGLNHTMSSKQELGHPFSLAFLNLTQND 546
QY 578 VACICEQNLQVWQKQKFLVNVVEQMKASPLDKASLYLDFNTSTCYITKTIISVSV 633

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Db	600	SVTVSVAVVLVYKKEFPHMLLAGOIKYGRGENTYDAFVITYSSODEQWVRELVKQNEEG	655
Qy	698	VPRFQCLHYRDFIPGVAIVANIIOEGFHKSRYVIVVSRHFIOSRWCFIPEYELAQTMQF	757
Db	660	VPPFQCLHYRDFIPGVAIVANIIEGHFKHSRYVIVVSRHFIOSRWCFIPEYELAQTMQF	715
Qy	758	LSRSRGIIFIVLEKVEKSLRQOVELYRLSSNTYLVEMEDNALGRHIFWRRLKALLDGK	817
Db	720	LSRSRGIIFIVLQVEKTELLRQOVELYRLSSNTYLVEMEDSVLGRHIFWRRLKALLDGK	779
Qy	818	ALMPD---ETSEBEOQATTL	834
Db	780	SNMPEGTVGTGCMQOEAATSI	799

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RESULT 4
US-10-732-563-8
: Sequence 8, Application US/10732563
: Publication No. US20040132079A1
: GENERAL INFORMATION:
: APPLICANT: Gupta, Shallely K.
: APPLICANT: Ghosh, Tarun K.
: APPLICANT: Fink, Jason R.
: TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
: FILE REFERENCE: 58193W003
: CURRENT APPLICATION NUMBER: US/10/732,563
: CURRENT FILING DATE: 2003-12-10
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 8
: LENGTH: 799
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-732-563-8

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Query Match	62.9%	Score 2726	DB 16	Length 799
Best Local Similarity	66.5%	Pred. No. 5e-213		
Matches 532	Conservative 111	Mismatches 151	Indels 6	Gaps 4

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QY 100 LNOJSLTVLTGNPISFSPGSFSGJTNLENLVAYETKMTSLSEGHIGQJLSLKKULVAHN 155
Dh 61 LSHSLSTLITLGNPIOSIALGAFSGSGSLQCKVAVEATNLASLENPPIGHLKTLKELVAHN 120
QY 160 LHSFPLPEYPSNLTLELHVDSYNYVYIOTISVKLOQPLREMPQVNLSDLSLNEPDSIOA 215
Dh 121 LIOSFPLPEYPSNLTLELHVDSNKKIOSIYTTDLRVLHQPMLNLSJDSLSLNPMTIOP 180
QY 220 QAFQGIIRLHELTLRSNFNSNVLKNCLONMTGLAHRLLILEPFXYERNLSEFDRSVMEGJ 275
Dh 181 GAKKEIRKRLKTLRNNPFDNLNWKTCIOGLAGLEBVRHVLVLEPFNREGNLEKFDKSALEGL 240
QY 280 CNVSIDEFRLTYINHSDIYNL-NCLANISAMSTGYAHIKHLADVPRHFQWQSLSIIRC 335
Dh 241 CNLTIEEFLAYLDYLDIIDLFPNCLTNVSSFSLVSTIRVXDFSYNFCMQHLELVNC 300
QY 339 HLMKPEKLSLPELKSMTLFTNRNEDISFQGLALPSLRYLDRNMAFPGCCSYSDPGTNN 395
Dh 301 KPGQPFYLLKLSIKRLFTSNKGNAGFSFVDPJPSLEFLDLSRNGLSFRGCCSQSDPGTTS 360
QY 399 LKTYLDSFNGVILMSANFWGLEBEYLDPOHSTLKKVLEFSVPLSLEKLYLDISYNTK 455
Dh 361 LKTYLDSFNGVILMSSNFGLEQLEHLDPOHSNLMKQMSFVPLSLRVLTYLDISHTTR 420
QY 459 IDDDGIFLGLISLNTKXAGNSFKONTLSNVFTNTNLFLDLSKQOLQSRKVPPTLY 515

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Db 421 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSOCCOLEQSLPTAFNSLS 480
Qy 519 RLQOLNMSHNHNLFLDPESHYKQLYSLRTLDCSPNRLET-S-KGILQHPKSLAFVNLTNNS 577
Db 481 SLQVLMNSHNHNFSLDTPPYKCLNSLOVLDYSLNHNMTSKQELQHPFSSLAFLNLTOND 540
Qy 578 VACICEYONFLOMWYDQKMFVNEQMKCASPIDMKASIVLDFTNSTCYIYKTIISVSV 637
Db 541 FACTEHOSFLOMIDKQQLLVEVERMECATPSDQKQNPVLSL-NITQNMKTIIGVSL 599
Qy 638 SVLVATYAFLLIYHFYFHLIIAGCKKYSRSESIYDAFVIYSSQNEDEWVRNELYKNLEEG 697
Db 600 SVLVSVVAVALVYKFYFHLMLAGCIKYGGENIYDAFVIYSSQDEDEWVRNELYKNLEEG 659
Qy 698 VPRFOLCHYRDFIPGVAIAANNIOEGPHKSRKVIYVVSRRHFIQSRWCIFEYELAQTMQF 757
Db 660 VPRFOLCHYRDFIPGVAIAANNIIEGPHKSRKVIYVVSRRHFIQSRWCIFEYELAQTMQF 719
Qy 758 LSSRSGLIFIVLEKVEKSLRQVLEYRLSRNTYLEMEDNALGRHIFWRRLKALLDQK 817
Db 720 LSSRAGIIFIVLOKVEKTLRQVLEYRLSRNTYLEMEDSVLGRHIFWRRLKALLDQK 779
Qy 818 ALNPD--ETSEEEOEATTL 834
Db 780 SWNEGTGVTGCMNOEATSI 799
RESULT 5
US-10-732-796A-8
; Sequence 8, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Taron K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732,796A
; EARLIER FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-796A-8
Query Match 62.9%; Score 2726; DB 16; Length 799;
Best Local Similarity 66.5%; Pred. No. 56-213;
Matches 532; Conservative 111; Mismatches 151; Indels 6; Gaps 4;
Qy 40 MDQNLSTKPHDIPYSTKNLDSFNPILKILRSYFTNFQOLQWLDLSRCEIETEDKAMHG 99
Db 1 MEAINPKIPDNLPSTKRLDLSFNLRLHGSYFSPFELQVLDLSRCEIETEDKAYQS 60
Qy 100 LNOJSTLVLTGNPKISFSPGSGSLTNLENVAVETKMTSLSEGFHIGQLISLKLNVAN 159
Db 61 LSHLSTLITLGNPISLALGAFSGSLQKLVAVETNLASLENFPIGLKLTKELVAN 120
Qy 160 LIHSFKLEBYPSNLTNLEHVDSYNYIQTISKDIQFLRENQVNLSDLSNPFDSIOA 219
Db 121 LIQSKLEBYPSNLTNLEHLDLSNKSIOIYCTDLRVHQMPLNLSLDSINPNFTOP 180
Qy 220 QAFQGRIRLHELTLRNSFNSSNVLMKCLONMTGLVHRLILGFKNERNLSPDRSVMGL 279
Db 181 GAFKIRLRLHKLTLRNNFDSINVMKTCIGLAGLEVHRLVLEGFRRBGNLEKDKSALBGL 240
Qy 280 CNVSIIDEFLRYINHFSDIYNL-NCLANISAMSGVHIKIDVDPHFKQSLISIR 338
Db 241 CNLITIEBRLAVLDYLDIIDLFNCLTNVSSFLSVSTIERVDFSYNFGMLLEVNC 300
Qy 339 HLKPPKSLPFLKSWTLTTRNEDISFQGLALPSRLYDLSNNANSPFGCCSYSPFTNN 398

Db 301 KFGQFPIKLKSLKRLFTSKNGNASEVDLPSEFLDLSRNGLSFPGCCSQSDPFTTS 360
Qy 399 LKYLDLSFNGVILMSANFMGEELELYDFOHSTLKATYEFVSFLKELLYLDISYNTK 458
Db 361 LKYLDLSFNGVITMSNNTLGLEJLHDFQHSNKLKQNSEFVPLSLRNLILYLDISHHTR 420
Qy 459 IDPDGIFLGLISLNTLKAAGNSFKDNTLSNFTNTNLTFLDLSKQQLBQISRGVFTLY 518
Db 421 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSOCCOLEQSLPTAFNSLS 480
Qy 519 RLQOLNMSHNHNLFLDPESHYKQLYSLRTLDCSPNRLET-S-KGILQHPKSLAFVNLTNNS 577
Db 481 SLQVLMNSHNHNFSLDTPPYKCLNSLOVLDYSLNHNMTSKQELQHPFSSLAFLNLTOND 540
Qy 578 VACICEYONFLOMWYDQKMFVNEQMKCASPIDMKASIVLDFTNSTCYIYKTIISVSV 637
Db 541 FACTEHOSFLOMIDKQQLLVEVERMECATPSDQKQNPVLSL-NITQNMKTIIGVSL 599
Qy 638 SVLVATYAFLLIYHFYFHLIIAGCKKYSRSESIYDAFVIYSSQNEDEWVRNELYKNLEEG 697
Db 600 SVLVSVVAVALVYKFYFHLMLAGCIKYGGENIYDAFVIYSSQDEDEWVRNELYKNLEEG 659
Qy 698 VPRFOLCHYRDFIPGVAIAANNIOEGPHKSRKVIYVVSRRHFIQSRWCIFEYELAQTMQF 757
Db 660 VPRFOLCHYRDFIPGVAIAANNIIEGPHKSRKVIYVVSRRHFIQSRWCIFEYELAQTMQF 719
Qy 758 LSSRSGLIFIVLEKVEKSLRQVLEYRLSRNTYLEMEDNALGRHIFWRRLKALLDQK 817
Db 720 LSSRAGIIFIVLOKVEKTLRQVLEYRLSRNTYLEMEDSVLGRHIFWRRLKALLDQK 779
Qy 818 ALNPD--ETSEEEOEATTL 834
Db 780 SWNEGTGVTGCMNOEATSI 799
RESULT 6
US-10-114-893-10
; Sequence 10, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; EARLIER FILING DATE: 2002-04-02
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-10
Query Match 13.9%; Score 602.5; DB 13; Length 661;
Best Local Similarity 28.2%; Pred. No. 4,66-40;
Matches 185; Conservative 127; Mismatches 236; Indels 47; Gaps 18;
Qy 28 CIEVLPNTYOCMOONLSKIPHDIPYSTKNLDSFNPILKILRSYFTNFQOLQWLDLSRCEI 87
Db 28 CIEKANTYNCENIGLSEIPDTLPNTTLEFSFNLPTIHNRTFSRLMNLTLDTLRC 87


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QY      88 E1ETEDKAMG1N0LSTVL7GPNPKSFGSGLTNLEMLVAVETKMTSLGEGHIQ 147
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      88 Q1NW1HEDTFOGHHQ1STVL7GNPL1MAE1SLNPKSLKHLFL1Q1G1S1NLEF1PV1N 147
QY      148 L1SLK1LVANHL1HSFKLPEYFSNLTNLEHVDLSYNY1Q1TSVKDLOFLRNPQVNL 207
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      148 L1NLESLV1GSHN1S1K1P1K1D1P1-AR1N1K1V1D1FQNN1A1H1YS1REDMS1EQ--A1N1SL 204
QY      208 D1SLN1D1S1Q1A1FQ1G1L1H1E1L1T1R1SN1PNS1SV1K1C1Q1N1T1G1L1H1V1H1L1G1E1F1N1E1N 267
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      205 N1F1G1N1N1V1K1E1L1G1A1F1S1T1V1FQ1S1---N1G1G1P1N1L1S1V1F1N1G1Q1N1S1T1G1S1L1M1G1T1E1D1D 260
QY      268 L1S1P1R1S1V1M1E1G1C1N1V1S1D1E1F1R1L1Y1N1H1F1S1D1-D1V1N1L1C1A1N1S1A1M1S1F1T1G1H1K1I1A1D1V1R 326
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      261 -E1D1S1A1M1L1K1G1C1E1M1S1V1S1A1N1Q1E-H1R1F1D1S1S1T1FQ1C1TQ1O1E1D1L1T1A1T1H1K---G1L1S 315
QY      327 H1R1K1W1S1L1I1R1-----C1H1K1P1--F1P1K1L1P1L1K1S1W1L1T1T1R1E1D1S1F1G1Q1--A1L1P 371
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      316 G1M1K1--G1N1L1K1K1L1V1S1V1N1H1F1D1L1C1Q1S1A1N1F1P1L1T1H1Y1R1G1--N1V1K1L1H1G1V1C1E1K1G 370
QY      372 S1L1R1Y1D1L1S1N1A1M1S1F1R1C1C1S1Y1S1D1G1T1N1L1K1Y1D1S1F1N1G1V1--L1M1S1A1N1M1G1E1E1L1E1Y1D1FQ1S 430
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      371 N1Q1T1D1L1S1H1N1D1E1A1S1D1C1S1L1Q1L1K1N1S1H1Q1T1N1S1H1E1P1L1G1L1O1S1Q1A1E1K1E1C1P1O1E1L1D1A1T 430
QY      431 T1L1K1V1T1E1S1V1P1L1E1K1L1Y1L1D1S1Y1T1N1K1I1D1P1G1I1F1L1G1I1S1N1T1L1K1M1A1G1N1S1F1K1D1N1T1--S1N 488
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      431 R1H1I1N1A1P1Q1P1Q1N1H1F1Q1V1N1L1T1Y1C1F1D1S1N1O1H1L1A1G1V1L1R1L1N1L1K1G1N1H1P1D1G1I1T1T1K1N 490
QY      489 V1T1N1T1N1L1T1F1D1L1S1K1Q1E1Q1S1R1G1V1P1D1L1Y1R1Q1L1M1S1H1N1L1--F1L1D1-S1H1Y1K1O1L1S1R 545
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      491 L1Q1T1V1S1L1E1V1L1I1S1C1G1L1S1I1D1Q1A1F1H1S1G1K1M1S1H1V1D1S1H1N1S1L1T1C1D1S1D1S1H1K1G1Y1-- 547
QY      546 T1L1D1C1S1N1R1I1E1T1S1K1I1Q1H1P1K1L1A1V1N1L1T1N1S1V1A1C1C1E1Y1Q1N1F1Q1W1K1D1K1M1F1V1N1E1Q1M1K 605
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      548 -N1L1A1N1S1I1N1I1S1P1L1P1L1S1Q1S1T1N1L1N1H1P1D1C1S1N1H1F1T1W1K1E1M1L1K1E1G1S1E1T1 606
QY      606 C1A1S1P1I1M1K1A1S1L1V1D1F1T1N1S1---T1C1Y1K1T1I1S1V1S1V1V1V1A1T1A1F1H1Y1F1H1 656
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      607 C1A1N1P1E1L1R1E1V1L1S1D1V1K1L1S1C1G1T1A1I1G1F1L1V1L1L1A1I1L1F1A1V1K1L1M1K1O1H1 661
Db

```

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APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 134
LENGTH: 661
TYPE: PR
ORGANISM: Homo sapiens
US-10-038-854-134

Query Match      13.9%; Score 602.5; DB 15; Length 661;
Best Local Similarity 28.2%; Pred. No. 4.6e-40;
Matches 185; Conservative 127; Mismatches 296; Indels 47; Gaps 18;

QY      28 C1E1V1P1N1T1Y1O1C1M1D1N1S1K1I1P1D1P1Y1T1K1N1D1S1F1N1P1K1I1L1S1Y1S1F1T1N1S1O1L1M1D1L1S1R1C 87
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      28 C1E1K1A1N1K1T1Y1C1E1N1G1L1S1E1P1D1L1T1N1T1E1F1E1S1N1F1L1T1N1K1R1F1S1R1M1L1T1F1D1L1T1C 87
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QY      88 E1ETEDKAMG1N0LSTVL7GPNPKSFGSGLTNLEMLVAVETKMTSLGEGHIQ 147
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      88 Q1NW1HEDTFOGHHQ1STVL7GNPL1MAE1SLNPKSLKHLFL1Q1G1S1NLEF1PV1N 147
QY      148 L1SLK1LVANHL1HSFKLPEYFSNLTNLEHVDLSYNY1Q1TSVKDLOFLRNPQVNL 207
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      148 L1NLESLV1GSHN1S1K1P1K1D1P1-AR1N1K1V1D1FQNN1A1H1YS1REDMS1EQ--A1N1SL 204
QY      208 D1SLN1D1S1Q1A1FQ1G1L1H1E1L1T1R1SN1PNS1SV1K1C1Q1N1T1G1L1H1V1H1L1G1E1F1N1E1N 267
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      205 N1F1G1N1N1V1K1E1L1G1A1F1S1T1V1FQ1S1---N1G1G1P1N1L1S1V1F1N1G1Q1N1S1T1G1S1L1M1G1T1E1D1D 260
QY      268 L1S1P1R1S1V1M1E1G1C1N1V1S1D1E1F1R1L1Y1N1H1F1S1D1-D1V1N1L1C1A1N1S1A1M1S1F1T1G1H1K1I1A1D1V1R 326
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      261 -E1D1S1A1M1L1K1G1C1E1M1S1V1S1A1N1Q1E-H1R1F1D1S1S1T1FQ1C1TQ1O1E1D1L1T1A1T1H1K---G1L1S 315
QY      327 H1R1K1W1S1L1I1R1-----C1H1K1P1--F1P1K1L1P1L1K1S1W1L1T1T1R1E1D1S1F1G1Q1--A1L1P 371
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      316 G1M1K1--G1N1L1K1K1L1V1S1V1N1H1F1D1L1C1Q1S1A1N1F1P1L1T1H1Y1R1G1--N1V1K1L1H1G1V1C1E1K1G 370
QY      372 S1L1R1Y1D1L1S1N1A1M1S1F1R1C1C1S1Y1S1D1G1T1N1L1K1Y1D1S1F1N1G1V1--L1M1S1A1N1M1G1E1E1L1E1Y1D1FQ1S 430
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      371 N1Q1T1D1L1S1H1N1D1E1A1S1D1C1S1L1Q1L1K1N1S1H1Q1T1N1S1H1E1P1L1G1L1O1S1Q1A1E1K1E1C1P1O1E1L1D1A1T 430
QY      431 T1L1K1V1T1E1S1V1P1L1E1K1L1Y1L1D1S1Y1T1N1K1I1D1P1G1I1F1L1G1I1S1N1T1L1K1M1A1G1N1S1F1K1D1N1T1--S1N 488
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      431 R1H1I1N1A1P1Q1P1Q1N1H1F1Q1V1N1L1T1Y1C1F1D1S1N1O1H1L1A1G1V1L1R1L1N1L1K1G1N1H1P1D1G1I1T1T1K1N 490
QY      489 V1T1N1T1N1L1T1F1D1L1S1K1Q1E1Q1S1R1G1V1P1D1L1Y1R1Q1L1M1S1H1N1L1--F1L1D1-S1H1Y1K1O1L1S1R 545
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      491 L1Q1T1V1S1L1E1V1L1I1S1C1G1L1S1I1D1Q1A1F1H1S1G1K1M1S1H1V1D1S1H1N1S1L1T1C1D1S1D1S1H1K1G1Y1-- 547
Db

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QY 546 TLDCSFNRIETSKGILQHPKSLAVFNLTNNSVACICEYONFLOWVKQKMFVNVVEQMK 605
Db 548 -LNLANSINIIISPRLPILSQSTINLSHNPLDCTCSNIHFLTWYKENVLHLEGSSEERT 606
QY 606 CASPIDMKASLVLDFTNS-----TCYIKTIIISVSVSIVVATVAFLIYHFPHL 656
Db 607 CANPSPRLGVKSLDVKLSGCGTAIGIFLIVFLLLATLLFPFAVKYLLMKYQHI 661

RESULT 8
US-10-038-854-135
; Sequence 135, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Verneer, Corine
; APPLICANT: Eissen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shinkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderne, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patuturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Bha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Elberman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Mus musculus

US-10-038-854-135
Query Match 13.8%; Score 597.5; DB 15; Length 661;
Best Local Similarity 27.9%; Pred. No. 1,2e-39;
Matches 187; Conservative 125; Mismatches 314; Indels 45; Gaps 15;

QY 12 TMAFLSCLR--PGSLNFCIEVLNPTTYQCDONLSKIIPHDIYSTKNLDSFNPDLKLR 69
Db 10 LVALFLASCRAVTSDDQKCIKEKVKYVCNENGLINEIGTILPNSTECLEFSFNVLPITQ 69
QY 70 SYSPFNFSQLOMIDRSCEITIEDKAMHGNQSLTVLTGNPIKSPGFSFGTNTNEN 129
Db 70 NTFESRLINLFTLDRRCQIYWIHEDTQSOQHRDLTVLTNPILFMAETLSGKALKH 129
QY 130 LVAVETKMTSLSEGFHIGQLISLKKLVANHLIHSFKLPEYFSNLTNLEHVDLSVNYIOTI 189
Db 130 LFFIOTGSSIDFPIRHNQKTLBSYLGSSNISSIKLPKGFPT-EKLVLPQNNALHYL 188
QY 190 SVKDIQFLRENPNQVNLSDLSLNPIDISIOAQAFQIGIRLHELTLNSFNNSVNLKKYCLQM 249
Db 189 SKEDWSSIQQ--ATVLSINLNGNDIAGIEPAFSAVFOSL---NFGTONLVIFKGL 242
QY 250 TGLVHRLILGEFKNERULSESFDSVMEGLCNVGSIDERLTYIHFSDIYNINCLANIS 309
Db 243 KNSTIQSLMDLTFE-DMDDEDISPAVEFGLECMSVESINLQKHFFENISSNTFHCFSGLQ 301
QY 310 AMSFTGVHIIKIID-----VPRHFKQSIIRCHLKP--FPKLSLPFLKSWTL 356
Db 302 ELDLTATLSLPSGLVGLSTLKKLVLSANKFENV---CQISANFSLHLSTKSG--- 354
QY 357 TTNREDISFGOLA-LPSLRVYLDLSRNAMSFRGCCSYSDFTGNMLKYLDLSFNGVI-LMSA 414
Db 355 NTKRLLEGTGCLLENLENIRELDSHDLETSDCCNLQLRNLSHQSILNLSYNEPLSLKTE 414
QY 415 NPMGLEBELEYLDFOHSTLTKKXTEPSVPLSLKLYLDISYNTXIDPDGILGLISLNTL 474
Db 415 AFKECPQELDLDLAFTRKLVKQADSPQNLHLKVLNLSHSLDLSISQQLDGLPALQHL 474
QY 475 IMAAGNSPKDNTL--SNVFTNTNTLFTLDSKCOLSEIISRGVDTLYRLQNLMSHNHLLF 532
Db 475 NLQGNHFPKGNIOKTNLSQTLGRLEILVLSLSCDLSIDQHAFTSLXMMNHHVDSNRRLTS 534
QY 533 LD---PSHYKQLYSLRTIDCSFNRIETSKGILQHPKSLAVFNLTNNSVACICEYONFLO 589
Db 535 SSIEALSHLKGIV-----LNLASNHISILPILPILSQORTINRQNPDLCTCSNIYPLE 590
QY 590 WVKDQKMFVNVVEQMKASPIDMKASVLDFTNSCY----IYKTIISVSVSIVVATV 645
Db 591 WYKENVQKLEDTEDTLCENPPLNGVRLSDVTLSCSMAAVGIFLIVFLVFAILLIPAV 650
QY 646 AFLIYHFPHL 656
Db 661 KYFLRMKYQHI 661

RESULT 9
US-10-037-417-107
; Sequence 107, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patuturajan, Meera
; APPLICANT: Grobse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Verneer, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R

```
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malvankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigara, Muraidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 107
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus
US-10-037-417-107

Query Match      13.8%; Score 597.5; DB 15; Length 661;
Best Local Similarity 27.9%; Pred. No. 1.2e-39;
Matches 187; Conservative 125; Mismatches 314; Indels 45; Gaps 15;

QY 12 IMALPLSLCR--PGSLNPCIETVLPNTTYQCMQNTSKTHDIPYTKNLDLSPNPKIKR 69
DB 10 IVALPLASGRATTSDDQCIKEKVKNTVCENLGINETGLPNSTECLEFSFNVLPTIQ 69
QY 70 SYSFTNSQLWLDLRSCEITETEDKAMHGLNQLSTLVLTGNPIKSPSGSGTLNLEN 129
DB 70 NTFERLNLTPDLTRCOIYIMHEPTFOSGRDLDTLTANPLFMATALSGPKALWH 129
QY 130 LVAVETKMTSLSEGFHIGQLISLKLNVANLTHSFKLPEYFSGNLTVLBEHVDLSYNYQTI 189
DB 130 LFFIQTGSSIDFIFLPHNQKTLESYLGSNHSIKLPGKPT-ELTKYLDLQONNAIHL 188
QY 150 SYKDLQFRENQVNLSDLSNLPIDSIQAQAFQIGIRLHELTLRSNNSNVLKMKCLQM 249
DB 189 SKEDMSLSQQ--ATMISLNLNGNDIAGIEPGAFAFDSAVFQSL---NFGTQMLLVFKGL 242
QY 250 TGLVHRLILGEPKERNLSEFDSVMEGLCNVSTIDEPLTYINHPSDDIYNLNCIANIS 309
DB 243 KNSITQSLWLTGE--DMDEDISPATFBGLCEMSVESINLQKHYPFNISNTFHCFSGIQ 301
QY 310 AMSFTGVHIXIAD-----VPRHFKWQSLIIRCHLKP--FPKLSPFLKSWTL 356
DB 302 ELDLATHLSLPSGLVGLSTLKLVLANKFENL---CQLSASNFPDLTHLSIKG--- 354
QY 357 TTNREDISGQLA-LPSLRYLDSLRNAMSFGCCSVDGTNNKTKLSDSPNGVI-LMSA 414
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DB 355 NTKRLLELGTGCELENENRELDLSDHDIETSPCCNLQLRNLSHLOSINLSTNEPLSLKTE 414
QY 445 NEMGLEBELEYLDFOHSTLKKVTEFSVPLSEKLYLYDISYNTWKIDFDGIPLGLISLNTL 474
DB 445 AFKECPQLELDLAVTRLRKVAQSPFQNLHLTKVLNLSHSLDLSSEQLPGLPALQHL 474
QY 475 KMAQNSFKDNTL--SNVFTNTNLTPDLISKQLEQISRGVDDTYRLQDLNMSHNNLP 532
DB 475 NLQGNHFPKGNIOKNTNSIQTLGRLEILVLSFCDSLSDQHAFTSLKMMNHVDSLNRHRTS 534
QY 533 LD---PSHYKOLYSRTLDSCSPNRLETSGILQHFPEKSLAVENLTNNSVACICEYQNFLO 589
DB 535 SIEALSHKGIY----LNLASNHSIILPILPLISOQRTNLKRONPLDCTCSNYFIE 590
QY 590 WVKDQKMLVNEQMKCASPIDMKASLYLDFTNSTCY---YKTLISVSVSVLVAVATV 645
DB 591 WYKEMNQLEDEDEDLPCENPPLLRGVRLSDVTLSSMAVGLFPLVPLVAILIIPAV 650
QY 646 AFLIYHFYFHL 656
DB 651 KYFLRWKYQHI 661

RESULT 10
US-09-954-987B-192
Sequence 192, Application US/09954987B
Publication No. US20030104523A1
GENERAL INFORMATION:
APPLICANT: Stefan Bauer
APPLICANT: Grayson B. Lipford
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
FILE REFERENCE: C1041/7016 (AMS)
CURRENT APPLICATION NUMBER: US/09/954,987B
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/233,035
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/263,657
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: US 60/291,726
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 60/300,210
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 230
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 192
LENGTH: 1032
TYPE: PRT
ORGANISM: Mus musculus
US-09-954-987B-192

Query Match      13.3%; Score 575; DB 10; Length 1032;
Best Local Similarity 25.1%; Pred. No. 1.5e-37;
Matches 242; Conservative 153; Mismatches 318; Indels 252; Gaps 40;

QY 32 LPNITYQCMQDN-LSKTHDIPYTKNLDLSPN-----YIQTISV----- 63
DB 120 LRLNLTLLLEDDNQLTYTTPAGLPESLKELSLIONNIFOYTKNTFGRLNLERLYLGWNCYF 179
QY 64 -----PLKTLIRSYSFTNF-----SOLQWLDLRSCEITETEDKAMH 98
DB 180 KGNQTFKVEDGAFKVLHLKVL-SLSFNNLFPVPPKLSLSLKLFLSNKAKIMNITQEDPK 238
QY 99 GLNQSLTVLVGN-----PIKSF-----PSFGSLTNLEMLVAVETQMTSIE 141
DB 239 GLENLTLLDLSGNCRCYNAPPTCTPKCKENSIIHHPAFOSLTQLLYLNTSSTSLRTIP 298
QY 142 GFHIGQLISLKLNVANL-LHSFKLPEYFSGNLTVLBEHVDLSY-----YIQTISV----- 191
DB 239 STWFENLNLKELHLEPRLVQELISGAFYTLTLPQLDLSFNFQYKEYEYLOFINISSNF 358
QY 192 -----KDLQFLENQVNLSDLSNLPIDSIQAQAFQIGIRLHEL 230
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Db          359 SKLRSLKTLHNGYFRELKKKHFEHLQSLPML-ATINLGINFTEKIDPKAQ----- 410
Qy          231 TLRSNFNSNVLMKCLQNTGLHVRLLIG-EFKNERNL-----ESP----- 272
Db          411 ----NFSKLDVI-----YLSGNRIASVLDGTDYSSMRNLKRPKSLTDDDEFPDHVNFYHS 461
Qy          273 -RSVMEGLCNVSIDERFLTYINH-----SDDIYNLANCIANSAMSFVGHAKIA 322
Db          462 TKPLIKPQCTAYGAKALDLSINNIFITGSGQFEGFQIACINLSFNANTQVFNGETFS--- 518
Qy          323 DVPRHFKMOSLSIRCHLKRPRLSLPLKSWTLTTNREDI-----SFGQALPSLRYLDL 378
Db          519 -----SMPHKKYLDLTNNRLDPDNNAFSD--LHDEVLVDL 552
Qy          379 SRNA--MSFRGCCSYSDFGTN--NLKYLDLSFNGVILMS-----ANFMGLELEYLDFOHS 430
Db          553 SHNAHFSAIGVTHRGFIQNLINLRVNLSHNGIYTLTBESLKSISLKELVFSGNRDL 612
Qy          431 TLKKYTE--FSVFLSEKLALYLDISYNTKIDPDGIFLG-LSLNTLMAGNS--FKDN 484
Db          613 HLMNANDGKYSIFKSLQNLIRLDLSYNNLQOIPNGAFINLPQSLQELLISGNKLRFFNW 672
Qy          485 TLSNVFTNTNLTFLDLSEKQLEQISRGVPTLYRLQULNMSHNNLFLDPSHYKQLYSL 544
Db          673 TLLQYF--PHLHLLDSRNELYFLPNCLSKFAHSLFTLLSHNFSHLPSGFLSEARNL 729
Qy          545 RTLDSEFNRIE-TSKGILQHPK-SLAVFNLTNNSVACICEYQNFLOWKQKMF---L 598
Db          730 VHLDSFNTIKMINSSLOTKTKNTSLIELHGNVYDCTCDSIDPSRWLDENLNTITPCL 789
Qy          599 VNVEQMKASPIIDMKASVLDPFTNSTC-----YIKTIISVSIVSLVAVATAFILY 650
Db          790 VNV---ICSNPDQSKSISMSLDLTTCVSDTTAAVLFPLTFLTSM--VMLAALVHHLFY 844
Qy          651 ---HFYFHL--ILAGCKKYSRGESITYDAFYYSQN---EDWVNNELVKMLEEGVPR-F 701
Db          845 MDWVFTHMCSAKLKGYRTSISQTFYDAYISDTYKASVTVMVNLRYHLESEDEKSV 904
Qy          702 QCLHYRDFIPGVALAANIIOGFHRSKRYIVVSHFIOSRWCIPFEYIACTOWPLS-- 759
Db          905 LCLCEBMDWDPGLPIIDIMQ--SINOSKKTIFVLTKY-----AKSNPKTAF 951
Qy          760 -----SRSGIIFVLEKVESLLRQOVELYRLSRNTYLEMEDNALGRHIFWRLL 809
Db          952 YLALQRLMDENMDVILFILLEPVLQ--YSQYLRLRORICKSSILQWPNPKAENLFWQSL 1009
Qy          810 KKALL 814
Db          1010 KVVVL 1014

RESULT 11
US-10-272-502A-31
; Sequence 31, Application US/10272502A
; Publication No. US20030139364A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetler, Christian
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Vollmer, Dory
; APPLICANT: Bauer, Stefan
; APPLICANT: Jurk, Marion
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
; FILE OF INVENTION: IMIDAZOQUINOLINE COMPOUNDS
; FILE REFERENCE: C01039.70065 US
; CURRENT APPLICATION NUMBER: US/10/272,502A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,208
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
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; LENGTH: 1032
; TYPE: PRF
; ORGANISM: Mus musculus
US-10-272-502A-31
Query Match      13.3%; Score 575; DB 14; Length 1032;
Best Local Similarity 25.1%; Pred. No. 1.5e-37;
Matches 242; Conservative 153; Mismatches 316; Indels 252; Gaps 40;

Qy          32 LENITQCGMDQW-LKIRPHDIPYSTKNLDLSEN----- 63
Db          120 LRLNLVLLLEDNQLTYTTIAGCPESLKELSLIONNIFQYTKANTPGLRLERLYLGMNCF 179
Qy          64 -----PKILRSYSFTNF-----SOLQWLDLSCIEITIEDKAMH 98
Db          180 KGNQTFKVEDGAFKYLHLKVL-SLSFNNLFFVPPKLPSPSLRKLPLSNAKINNIIOQBPK 238
Qy          99 GLNQSTLYLVGN-----PIYSFS-----PSFGSLTNLENLVAVETQMTSL 141
Db          239 GLENLTLLDLSGNCPCRCYNAPPTCPCKENSIHHPILAFOSLTQLLYLNLSTSLRTIP 298
Qy          142 GFHIGQLSLKKLVANAH-LIHSFPLREYFSNLTLNLEHVDLSYN-----YIQTISV--- 191
Db          299 STWFENLSNLKELHLEFNYLVQELASGAFLTKLPSLQTLDSFNFQYKRYELOFINISSNF 358
Qy          192 -----KDLQFLRENPDQVNLSDLSINPLDISIOAQAFQGIRLHBL 230
Db          359 SKLRSLKTLHNGYFRELKKKHFEHLQSLPML-ATINLGINFTEKIDPKAQ----- 410
Qy          231 TLRSNFNSNVLMKCLQNTGLHVRLLIG-EFKNERNL-----ESP----- 272
Db          411 ----NFSKLDVI-----YLSGNRIASVLDGTDYSSMRNLKRPKSLTDDDEFPDHVNFYHS 461
Qy          273 -RSVMEGLCNVSIDERFLTYINH-----SDDIYNLANCIANSAMSFVGHAKIA 322
Db          462 TKPLIKPQCTAYGAKALDLSINNIFITGSGQFEGFQIACINLSFNANTQVFNGETFS--- 518
Qy          323 DVPRHFKMOSLSIRCHLKRPRLSLPLKSWTLTTNREDI-----SFGQALPSLRYLDL 378
Db          519 -----SMPHKKYLDLTNNRLDPDNNAFSD--LHDEVLVDL 552
Qy          379 SRNA--MSFRGCCSYSDFGTN--NLKYLDLSFNGVILMS-----ANFMGLELEYLDFOHS 430
Db          553 SHNAHFSAIGVTHRGFIQNLINLRVNLSHNGIYTLTBESLKSISLKELVFSGNRDL 612
Qy          431 TLKKYTE--FSVFLSEKLALYLDISYNTKIDPDGIFLG-LSLNTLMAGNS--FKDN 484
Db          613 HLMNANDGKYSIFKSLQNLIRLDLSYNNLQOIPNGAFINLPQSLQELLISGNKLRFFNW 672
Qy          485 TLSNVFTNTNLTFLDLSEKQLEQISRGVPTLYRLQULNMSHNNLFLDPSHYKQLYSL 544
Db          673 TLLQYF--PHLHLLDSRNELYFLPNCLSKFAHSLFTLLSHNFSHLPSGFLSEARNL 729
Qy          545 RTLDSEFNRIE-TSKGILQHPK-SLAVFNLTNNSVACICEYQNFLOWKQKMF---L 598
Db          730 VHLDSFNTIKMINSSLOTKTKNTSLIELHGNVYDCTCDSIDPSRWLDENLNTITPCL 789
Qy          599 VNVEQMKASPIIDMKASVLDPFTNSTC-----YIKTIISVSIVSLVAVATAFILY 650
Db          790 VNV---ICSNPDQSKSISMSLDLTTCVSDTTAAVLFPLTFLTSM--VMLAALVHHLFY 844
Qy          651 ---HFYFHL--ILAGCKKYSRGESITYDAFYYSQN---EDWVNNELVKMLEEGVPR-F 701
Db          845 MDWVFTHMCSAKLKGYRTSISQTFYDAYISDTYKASVTVMVNLRYHLESEDEKSV 904
Qy          702 QCLHYRDFIPGVALAANIIOGFHRSKRYIVVSHFIOSRWCIPFEYIACTOWPLS-- 759
Db          905 LCLCEBMDWDPGLPIIDIMQ--SINOSKKTIFVLTKY-----AKSNPKTAF 951
Qy          760 -----SRSGIIFVLEKVESLLRQOVELYRLSRNTYLEMEDNALGRHIFWRLL 809
Db          952 YLALQRLMDENMDVILFILLEPVLQ--YSQYLRLRORICKSSILQWPNPKAENLFWQSL 1009
```

QY 810 KCALL 814
Db 1010 KNAVVL 1014

RESULT 12
US-10-407-952-32

Sequence 32, Application US/10407952
Publication No. US20030232074A1
GENERAL INFORMATION:
APPLICANT: Lipford, Grayson
APPLICANT: Bauer, Stefan
TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligonucleotides
FILE REFERENCE: C01041.70037.US
CURRENT APPLICATION NUMBER: US/10/407,952
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/421,966
PRIOR FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US 60/370,515
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 1032
TYPE: PRT
ORGANISM: Mus musculus
US-10-407-952-32

Query Match 13.3%; Score 575; DB 15; Length 1032;

Best Local Similarity 25.1%; Pred. No. 1.5e-37;
Matches 242; Conservative 153; Mismatches 318; Indels 252; Gaps 40;

QY 32 LENITVQCDON-LSKIPHDIPYSTKNLDSFN----- 63
Db 120 LKNLVLLLEDQVITIPAGLPESLKEKSLIGNNIFQVTKNTFGRLNERLYLGNCF 179
QY 64 -----PIKIRSYSTNF-----SOLMDLSRCEITIEDKAM 98
Db 180 KCONTFKVEDGAFKNLILHKVL-SLSFNNLFYVPPRLPESLKRKLFLSNKAKIMNITQEDPK 238
QY 99 GKNOSTVLNGN-----PIKFSF-----PSFSGLTJNENVAVETKMTSL 141
Db 229 GLENLTLDLSDGNCRCYNAPPCTPCCKNSSIHHPILAFQSLTQLLYNLISSTSLRTIP 298
QY 142 GFHIGQLISKLLVAHN-LHSFKLPEYFNSMLTNEVDLSYN-----YIQTISV----- 191
Db 229 STWFENLSLTKELHLEFNYLVEIASGALVTKLPISQIIDLSPNQYKRYLOFININSNP 358
QY 192 -----KDLQFLRENPOVNLSLDISLNPIDISIQAOAFQIRLHEL 230
Db 359 SKLRSLKLLHRLRGVYFRELKKHFEHLQSLPNL-ATINLGINFIEKIDFKAFQ----- 410
QY 231 TLKSPNSNSVAKMCLQNTTGLHVRLLIG-EFKKERNL-----ESPD----- 272
Db 411 -----NFSKLDVI-----YLGNRIASVLDGTDYSSWRNRLKRLSTDDEFPDVNFYS 461
QY 273 -RSVMEGLCNVSIDEFRLTYINHF-----SDIYVLANCIANISAFGVHAKHA 322
Db 462 TKPLKPCQTAAGKALDLSLNNIFITGKSQFPGFODIACILANSFANQVFGTGRS----- 518
QY 333 DVPRHFKWOSLSIRCHLKPFPKLSLPLKSWTLTTNREDI-----SEGOALPSLRKYDL 378
Db 519 -----SMFHIXYLDLTNNRLDPDNNAFSD--LHDLVLDDL 552
QY 379 SRNA--MSFRGCCSYSDPGTN--NLKYLDLSPNGVILMS-----ANFMGLEELEYDFOHS 430
Db 553 SRNAHYFSLAGVTHRLGFTQNLINLKVLSHNGIYTLTESELSISLKEIVFSGNRDL 612
QY 431 TLKYTE--FSVFLSEKLLYLDISYTNKIDFDGIFGL-LSLNTLTKAGNS--FKDN 484
Db 613 HLMNNDGKYSWISFSLQNLIRLSDSYNNLQOIPNCAFNLPSQLOELLISGNKLRFFMW 672
QY 485 TLSNVTNTNTNLTFDLDSKQLEQISRGVPTLYRLQLINMGNHNLFLDPSHYKQLYSL 544

Db 673 TILQYF-----PHLHLDLSRNELYFLPNCLSKFASHLETLTLLSHNHFSLPSGFLSEARNL 729
QY 545 RLDCSFNRIB-TSKGIIQHPK-SLAVFNLTNNSVACICEYONFLQWKQKMF-----L 598
Db 730 VHLDSFNTIKINSSIQTKKTNLSTLELHGNVFDCTCQSDSRSMLEMLNTTIPKL 789
QY 599 VNEQMKCASPDMKASVLDFTNSTC-----YIKTIISSVSVLVVATVAFELIY 650
Db 790 VNV-----ICSNPDQSKSISMSLDLTTCVSDTAAVLFLTELTSM--VMLAALVHHLFY 844
QY 651 ---HFYHL--ILLGCKKYSRGEISYDAFYISSQN---EDWVNELYKNEEGVPR-F 701
Db 845 MDWFIYHMCASAKLKGRTTSQTFYDAVISYDTRKASVTDWVINELRHLESEDSKV 904
QY 702 QLCIHRDFIPGVAIAANIOGFPKSRKVIVVSRHRTQSRWCIFEYEAQTOFLS-- 759
Db 905 LILCEERWDGRLPIIDNMQ-SINOSKTIFFVLTKY-----ASWYFKYAF 951
QY 760 -----SRSGIIFVLEKVEKSLRQVELYRLSRNTYLEMEDNALGRHIFWRRL 809
Db 952 YLALQRLMDENMDVIFILFEPVLQ--YSQYLRRLQRICKSIILOWPNNPKALELFWQSL 1009
QY 810 KCALL 814
Db 1010 KNAVVL 1014

RESULT 13

US-09-954-987B-175
Sequence 175, Application US/09954987B
Publication No. US20030104523A1
GENERAL INFORMATION:
APPLICANT: Stefan Bauer
APPLICANT: Grayson B. Lipford
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
FILE REFERENCE: C1041/7016 (AMS)
CURRENT APPLICATION NUMBER: US/09/954,987B
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/233,035
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/263,657
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: US 60/291,726
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 60/300,210
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 230
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 175
LENGTH: 1050
TYPE: PRT
ORGANISM: Mus musculus
US-09-954-987B-175

Query Match 12.9%; Score 559; DB 10; Length 1050;
Best Local Similarity 24.4%; Pred. No. 3.1e-36;
Matches 265; Conservative 153; Mismatches 327; Indels 342; Gaps 52;

QY 4 LHLAAGTILMALFLSCLRPSLNPICIEVLPNI-----TYQCDONLSKIPHDIPYSTKNL 58
Db 13 LIFLMLLVSRVFGFRWPKTL-PC-EYKVINPEAHVIVDCTDKHLTEIPBGIPNTTTL 70
QY 59 DLSFPLILKRSYSTNSQLOMDL-----SKCEIF-----IEDKAMHGLNQSL 104
Db 71 TLTINHIPSISDPSRRNLHEIDLRCNCVPLLGSKANVCTKRLQIRPGSFGSLDLK 130
QY 105 TVLNGNPIKSPS-----PSFSGLTNLB--NLVAVE-----TKMTSLGPHIQG----- 147
Db 131 ALYLDGNQLLEIPDLPSSLH-LLSLEANNIFSIKENTELVNIETLYLQGNCCYRRNCP 189

QY 148 -----LISTKLANVA-----HN1- 160
Db 190 NVSYSIEKDAFLVMRNKVLKSLKDNVAVPTTLBPNNLELYNNI1KKIOENDFNNTN 249
QY 161 -----IHSFKL-----PEY 169
Db 250 ELQVLDLSGNCRCVNVYPCTPCENNSPLQIHDAFNSLTELKYLRLHSNLSLOHVPFW 309
QY 170 FSNLTNLEHVDLSYNYIQTISVKDLOFLRENQVNLSDLSNPIDSIOQAFOGIRLHE 229
Db 310 FKNMNTLOELDSQVYLAR-EIEBAKFLHFLPNL-VELDFSFN---YELQVYHA-----S 359
QY 230 LTLRNSNSNVLKNC-----LQNTGHLNHL-----IIGEFKN 264
Db 360 ITPHLSLSLENLKLIRVKGYPFKELKNSLSVLHKLPRLEVLDTGTFNFIKIDJADNIFKH 419
QY 265 ERNLESFDRSVME-----GLC---NVSIDEFR---LTYINHPSDDIYNLNC-LAN 307
Db 420 FENMLKLIDLSVNIKISPSBSREVGFCRNAQTSVDRHGPVLEALHAFRYDEYARSCRKN 479
QY 308 ISAMSGTGVHIXIADVPRHFKWQSLIIRCH---LKPPKLSLPFLKSWTLTTNREDIS 364
Db 480 KEPPSFLPLN---ADC-HIYGQTLDSRNNIFFIKPSDPQHLSPKLANLSGN---T 529
QY 365 FGOL-----ALPSLKYDLSRNAMSGCCSYSDFGTNNLKLYDLSFNGVILMSANFM 417
Db 530 IGQTLNGSELMPLELRLYLDPSNNRLD-----LTYSTAFE 564
QY 418 GLEBELEYLD-----FOHSTLKVTESFVPLS-LEKLLY--LDISYNTK-IDPDGIFL 466
Db 565 ELQSLBEVLDLSNSHYFOABEGITMNLNFTKRLDLKMMNDNDISTASRTMESD--- 620
QY 467 GLISLNTLKMAGNSFK-----DNTLSNVFTNTNLTFDLSKCOLBOISRGVDP----- 515
Db 621 ---SLRIEFGRNHLDVLRAGDNRYLDFPKULFNLBVLDISRNSLSNLSPPREVEFGMPN 677
QY 516 -----TLYRQLNMSHNL-----LFDPSSHK 539
Db 678 LKNLSLAKNGKSPFMDRLQLLKLEIIDLSSHQTLKYPERLANCSKSLTTLILKHNOIR 737
QY 540 QL-----YSLRTLDSPNRIFTSKGLQ--HFPPK---SLAVENLTNNSVACICEYQ 585
Db 738 QLTKEFLDALQRLTLDISSNKIQ-----VIQKTSFPEVNLNLEMLVHHRFLCNCDAV 793
QY 586 NPLQWQKQKFLVNV-EQMKCASPIDMKASLVDFTNSTCYIKT---IISVSVSYL- 640
Db 794 WFWVNVNHTDVTIPLYATDVTGCVGAKHGQSVISLDLYTCELDTNLIILSVSISVLF 853
QY 641 --VYATVAFI-----YHFYPHLIIAGCKKYSRGEIYDAFYISSQNE--DWYRNEL 690
Db 854 LMVNVTTSHLFFWDMWYIYFWRKAKIKGYOHLQSMESCDAFIYDVTGSAVTEWVLQEL 913
QY 691 VKNLEEGVPR---FOLCLHYRDFIPGVAIAANIIOEGFHKSRYVWVSRHPIOSRWCIF 747
Db 914 VAKLED--PREKHFLCLBERDMLFGQVLEHLSQ-SIQLSKTYFVNTQYAKAKESKRM 970
QY 748 EYEIAQTQWPLSSRSGIIFIVLEKYEKSLRQO-VELYRLLSRNTYLEMEDNALGRHIFW 806
Db 971 AFYLSHQ-RLLDEKVDVILILF--LEKPLQSKFLQLKRLCRSSVLEMPANPQAHPRFW 1027
QY 807 RRLKAL 813
Db 1028 QCLKNAL 1034

RESULT 14

US-10-272-502A-22
; Sequence 22, Application US/10272502A
; Publication No. US20030139364A1
; GENERAL INFORMATION:
; APPLICANT: Kriesel, Arthur M.
; APPLICANT: Schaefer, Christiaan
; APPLICANT: Bratzler, Robert L.

; APPLICANT: Vollmer, Jorg
; APPLICANT: Bauer, Stefan
; APPLICANT: Jurk, Marion
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
; TITLE OF INVENTION: IMMIDZOOINOLINE COMPOUNDS
; FILE REFERENCE: C01039.70065.US
; CURRENT APPLICATION NUMBER: US/10/272.502A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,208
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent version 3.1
; SEQ ID NO 22
; LENGTH: 1050
; TYPE: PRN
; ORGANISM: Mus musculus
US-10-272-502A-22
Query Match 12.9%; Score 559; DB 14; Length 1050;
Best Local Similarity 24.4%; Pred. No. 3,1e-36;
Matches 265; Conservative 153; Mismatches 327; Indels 342; Gaps 52;
QY 4 LHLHAGTILMLFLSLCPGSLNPCIYVLPNI-----TYQCMDQNLKIPHDIPSTKUL 58
Db 13 LIFLMLLVSVFGRFWPPKTL-PC-EVKVNIPEAHVIVDQTDKHLTEIPGIPNTNTNL 70
QY 59 DLSFNPFLKILRSYFTNFSOLQWLDL-----SRCIEFT-----TEDKAMGLNOLS 104
Db 71 TLTINHISIPDSFRRLNHLBEIDLRNCYCVULLGSAVYCTRLQIRPSFGSLDLK 130
QY 105 TLVITGNPIKSPS---PGSFGTLNLE--NLVAVE---TYWTSLEGPHIQO----- 147
Db 131 ALYDGNQILRIPODLPSLHL-LSLSEANNIFSTKENUTELVNIETLYLGQNCYRNPC 189
QY 148 -----LISTKLANVA-----HN1- 160
Db 190 NVSYSIEKDAFLVMRNKVLKSLKDNVAVPTTLBPNNLELYNNI1KKIOENDFNNTN 249
QY 161 -----IHSFKL-----PEY 169
Db 250 ELQVLDLSGNCRCVNVYPCTPCENNSPLQIHDAFNSLTELKYLRLHSNLSLOHVPFW 309
QY 170 FSNLTNLEHVDLSYNYIQTISVKDLOFLRENQVNLSDLSNPIDSIOQAFOGIRLHE 229
Db 310 FKNMNTLOELDSQVYLAR-EIEBAKFLHFLPNL-VELDFSFN---YELQVYHA-----S 359
QY 230 LTLRNSNSNVLKNC-----LQNTGHLNHL-----IIGEFKN 264
Db 360 ITPHLSLSLENLKLIRVKGYPFKELKNSLSVLHKLPRLEVLDTGTFNFIKIDJADNIFKH 419
QY 265 ERNLESFDRSVME-----GLC---NVSIDEFR---LTYINHPSDDIYNLNC-LAN 307
Db 420 FENMLKLIDLSVNIKISPSBSREVGFCRNAQTSVDRHGPVLEALHAFRYDEYARSCRKN 479
QY 308 ISAMSGTGVHIXIADVPRHFKWQSLIIRCH---LKPPKLSLPFLKSWTLTTNREDIS 364
Db 480 KEPPSFLPLN---ADC-HIYGQTLDSRNNIFFIKPSDPQHLSPKLANLSGN---T 529
QY 365 FGOL-----ALPSLKYDLSRNAMSGCCSYSDFGTNNLKLYDLSFNGVILMSANFM 417
Db 530 IGQTLNGSELMPLELRLYLDPSNNRLD-----LTYSTAFE 564
QY 418 GLEBELEYLD-----FOHSTLKVTESFVPLS-LEKLLY--LDISYNTK-IDPDGIFL 466
Db 565 ELQSLBEVLDLSNSHYFOABEGITMNLNFTKRLDLKMMNDNDISTASRTMESD--- 620
QY 467 GLISLNTLKMAGNSFK-----DNTLSNVFTNTNLTFDLSKCOLBOISRGVDP----- 515
Db 621 ---SLRIEFGRNHLDVLRAGDNRYLDFPKULFNLBVLDISRNSLSNLSPPREVEFGMPN 677
QY 516 -----TLYRQLNMSHNL-----LFDPSSHK 539
Db 678 LKNLSLAKNGKSPFMDRLQLLKLEIIDLSSHQTLKYPERLANCSKSLTTLILKHNOIR 737

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QY 540 QI-----YSLRTLDCSFNRIETSKGILQ--HPPK-----SLAVFNLTNNSVACICEYO 585
DB 728 QLTXYFLDALQRLYDLISSNKIQ-----VIQKTSFPENVNLNLEMLVHNNFPLGNCDAV 793
QY 586 NPLQWVKQKMFVNV--EQMKCASPDMKASVLDFTNSTCYIKT---IISVSVSVL- 640
DB 794 WFWWWNHTDVTIIPYLATDVTCTVCGPAHKGQSVISLDLYTCEDLDLTNLLIFSVSISSVLF 853
QY 641 --VVAATVAFLI-----YHFPHLLIAGCKKYSRGSISYDAFVYSSONE---DWVRNLT 690
DB 854 LMVWVTTSHLFPWDMWYIYFWKAKIKGYQHLQSMESCYDAPVDTKASAVTEWVLOEL 913
QY 691 VNLEEGVPR---FOLCLHYRDFIPGVAIAANIIOEGFHKSARKVIVVSRHFIQSRWCIF 747
DB 914 VAKLED--PREKHFNLCLEERDMLPGQPYLENTLSQ--SIQSKTYVFWMTQKAKTESFPM 970
QY 748 EYEIAQTWQFLSSRSGIIFIVLEKVEKSLRQO--VELYRLLSRNTYLEMEDNALGRHIFW 806
DB 971 AFYLSHQ--RLDEKVDVILIF--LEKPLQSKFQLRLCRSSVLEWPAHPQHPYFW 1027
QY 807 RLKRLAL 813
DB 1028 QCLKNAL 1034

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RESULT 15
US-10-407-952-26
; Sequence 26, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Baurer, Stefan
; TITLE OF INVENTION: Immunostimulatory G,U-containing Oligonucleotides
; FILE REFERENCE: C01041.70037 US
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent version 3.1
; SEQ ID NO 26
; LENGTH: 1050
; TYPE: PRN
; ORGANISM: Mus musculus
US-10-407-952-26

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Query Match 12.9%; Score 559; DB 15; Length 1050;
Best Local Similarity 24.4%; Pred. No. 3,1e-36;
Matches 265; Conservative 153; Mismatches 327; Indels 342; Gaps 52;

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QY 4 LIHLAGTILMALFLSCLPRGSLNPCIIEVLNPI---TYQCMDONLSKPHDIPYSTKML 58
DB 13 LIFIMMLVSRVFGFRWPKTL-PC-EVKVNIPEAHVIVDCTDKHLELTPBGIPTNTNLT 70
QY 59 DLSFNPCLKIRSYSTNFSQLOMLD-----SRCEIF---IEDKAMHGINS 104
DB 71 TLTINHIISIPDSFRRLLNHEIDLRNCVCVVLSSKANVCTKRLQIRPFSGLSDLK 130
QY 105 TLVLGNPKISFS---PGSFGIYNLE--NLVAVL---TKMTSLGPHIQO----- 147
DB 131 ALYLDGNQLBEIPQLPSSLH--LISLEANNIPSITKENLTELVTETVLGQNCYRNP 189
QY 148 -----LISIKLANVA----- 160
DB 190 NVSYSEKDAFLWMLKVLSLKDNNTAVPTLTPENLLEYLYNNIIKKIOENDNNIN 249
QY 161 -----IHSFPL-----PEY 169
DB 230 ELQVLDLSGNCRCYVPIPTPCERNNSPLQIHDAFNLSLTCLKVLRHSHNSLQHVPTW 309

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QY 170 FSNLTNLEHVDLSNVIQITISVKDIQFLRENDQVNLSDLSLNPIDSIQAOAFQIGIRLHE 229
DB 310 FKNMNLQELDLSQVYLAR--EIEAKFLHFLPNL--VELDFSFN-----YELQVYHA-----S 359
QY 230 LTLRENFNSNVLKMC-----LQWNTGHLVRL-----ILGEFKN 264
DB 360 ITLPHSLSLLENLKLIRVKGVYFKEKNSSLSVLKHLPRLEVLDTGTFNFIKADLNTFPH 419
QY 265 ERNLSFPRSVM-----GLC---NVSIDEFR---LTYINHFSDDIYNLNC--LAN 307
DB 420 FENLKLIDLSVVKISPSBSREVGFCPNAQISVDHGPQVLEALHYFRDEVARSCRFPKN 479
QY 308 ISAMSPFGVHIKHADVPRHFKQSLSTIRCH---LKEPKLSLPLKSWTLTTRNEDIS 364
DB 480 KEPPSFLEPLN---ADC--HIYGQTLIDLSRNNIFPKSDFOHLFLKLNLSGN-----T 529
QY 365 FQOL-----ALPRLRYLDSRNMSFRGCCSYSDFGNNIKYVLDLSNGVILSANFM 417
DB 530 IQOTLNGSELMPRLRLRYLDFSNRLD-----LVSITAE 564
QY 418 GLELELYD-----FOHSTLKKVTEFSVFLS--LEKLY--LDISYTNTK--IDPDGIFL 466
DB 565 ELQSLLEVLDLSNSHYFOABEGITHTMLNFTKKRLDKLMDNDNDISTASRTMESD----- 620
QY 467 GLISLNTLKMAGNSFK-----DNTLSNVFTNTNLFTLIDLSKQLEQISRGVFD----- 515
DB 621 ---SLRIIEFRGNHLDVLMRAGDNRVLDFFKMLFMLEVLDISRNLSNLSLPPPVFEQMPN 677
QY 516 -----TLYRQOLNMSHNNL-----LFLDPSHK 539
DB 678 LKNLSLANGLKSPFWDRLQLLKHLLELDLSHNLQTKVPERLANCSKSLTTLILKHNQIR 737
QY 540 QI-----YSLRTLDCSFNRIETSKGILQ--HPPK-----SLAVFNLTNNSVACICEYO 585
DB 728 QLTXYFLDALQRLYDLISSNKIQ-----VIQKTSFPENVNLNLEMLVHNNFPLGNCDAV 793
QY 586 NPLQWVKQKMFVNV--EQMKCASPDMKASVLDFTNSTCYIKT---IISVSVSVL- 640
DB 794 WFWWWNHTDVTIIPYLATDVTCTVCGPAHKGQSVISLDLYTCEDLDLTNLLIFSVSISSVLF 853
QY 641 --VVAATVAFLI-----YHFPHLLIAGCKKYSRGSISYDAFVYSSONE---DWVRNLT 690
DB 854 LMVWVTTSHLFPWDMWYIYFWKAKIKGYQHLQSMESCYDAPVDTKASAVTEWVLOEL 913
QY 691 VNLEEGVPR---FOLCLHYRDFIPGVAIAANIIOEGFHKSARKVIVVSRHFIQSRWCIF 747
DB 914 VAKLED--PREKHFNLCLEERDMLPGQPYLENTLSQ--SIQSKTYVFWMTQKAKTESFPM 970
QY 748 EYEIAQTWQFLSSRSGIIFIVLEKVEKSLRQO--VELYRLLSRNTYLEMEDNALGRHIFW 806
DB 971 AFYLSHQ--RLDEKVDVILIF--LEKPLQSKFQLRLCRSSVLEWPAHPQHPYFW 1027
QY 807 RLKRLAL 813
DB 1028 QCLKNAL 1034

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Search completed: March 12, 2005, 20:27:59
Job time : 80.8956 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:01 ; Search time 21.5445 Seconds
(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985b-6

Perfect score: 4335
Sequence: 1 NMPLHLAAGTLTALFLSCL.....GKALNPDETSEEQATTLT 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597.5	13.8	661	2 I56258	RP105 - mouse
2	465.5	10.7	786	2 T06864	Toll protein-like
3	397	9.2	1097	2 A29943	Toll protein precu
4	374	8.6	1389	2 T13852	gene wheeler prote
5	371	8.6	1385	2 T13857	clt protein - fru1
6	320.5	7.4	1134	1 A29944	chaoptin precursor
7	303	7.0	1066	2 T15864	hypothetical prote
8	301.5	7.0	603	2 JC6128	insulin-like growt
9	300.5	6.9	605	2 JC5239	insulin-like growt
10	290.5	6.7	603	2 UC1282	insulin-like growt
11	287.5	6.6	1112	2 T10504	insulin-like growt
12	285.5	6.6	1051	2 T13174	gpi10 protein - fr
13	281.5	6.5	605	2 A41915	insulin-like growt
14	279	6.4	1469	2 B36655	slit protein 2 pre
15	279	6.4	1480	2 A36665	slit protein 1 pre
16	274	6.3	1592	2 A33988	adenylate cyclase
17	270.5	6.2	1143	2 T10636	hypothetical prote
18	270	6.2	907	2 JG0193	G protein-coupled
19	266.5	6.1	1523	2 T13953	MEGF5 protein - ra
20	266	6.1	1531	2 T42218	slit-1 protein hom
21	265.5	6.1	1016	2 T30553	disease resistance
22	264.5	6.1	1027	2 B85089	receptor protein X
23	261	6.0	1232	2 T05322	hypothetical prote
24	259	6.0	910	2 G84648	probable disease r
25	256	5.9	560	2 A60164	platelet membrane
26	253	5.8	907	2 JB0176	orphan G protein-c
27	252	5.8	1120	2 B86479	hypothetical prote
28	250	5.8	1068	2 H96769	hypothetical prote
29	249	5.7	662	2 S42799	garp precursor - h

30	249	5.7	855	2 T17460	disease resistance
31	247.5	5.7	1778	2 AF1116	internein protein
32	247	5.7	890	2 T00800	disease resistance
33	246.5	5.7	853	2 T17461	disease resistance
34	246.5	5.7	910	2 B96770	hypothetical prote
35	243.5	5.6	738	2 T19938	hypothetical prote
36	243	5.6	1091	2 A58532	glial cell membran
37	243	5.6	1784	2 C96615	hypothetical prote
38	242.5	5.6	603	2 T24315	hypothetical prote
39	242.5	5.6	800	2 H84740	hypothetical prote
40	242.5	5.6	951	2 A96770	hypothetical prote
41	239	5.5	855	2 T07015	Cf-4A protein - to
42	237	5.5	994	2 H96510	probable disease r
43	236.5	5.5	622	2 JC7973	synleutin - human
44	235.5	5.4	983	2 G84524	probable disease r
45	235.5	5.4	2026	1 OYBY	adenylate cyclase

ALIGNMENTS

RESULT 1

I56258
RP105 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: I56258
R/Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A/Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a m
A/Reference number: I56258; MUID:95204928; PMID:7897216
A/Accession: I56258
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-661 <RES>
A/Cross-references: UNIPROT:O62192; GB:D37797; NID:G761711; PIMN:BA07043.1; PID:G761712

Query Match

Best Local Similarity 13.8%; Score 597.5; DB 2; Length 661;
Matches 187; Conservative 125; Mismatches 314; Indels 45; Gaps 15;

QY	12	IVALLFLSCRR--PGSLNPCTIEVLPNTTQCMDQNTSKIPHDIPYSTKXLDLSPNPKIKR	69
DB	10	IVALLFLSCRRATTTSDQCKIEKVKYKNCENIGINEIPGLPNSECEFFSNVLPITD	69
QY	70	SVSPFNPSQLQWLDLSRCEIETIEDKAMHGQNLSTVLTGNPIKSPSGSGLTNLEN	129
DB	70	NTTFERLNLVPLDLTRCQYWIHEDTFQSGHRLDTLVLTANPLFMAETALSGPKALX	129
QY	130	IVAVETKMTSLBGFHIGQLISLKLNVANLHSEKLPDYFNSLNTNLEHVDLSYNYQTI	189
DB	130	LFFIQTGSSIDFIFLHNGKTESLYGNSHLSIKLPKGFPT-EKLYKLDQNNANLHVL	188
QY	190	SVKDIQFTRENDQVNLSDLSNPIDTSIOAQAFQIGRIHELTLRSNFSNVLKQCLQNM	249
DB	189	SKEDMSLQO--ATNLINLNGNDIAGIEPGAFAVFSGL---NFGQTMVLVFEKL	242
QY	250	TGLAHRLILGSEKERNIESFDRSVMBGLCNVSIDEFPLTYINHFSDIYNLNCIANIS	309
DB	243	KNSTQSLMLGTFE-DMDEDISPVFEGLCMSVESINLQKHYPFNISNTFHCPSGLQ	301
QY	310	ANSPGVHAKHKLAD-----VPRHFKWQSIIRCHLKP--FPKLSLPLKSWTL	356
DB	302	EIDLRAHSLSELPGLVGLSTLKKVLANKRENT---CQISANFPLTHLSIKG---	354
QY	357	TNNREDISFGQLA-LPSRLYLDLSRNANMSFRCCGYSDFGTNNLKYLDSENGVT-LMSA	414
DB	355	NTRKRELGTGCLENENLRELDISHDDIETSDCCNLOARNLSHOSLNISYNEPLSLKTE	414
QY	415	NFMGLSELEVLDFQSTLKKVTEFSVFLSEKLVLDISYNTKLDPOGIFGLSLNTLT	474
DB	415	AKKCPQHELDLAFTRLKVKAQSPFQMLHLKLVNLHSLDLSSEQLFDGLPALQHL	474

QY	475	KMAGNSFKDNTLT--SNVFNTNTNLTFLDLSKQLEQISGVDPDTLYRLDLMASHNNLTF	532
QY	475	KMAGNSFKDNTLT--SNVFNTNTNLTFLDLSKQLEQISGVDPDTLYRLDLMASHNNLTF	532
Db	475	NLQGNHFPEKGNIOKTNISLDTGLRLLEIYLSFCDLSIDQHATSLKMGHVDLSHNRLLS	534
QY	533	LD--PSHYKQDLSRLTDCSFNRJETSXGILLQHPFKSLAVENLTNNSVACICEYONFLQ	589
Db	533	LD--PSHYKQDLSRLTDCSFNRJETSXGILLQHPFKSLAVENLTNNSVACICEYONFLQ	589
QY	535	SIEMALSHLKGIY----LNLASNNHISILPSLLPLISQQRITNLRQNPIDCTCSNIYFE	590
Db	535	SIEMALSHLKGIY----LNLASNNHISILPSLLPLISQQRITNLRQNPIDCTCSNIYFE	590
QY	550	WYKQDKMFLVANVEQKCKSPIDMKASLYVDFNNSCY----YKTIISVSVSVLVVATV	645
Db	551	WYKEMQKLEDEDTEDTLCENPFLRGVRLSDVTLSGMAAVGIFFLVFLVPAIILIEFV	650
QY	646	AFLIHYFYEHL 656	
Db	651	KYFLRWKTYOHI 661	
RESULT 2			
T08664			
Toll protein-like receptor DKFZp54710610.1 - human			
C/Species: Homo sapiens (man)			
C/Date: 11-Jun-1999 #sequence _revision 11-Jun-1999 #text_change 09-Jul-2004			
C/Accession: T08664			
R/Pousterka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.			
submitted to the Protein Sequence Database, May 1999			
A/Reference number: Z16466			
A/Accession: T08664			
A/Molecule type: mRNA			
A/Residues: 1-786 <PO>			
A/Cross-references: UNIPROT:O15399; EMBL:AL050262			
A/Experimental source: fetal brain; clone DKFZp54710610			
C/Genetics:			
A/Note: DKFZp54710610.1			
Query Match			
Best Local Similarity 24.8%; Score 465.5; DB 2; Length 786;			
Matches 203; Conservative 131; Mismatches 287; Indels 197; Gaps 33			
QY	120	SPSGITNLENTLVAVETKMTSLGPHIGQI-----ISLKKLN--VAHNLHSFKLPERYS	171
Db	32	SKNGIHHPKDLSQKTTILINISQNIYSELMTSDILSKRLITLISHNRIGYLDISVFKE	91
QY	172	NLTNLEHDLSTNYIQTISVYDLOFLRENPQYNLS-LDLSLNPDISIQ-AQAQGI-RLLH	228
Db	92	N-QELELYDLDSHNKLVKISC-----HPTNLKRLDLSFNAFPALPICKKEFGNMSQLK	142
QY	229	ELTL-RSNFNSNNTVKMGCLQMMTGAAHYRLILGEPFNERNLSPRSVWEGICNVSIDBF	287
Db	143	FLGLSTLHLEKSSVLPPIAHNLISKY--LVLGELYGKEEDG-----GIQDFYTESL	192
QY	288	RLTYIN---HESDDIYNLCLANISAMSFTGVHAKHADVPRHFQMOGLSIIRCHLXPF	343
Db	193	HIVPFTNKEFPH-----ILDVSVKTVANLLELSNIKCVLEDESKCSFSLIAKLTQIN	243
QY	344	PKLSTLPEPLKS-----WTLTNNEDIS---FQQLALPSIRIYDLSRNAMS	384
Db	244	PKLSTLTLNLIETTNWSEFIRILQLVHMTTWYSSISNVQLQQLDFRDEYDGTSLKALS	303
QY	385	FRGCS-----YDFGTNNLK-----YLDSTNGVILMSA	414
Db	304	IHQVAVDFGFPQSYIYEIIFSNMNIKNFTVSGTRVHMLCPSKISPFLLDPSNNLLDT	363
QY	415	NPMG---LELELYLDFOHSTLTKVTFES-VPLSEKLVLVDISYNTKID-PDGI-FLGLI	469
Db	364	VFENQGHLELETLTLQNMQLKELSKIAEMTQMSLQQLDISQNSVSIDEKKGDCSWK	423
QY	470	SLNTLKMAGNSFKDNTLSNVFTNTNLTFLDLSKQLEQISRGVDTL-YRLQLLMSHN	528
Db	424	SLLSLAMS-----SNILLDT-----IPRCLEPRRIKVDL-HS	454
QY	529	NULFLDPBHHYKQDLSYLRFLDGSFNRJETSXGILLQHPFKSLAVENLTNNSVACICEYONFLQ	579
Db	455	NKIKSIPQVAVYGLLEQLOELNVAFNSLTLDPGCGSF--SLSTVLIIDHNSHPSADFPQS	512

QY 580 -----CICEQNPLQWYKQDKMFVIANEQA-----KCA5PIDM 612
 Db 513 CQKRSIKAGDNPPQCTCELGEFVK-----NIDQVSSEVLBEQMPDSYKCDYDESY 562
 QY 613 KASLVLDFTNSTCYIKYTTISVSVSVLVAATVAFLLIHFYFHL-----TLIAGCKYRS 667
 Db 563 RGTLLKDFHMSSELSCNITLLITVITVATMLVLAIVTSLCYTLDLPWLYRMVQCWTQRRR 622
 QY 668 GEGT-----YDAFVYSSQNEEDWPNELVKNLE-EGVRFQCLAHYRPIPSVAI 716
 Db 623 ARNIPLEELQRIQFAFISYSGHDSFWVKNELLPLNLEKGM--QICLHERNFVPEKSI 679
 QY 717 AANIQGFHRSRVYIVVSRRHFIQSRWCIFEEYELIAOTWQFSLRSGLIFIVLEKY-EKS 775
 Db 680 VENIT-TCIEKSYKSIIVLSPNFQSEMCHELYFAHNLPHGCSNLIILLLEPIFYQS 738
 QY 776 LLRQVELYRLISNTYLEWEDNALGRHIFRRILKAL 813
 Db 739 IPSSTYHKLKSLMARRTYLEWPKESKRGKGLFWAMLRAL 776

 RESULT 3
 A29943
 Toll protein precursor - fruit fly (Drosophila melanogaster)
 C|Species: Drosophila melanogaster
 C|Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
 C|Accession: A29943
 R|Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
 Cell 52, 269-279, 1988
 A|Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, af
 A|Reference number: A29943; MUID:88135760; PMID:2449285
 A|Accession: A29943
 A|Molecule type: DNA
 A|Residues: 1-1097 <HAS>
 A|Cross-references: UNIPROT:P08953; GB:M1969; GB:J02682; NID:g158640; PIDN:AAA28941.1;
 C|Genetics:
 A|Gene: FlyBase:rl
 A|Cross-references: FlyBase:FBgn0003717
 C|Keywords: transmembrane protein
 F|1-17/Domain: signal sequence #status predicted <SIG>
 F|18-1097/Product: Toll protein #status predicted <MAT>

 Query Match 9.2%; Score 397; DB 2; Length 1097;
 Best Local Similarity 23.4%; Pred. No. 1e-16;
 Matches 196; Conservative 119; Mismatches 302; Indels 222; Gaps 30;

 QY 33 PNITYQMDNLSKIPHDl-PYSTK-NLDLSNPILKRSYSFTNFSQLOMILSRCEI 89
 Db 319 PELQILRLRAELQSLPGDLFEHSTQITNISLGDNLAKTLPATLLEHQVNLISDLSNNRL 378
 QY 90 ETLEDKAMHGLNQLSTVLVGNPIKSPSPSGFGLTLEVLVAVERMTSLLEG----- 142
 Db 379 THLPDSLFAHTNLTDLRLLEDNLTLGISGDI FENLGLVLTVLVMSRRNLRLIRIDRAFAVSTN 438
 QY 143 -----FHL-----GQLISLKLNVAMNLHSPFKLDEYPSNLT 174
 Db 439 GLRLHLHDNDIDLQQLPDLIMLQTYQINSFPGYMGHLLTLNLRNNSI-ITVYNDMKATML 457
 QY 175 NLEHVDLSYNYIQTISYKDLQFLRENPQVNLISDLSINPIDSIOAQAFQGIIRLHELTLS 234
 Db 498 QLRRLDLSYNNISSLGYEDLAFLSQN-----RLH----- 526
 QY 235 NFNSSNVLLKQCLQNMGTGLHVRLLIGEFKERNLLESFDRSVMEGLCNVSIIDERPLTYINH 294
 Db 527 -----VNMTHNKLRIALPE-----DYHLGGYNN-----NLVAVD- 557
 QY 295 FSDDIYVNLCLANISAMSFQVHIKHLADVPRHFKMOSIIRICHLLKPPKLSLPFLKSW 354
 Db 558 LNDNPVLCDDCTILMFIOLVGVYHKPQYS---RQFKLRTRDLV-----CSQPNVLLEG 605
 QY 355 TLATTNRDLSFGQALPSLRVYLDLSRRNMSFRCC-CSYSDFGTNNLKYLDLSFNGVYILMS 413

Db 606 TFEVROIEP-----QTLICPLDPSDDPRKRCPCRCNCHV-----TYDKALVIN 649
 Qy 414 ANFMGLEELLEYLDFOHSTIKKYTEFSEVPLSEKLYLDISYNTKIDPGLISLNT 473
 Db 650 CHSGNLTIVPRLPNLHKNNQLM-----LHLENNLTLLRPSANT-----GYESVTS 696
 Qy 474 LKAGNSFPDNTLSNVFTTNTLPLDLSKQLEQISRGVPTLVRLQLLNNSHNNLFL 533
 Db 697 LHLAGNNLT-----TSIDVDQLPTMLTHLDIS-----WNHLQMLN----- 730
 Qy 534 DSHVKQLYSLRTLDOSFNRISKGILOHFPKSLAVENLTNNVACICEYONFLQWMD 593
 Db 731 -----ATVLGFLRTMKMSV-KLSGPNMCDCTAPLFLFTD 768
 Qy 594 QMPLVNEQMKCAPIDMKASLYLDFTNSTCIYKTI-ISVSV-----SVLVAATVAFPI 649
 Db 769 NFERIGDRNEMCVN-AEMPTMVELSTNDICPAKGVFIALAVIALGLAGFAALY 827
 Qy 650 YHF-----YFH-LILLAGCKKYSRGESYIDAFVYSSQNEQWVKNELVKNLEGVPR 700
 Db 828 YKQTEIKIMLYAHNLLMFVTEEDLDKDKPDAPFISYSHKQSPFIEDVLPOLBHPQK 887
 Qy 701 FOLCHYRDFIPGVALIANNIOEGFHKSRKVIWVSRHPIQSRMCIFFEYIAQTWQFLSS 760
 Db 888 FOLCHYRDMVLVGHIPENIMR-SVADSRRITIVLSQNFISKEMARLEFRALHRSALMEG 946
 Qy 761 RSGIIFIV-----LEKVEKSLRQOVELYRLLSRNTYLEMEDNALGRHIFWRRLKAL 813
 Db 947 RSRIVITVYSDIGDEKDE-----ELKAVLKNNTYIKW-----GDFWFDKLRFL 993

RESULT 4

T13852
 gene wheeler protein - fruit fly (Drosophila melanogaster)
 C.Species: Drosophila melanogaster
 C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C.Accession: T13852
 R.Eldon, E.; Kooyer, S.; D'aveyln, D.; Duman, M.; Lawinger, P.; Botae, J.; Belien, H.
 Development 120, 885-899, 1994
 A.Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
 A.Reference number: Z17796; MUID:95524375; PMID:7600965
 A.Accession: T13852
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-1389 <EID>
 A.Cross-references: UNIPROT:Q24591; EMBL:I23171; NID:g415682; PID:g1019104; PIDN:AAA7920
 C.Genetics:
 A.Gene: wheeler
 A.Cross-references: FlyBase:FBgn004364

Query Match 8.6%; Score 374; DB 2; Length 1389;
 Best Local Similarity 21.2%; Pred. No. 3.7e-15;
 Matches 230; Conservative 159; Mismatches 327; Indels 366; Gaps 48;

Qy 41 DONLSKITHDIPYSTKNDLSFNPLKIRSYSTNF-----SQIQ 80
 Db 154 DNNIRQLPEGWCMSPSLQLNLTONIRSAFLFSEKLCAGSALSNANGAVSGSGSEIQ 213
 Qy 81 WLDSRCIEITIEDKAMHG--LNOLSTVLNTPISFSPGSGQLTNLENVAVETKMT 138
 Db 214 TLDSVFNELRSLPD-AMGASRLRLQTLSTLOHNNISTLAPNALAGLSSLRVNLINISYHNV 272
 Qy 139 SLEGHFIQILSLKLVNAHNLHSFKLPE-----YFS 171
 Db 273 SLPSFAFGNKEIRLHLQGNDL-YELPKGLHRLLEQLVLVDSGNQLTSHHVNSYFA 330
 Qy 172 NLTNLEHVDLSNYQTI---SVKLOPLRENPQVNLSDLSLPIDSIQAQAFQGI-RL 227
 Db 331 GLIRIVLNTSNNALTRIGSKFKELYPLO-----LIDMNNISIGHIEGAFPLVYL 383
 Qy 228 HELTLRSN-----FNSSNVL-KMCLQNMNTGLHVRHLIGE-FKXERNLESFDRS-- 274
 Db 384 HTLNLAEKRLHTLDNRIRNGLYLVLYKLTLLNN---NLVSVESQAFKNCSDLKEIDLSSN 439

Qy 275 -----VMEGLCNVS-----IDFRLTYINHSDIYINLCIANISAMS--FTGVH 317
 Db 440 QLTVEPAVQDLSMLKTLIDGENQISEFR-----NNTFRILNQLTGLRLDNRIGNIT 492
 Qy 318 ICHIDVPRHFQWQSLSIIRCHLKPPKLSL-PFLKSWTLTNREDISF-----GOLA-L 370
 Db 493 VQMFQDLPR-----LSVLNLAKNRIQSIERGAFAKNTIEIAIRLDKNTLTDINGIFAVL 546
 Qy 371 PSLRYLDSIRNAMSFRGCCSYSDPGNNLKLYLDLSFNGVILMSANPMGLEE--LEYLDF 427
 Db 547 ASLWLNLSSENLVW---FDYA-FIPSNLKMIDHIGNYIEAL-GNYKQOEIRVTTLLA 601
 Qy 428 QHSTLKYTEFSEVPLSEKLYLDIS-----YNT-----KIDPDIFFGLISLNTL 474
 Db 602 SHNRITBEGMSVPSRISL-LPFINNNIIGQIQANFVQDKTRIALRDLVAVNSKISLNL 660
 Qy 475 KMA-----GNSFKDNTLSNVFTTNTLT-----FLDKR----- 503
 Db 661 RVAPVSAEKVPEFYLGPNFECDSMELORINNLTTRQHPHVVDLGNIECLMPHSRGA 720
 Qy 504 -----COLBO----- 508
 Db 721 PLRPLASASDPFKYTESHCPTCHCEYQCEGEVLCPCNCSCFHATATATNYDCR 780
 Qy 509 -----ISRGVDTLY-----RLQLLNMGHNNLLPLDPHYKQL 541
 Db 781 QDLALPFRIPQDVSD-LYLDGNNMPELEVHILGRNRILALYLNASNNMTLQNGSLAQ 839
 Qy 542 YSLRTLDOSFNRISKSG-----ILOHFK-----SLAVNLTNNS 577
 Db 840 VNLRYLHLENNCLTALBETSEFRSLGLRLLYLNNMLTHISNATEPEVLSLEVLRLDNR 899
 Qy 578 V-----ACIC-EYONFLQWVDQKFLVNEQMKCA-SPIDMK 613
 Db 900 LSSLPHLOKRSLOGLTGRNASCRCOOLRELAQFSDNANVVDADHDYLDAGIKRE 959
 Qy 614 ASLYLDFTNST-----CYITKTIISVSVSVLVVAATVAFPI 649
 Db 960 LELIGNLNGPDCSDLLDASANSISSQDLGAGICPCMPAVL---VIFLVVLIIVPV 1016
 Qy 650 YHFYHLLILAG-----CK-KYSGESYIDAFVYSSQNEQWVKNELVKNLEGVPRQOL 703
 Db 1017 PRESVRMMLFPHYGRVCEPRFEDAGKYDAIILHSEKDYERVCNIAELEHGRPPFL 1076
 Qy 704 CLHYRDFIPGVALIANNIO--EGFHKSRKVIWVSRHPIQSRMCIFFEYIAQTWQFLSR 761
 Db 1077 CLQQRDLPP-----QASHQLVEGARSKTIILVLRNLATFEMNRIEPRNA---FHESL 1128
 Qy 762 SGII--FVLEK-----VEKSLRQOVELYRLLSRNTYLEMEDNALGRHIFWRRL 809
 Db 1129 RGLAQKVIITBETSVSAAEDVAELSPYKSVPSRLLTLCORY-----FWEXTL 1176
 Qy 810 KKAL 813
 Db 1177 RYAI 1180

RESULT 5

T13887
 tlr protein - fruit fly (Drosophila melanogaster)
 C.Species: Drosophila melanogaster
 C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C.Accession: T13887
 R.Chang, C.; Beachy, P.A.
 Mech. Dev. 47, 225-239, 1994
 A.Title: Expression of a novel Toll-like gene spans the parasite boundary and contri
 A.Reference number: Z17805; MUID:95151581; PMID:7848870
 A.Accession: T13887
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-1385 <CHI>
 A.Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AAB33383

F/854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
 F/879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
 F/903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
 F/928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR35>
 F/949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
 F/973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
 F/996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
 F/1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
 F/1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Query Match 7.4%; Score 320.5; DB 1; Length 1133;

Best Local Similarity 22.0%; Pred. No. 3,9e-12;

Matches 165; Conservative 111; Mismatches 236; Indels 237; Gaps 29;

42 QNLKIPHDIPYSTKNDLSFNPDLKIRSFSTNF-SQOMDLRSCEIETEDKAMGL 100
 148 RHLOLRH-----LDGYNHITHIQHDSFRGLEDISQTLILKENCISQMSHSFSL 199
 QY 101 NQSLTVLTGNPKSPSGF-SGLTNLENVAVETKMTSLGPHIGQLISLKLNVAN 159
 Db 200 LILETDLISGNLFEIDPVFVDMPRRLRLTLTNILSEIPYDALGPKSLRTLDISHN 259
 QY 160 LIHSKLEPYF---SNLTNLEHVDLSYNYIQTISVKQLFLRENPQVNLSDLSINPD 215
 Db 260 VYMSLSGNETYKIKASTKLNLDNLLEYNHIEVLPPNSEKYP---DYVNRTP-FDGNPIH 315
 QY 216 STIOAQFOGIRLHELTLR-----SNFNSSNVLKMCLOMGTGLAHYRL----- 257
 Db 316 TLREDAFAPARIRELYMYCGLTNISPAVFDLSVNSLOLDLSGNNLTGLH-HKLPNNPD 374
 QY 258 IL-----GEFKERNLESFDRSYMEGLCNVSIDEFRLTYINHPSDDIYNLCANISA 310
 Db 375 VLKVISMDNKKIKIQKPTFTFN-AVHYTLKLKDLGDR-----NDPTNLQTLRMNR 425
 QY 311 M-SFGVAKHIAVY---PRHK-----WQSLSTIRC-----HKRPKLSLPF 350
 Db 426 MNMMSLSLSRSGSSVGEDEKDFGVELEDQITRASLSGIQSHAFKVRGLKRLDF-- 483
 QY 351 LKSWTLTTRREDISFGQL-----ALP-----SLRYLDSRRAMSPR 386
 Db 484 --SENGISSEIENDAFHEIGHSLISLMSHGSGSALPAEPLAHLTSLQELDSNNHISM 541
 QY 387 GCCSYSDF-----GT-----NNLKYLDSFNGVILMSAN----- 415
 Db 542 SPTSHPLKNLLELHONRIEQLKGTQGDHSLGLEISLRPHNLTSISQHTFEDLEA 601
 QY 416 -----FGLBELRYLDPQHSSTLKKTVESVPLSEK----- 447
 Db 602 LRKLHLDNKKIDIERRAFNNLDELEYLSLRGNKINNLADES-FQVLPFLTEILDNAFNL 660
 QY 448 -----LY-----LDISYTNK 458
 Db 661 PNFNFDPQVQVTLNLYNVSHNOIRQIMYNSSSGNEHGGMHSNIIKILDSNNNS 720
 QY 459 IDPFDGIFL-GLISLNTLKKMAKNSFKDNTLSNVFTNTNLTFPLDSKQLEISRGVFDTL 517
 Db 721 IHPGFRFAEISLTHLHGYSIM-NTRDVFQGNPHIQWLDLSNWHHEIDPAFKMT 779
 QY 518 YRLQILNNSHNLFLDPESHYKQYSLRTLDCFN-----RIETSKGL 561
 Db 780 KQLQLVFPGHNYLSIDIPQDIFPKVQGLRIVDPSHNLRLGPDNLFYNGMEKLDVSHNM 839
 QY 562 QHPKPS-----LAVFNLTNNSVACI 581
 Db 840 LKIPSSSLSSLAALTLCBLHLSNNPISIT 868

RESULT 7
 T15864
 hypothetical protein C56B.6 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T15864

R/Fulton, L.
 submitted to the EMBL Data Library, November 1995
 A/Description: The sequence of C. elegans cosmid C56B.6.
 A/Reference number: 569019
 A/Accession: T15864
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1066 <FOL>
 A/Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIDN:AAA810
 C/Genetics:
 A/Gene: C56B.6
 A/Intons: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 9

Query Match 7.0%; Score 303; DB 2; Length 1066;

Best Local Similarity 22.8%; Pred. No. 6.6e-11;

Matches 145; Conservative 110; Mismatches 260; Indels 120; Gaps 23;

34 NITTCOMQNLKIPHDIPYSTKNDLSFNPDLKIRSFSTNFSGQLMDLSRCIEITE 93
 Db 131 NITH-LMDTNEVTESEMKVILRN-----NKVRLDKHSFSGFKRIREDISYNOIQVE 184
 QY 94 DKAMHGLNQSLTVLTGNPKSPSGSGLTNLENVAVETKMTSLGPHIGQLISLKL 153
 Db 185 DSSEFTGHMGSUDLSYRIAYLRGM-----LKNPAK-----TLKT 221
 QY 154 LNVANHLHSFKLPEYFNSLTNLEHVDLSYNYIQTISVKQLFLRENPQVNLSDLSINP 213
 Db 222 LKLAENMTHA--TPPALDLNRLTHLNLNGKLNRI--DGDVLKGTCDTLVELFLANNY 276
 QY 214 IDSIOAQFOGIR-LHELTLNSENSSNVLKMCLOMGTGL-----HYRLIL--GE 261
 Db 277 LEHIFPGVLSGKQLEHLDISK-----KIMSLKPPSLSTIYKEETSTYARMLIAGNR 330
 QY 262 FKNERNLESFDRSYMEGLCNVSIDEFRLTYINHPSDDIYNLCANISAMSPGVAKH 321
 Db 331 INNSDYILFEMFLITVYDVSFNRIKISPRVFK-----LKNLSLPLQNNQLAHF 383
 QY 332 ADVPRHFKWQSLSTIRCHLKEPKLS--LPFLKSWTLTTRREDI--SFQQLALPSIR 374
 Db 384 PSLPRLDLKRLHMDNNOIQKIDNFSIADLPQLQHLSLAGNQLDITTEMFGSSSSSELK 443
 QY 375 YLDSRRNMSFRGCCSYSDFGTNNILKYLDSPNGV-IIMSANFMLEBELRYLDPQHSSTL 433
 Db 444 SLNLAHNRKHSISRSFSDL--DNLQQLRLSHNNIRITTSFMSLRMLRIYLDLSHNRIT 501
 QY 434 KYTERSVF-LSEKLYLDISYTNKIDPFDGIFLGLISLNTLKKMAKNSFK----- 482
 Db 502 KILPSALYQLPALDVLHLDHNNLN-EIDRDA-FRSFSDLOSLKSHNAFRSPCEPLGSI 559
 QY 483 -----DNTLS--NVFTVNTNLTFPLDSKQLEISRGVFDTLYRLQILNNSHNL 531
 Db 560 SQVHQLDSSNQINIDIFCIARGIRKSLASNSVEKIKNRKLLQDATLTSIDISHNGII 619
 QY 532 FLDPESHYKQYSLRTLDCSFRIETSKGILQHPKSLAVFNLTNNNSVACICEYONFLOV 591
 Db 620 DVSDAPCECRKLSHIKSHYIR-----NLMKGTAVCI--PWI 656
 QY 592 KDQKMFV---NVQOMKASPIDMKASVLDFTN 622
 Db 657 SHLTTFCEFTYKHELRITTSFYIIVDSQSLTSFGN 691

RESULT 8
 JG6128
 Insulin-like growth factor binding complex acid labile chain - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
 C/Accession: JG6128
 R/Botclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T.
 Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996
 A/Title: Organization and chromosomal localization of the gene encoding the mouse acid I
 A/Reference number: JG6128; MUID:96413591; PMID:8816745
 A/Accession: JG6128

A:Molecule type: DNA
A:Residues: 1-603 <BOI>
A:Cross-references: UNIPROT:P70389; GB:U66900; NID:91621612; PID:AA17270.1; PID:916216
C:Comment: This protein is a serum protein and it is of the ternary complex in the phys
C:Genetics:
A:Gene: als
A:Map position: 17

Query Match 7.0%; Score 301.5; DB 2; Length 603;
Best Local Similarity 24.9%; Pred. No. 3.8e-11;
Matches 160; Conservative 87; Mismatches 240; Indels 155; Gaps 25;

```
QY 39 CMDQNLSTKIPHDIPYSTKNDLSFNPPLKILRSYSTNSQQLMDLSDCELETIEDKMH 98
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 60 CSSRLTLPDGIPTSTALMDGNLSSIPSAFQNLSDPFLMLQSQWLRSLPQALL 119
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 99 GLNQLSTVLTLGNPKFSFGSLTNLEMLVAETMTSLSEGFHIGQLISLKKLVANH 158
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 GLQNLVHILERNLRLSLAAGLFRTPPSLASISLGNLIGRLBGLPFGLSHMDNLGW 179
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 159 NLHSFKLPE-YFSNLTNLEHVDLSYN--YIQTISVKDLOFLRENPQVNLSDLSNPI 214
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 180 NSL--VVLPTVFGQLGNLHELVLAGNKLTYLQPLALGGLGELRE-----LDLSRNAL 230
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 215 DSIQAQAQGI-RLHELTLRSNFSNVKMCLOMTGVAHRLILGEFKNERLLESDR 273
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 231 RSVKANVPIHLPRLOKLYL-----RNLTVAVAPRAVLG----- 264
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 274 SVMELGNVSIDEFRLTYINHFSDDIYNLNCIANISAMSF--TGVHKKIAD-----V 324
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 265 --MKAL-----RMLDLSH-----NRVAGLLEDTFGLGLGHLVRLAHNAITSLR 306
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 325 PRHFKQSLSIIRCHLKPPLKSLPEFLKSWTLTTNREDISFGQL-----ALPSRLYDL 378
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 307 PRTEK-----DLHFLBELQGHNR-----IRQGEKTFEGGLGQLEVLTL 345
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 379 SRNMSFRGCCSYSPFGTNMLKYLDLSPNGVILMSAN-FMGLBELLEYDPOHSTLKATTE 437
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 346 NDNQHEVKAGF--FGLFNVAVMNLGNCRLSEHEHFGGIGRLSHLHESCLGIRTL 403
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 438 FSVFLSEKLKLYLDSYNTKIDFGIFLAGLISLNTLKMAGNSPKDNTLSNV---FTNT 493
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 404 HT-----FAGLSGLRLTL-----RDNISISIEEGSLAGL 433
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 494 TNLFLDLISKQLEQISRGVFDTRYLQLLMSHNNLLFLDP SHYKQYLSRLTDCSFNR 553
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 434 SELLELDITANQLFTLPRQLFGQLGQLEYLLSNQLTMSBDVGLQRAFMWLDLSNR 493
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 554 IET-SKGLQHPKSLAVFNLTNNSVACICRYQNFQWQKQKFLVNEQMKASPIDM 612
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 494 LETPAEGLFSSLGR-LRYLNLRRNSL-----QTFVPPQGLERLWL-DANPMDSCPLKA 545
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 613 KASIVLD-----FTNSTC-----YIKTIISVSVEV 639
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 546 LRDPALQNPVPRFVQIVCEGDDCQPYTYNNITCAGPANY 587
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

RESULT 9
JC5239
Insulin-like growth factor acid-labile chain - baboon

C:Species: Papio sp. (baboon)
C>Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: JC5239
R:Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like
A:Reference number: JC5239; MUID:97040714; PMID:8886027
A:Contents: liver
A:Accession: JC5239
A:Molecule type: mRNA
A:Residues: 1-605
C:Comment: This factor is structurally related to proinsulin and have insulin-like meta

Query Match 6.9%; Score 300.5; DB 2; Length 605;
Best Local Similarity 23.9%; Pred. No. 4.4e-11;
Matches 155; Conservative 81; Mismatches 238; Indels 175; Gaps 20;

```
QY 39 CMDQNLSTKIPHDIPYSTKNDLSFNPPLKILRSYSTNSQQLMDLSDCELETIEDKMH 98
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 60 CSSRLTLPDGIPTSTALMDGNLSSIPSAFQNLSDPFLMLQSQWLRSLPQALL 119
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 99 GLNQLSTVLTLGNPKFSFGSLTNLEMLVAETMTSLSEGFHIGQLISLKKLVANH 158
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 GLENLCHILERNLRLSLAAGTFAVTPALALGSSNRRLSEBGLPFGGLNMDNLGW 179
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 159 NLHSFKLPE-YFSNLTNLEHVDLSYN--YIQTISVKDLOFLRENPQVNLSDLSNPI 214
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 180 NSL--AVLPDAFRLGGLRELVLAGRLAYLQPLFSGLAELRE-----LDLSRNAL 230
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 215 DSIQAQAQGI-RLHELTLRSNFSNVKMCLOMTGVAHRLILGEFKNERLLESDR 273
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 231 RAITANVFAQLPRLOKLYL-----IAAVAAGAPLGL-----DRNL----- 253
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 274 SVMELGNVSIDEFRLTYINHFSDDIYNLNCIANISAMSFYGVHKKIADVPFRHFKQSL 333
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 254 -----IAAVAAGAPLGL-----KALRWLDL 273
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 334 SIIRCHLKPPLKSLPEFLKSWTLTTNR-----EDISFGQLALPSRLYDLSRNMSFRGC 388
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 274 S-----HNRVAGLLEDTFPGLL--GLRYLRISHNAIASLRP 307
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 389 CSYSPFGTNMLKYLDLSPNGVILMSANFPMGLBELLEYDPOHSTLKATTESVLSLEKL 447
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 308 RTFEDL--HFLBELQGHNRRLQRLAERSFEGGLGQLEVLTDHNLQEV-KVGAELGLTNV 364
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 448 LYLDISYNTKIDFGIFLAGLISLNTLKMAGNS-----FRDNTLSN 488
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 365 AVNMLSGNCLRNLPDQVFRGGLKSHLHESCLGIRTPHIFAGLSGLRRLFLKDNGLVG 424
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 489 V-----FTNTTNLTFLDLISKQLEQISRGVFDTRYLQLLMSHNNLLFLDP SHYKQYLSL 544
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 425 IEEQSLWGLAELELDITSNQTLTLPQLFGQLGQLEYLLSHRLAELEPADALGPLQRA 484
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 545 RTLCSFNRIETSGILQHPKSLAVFNLTNNSVACICRYQNFQ--WVQDQKQKFLVNE 602
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 485 FMDVSHNRLEALPGLSLASLGRLYLNLRRNSLRTFTPOPGLERLMLBS-----N 536
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 603 QMKASPID-----MKASIVLDFTNSTC-----YIKTIISVS 635
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 537 PMDCSCLKALRDPALQNPASVPRFQAICEGDDCQPYTYNNITCAS 585
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

RESULT 10
JC1282

Insulin-like growth factor-binding protein acid labile chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: JC1282

R:Del, J.; Baxter, R.C.

Biochem. Biophys. Res. Commun. 188, 304-309, 1992

A:Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac

A:Reference number: JC1282; MUID:93038676; PMID:1384485

A:Accession: JC1282

A:Molecule type: mRNA

A:Residues: 1-603 <DAI>

A:Cross-references: UNIPROT:P35859; GB:S46785; NID:G258002; PID:AA23770.2; PID:G570593

A:Experimental source: liver

A>Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205

F:1-27/Domain: signal sequence #status predicted <SIG>

F:28-603/Product: insulin-like growth factor binding protein, acid labile chain #status i

F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 6.7%; Score 290.5; DB 2; Length 603;
Best Local Similarity 22.4%; Pred. No. 1.8e-10;
Matches 152; Conservative 99; Mismatches 204; Indels 223; Gaps 26;

[illegible]

RESULT 11
T10504
disease resistance protein Cf-2.1 - currant tomato
C|Species: Lycopersicon pimpinellifolium (currant tomato)
C|Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C|Accession: T10504; T10515
R|Dixon, M.S.; Jones, D.A.; Keddie, J.S.; Thomas, C.M.; Harrison, K.; Jones, J.D.
Cell 84, 451-459, 1996
A|Title: The tomato Cf-2 disease resistance locus comprises two functional genes encoding
A|Reference number: Z17062; MUID:96190812; PMID:8608599
A|Accession: T10504
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-1112 <DIX>
A|Cross-references: UNIPROT:Q41397; EMBL:U42444; NID:g1184074; PIDN:AAC15779.1; PID:g1184077
A|Experimental source: cultivar Cf 2
A|Accession: T10515
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-1066, 'I', 1068-1085, 'E', 1087-1110, 'R', 1112 <DIX>
A|Cross-references: EMBL:U42445; NID:g1184076; PIDN:AAC15780.1; PID:g1184077
A|Experimental source: cultivar Cf 2

Query Match 6.6%; Score 287.5; DB 2; Length 1112;

[illegible]

RESULT 12
 T13174
 gp150 protein - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
 C:Accession: T13174
 R:Tian, S.S.; Zinn, K.
 J: Biol. Chem. 269, 28478-28486, 1994
 A>Title: An adhesion molecule-like protein that interacts with and is a substrate for
 A:Reference number: Z17630, M0ID:95050638, PMID:7961789
 A:Accession: T13174
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-1051 <T1>
 A:Cross-references: UNIPROT:Q24007; EMBL:U15220; NID:9595869; PID:9595860; PIDN:AAA617
 A:Experimental source: strain Oregon R
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0013272
 A:Map position: 2

Query Match 6.6%; Score 285.5; DB 2; Length 1051;

Best Local Similarity 24.0%; Pred. No. 7.9e-10;
Matches 155; Conservative 114; Mismatches 211; Indels 167; Gaps 34;

QY 82 LDRSCEIETIEDAMGMLNOLSTLVITGMPISFGSGSGLTNLENAVETKMTSLE 141
D 297 IKRANCTLEVLAAAFGLNELVAVNLTDGALINDPTFVGKKKRLMLTISGNDLSVMS 356
QY 142 GFH-IGQLTSLKLVANHLHSPKPEYPSNLTNLEHVDLSNVTISVKQLQFLREN 200
D 357 SIHYLKSSSIEELDPSRRNLMELN-PKAFSHLSNVVYINLSQNSKKCPPEKAFE----- 410
QY 201 PQVNL-SLDSLNPIDSIQAQAFQGRIRHELTLSN-----FNSSNVLKVCLOMTG 251
D 411 -KVTLLEEDLSYNSLTLEPRDIFNGTTLSLHLKNTNRGDLHFGTKLQOULDSFNSI 469
QY 252 LHVHRLIGEFKNERLLESFDRSVMGLQVST-----DEFRLTYINHFSDDIYN 301
D 470 VQVH-----SWFDK-MPGLTNLMKNGIKKIQPDSP-LTLKRLRHIDL-S 513
QY 302 INCLANISAMFTGVHKKIADVPKFKQSLIIRCHLKPPKLS-LP---FLKSWTLT 357
D 514 INDLQISGMF-----FKNSLIDVIR-LNDNPRLSOLPTDGF-L-SYS-- 554
QY 358 TNREDISFGQALPELRVLDLSRNAMSPFGCCSYSDPFGT-NNLKXVLDLSPNGVILMSANF 416
D 555 -----GEF---TVYYLIDISNCAI---GPIGHKAFSTMRHLTKLAMNI-----NH 595
QY 417 MGLEELEYLDPOHSTLKKVTEFSVLSLEKLIYLDISTY-NTKIDPDGIFLGLISANTLK 475
D 596 LPRE-----IFTGHLKLIIDLISNNLITRMD-DLIFPDNDELTKLS 635
QY 476 MAGNSFKDNTLS-NVFTNTNLTFLDLSKQLEQISKRVPTLYRLQLANSHNNLLFLD 534
D 636 LAGNPI--SRLSVRLFLRLHQLRCLDVNDCETTL-----LSDRDL----- 674
QY 535 PSNKKOYLSFTLDCSFNRI-ETSKGILQHPKSLAVENLTNNSVACICEQNLQWVKD 593
D 675 GAGYKIDPSLRSPNAGNLIKKISSBDVKSF-KYLRSLDITNNPLKCTPPQEFISY--- 730
QY 594 QKMFVNVQMKKASPIDMKASLYLDFTNSTCYITKTIISVSVSVLVAVTVAFLIHYFY 653
D 731 -----VTLQOMTPPKRLPVLANLEDAT-----IYQLETLAQAGSSSL 768
QY 654 FHLILAGCKKYSRGESIVDAFYISSQNEQWVRLNKLKESVPR 700
D 769 AHEV-----CKHAEGSLD-----EKKADSAKALKERLKESSVKK 804

Db 769 AHEV-----CKHAEGSLD-----EKKADSAKALKERLKESSVKK 804

RESULT 13
A41915
Insulin-like growth factor-binding complex acid-labile chain precursor - human
N/Alternate names: Acid-labile Subunit (ALS)
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A41915
R/Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A/Title: Structure and functional expression of the acid-labile subunit of the insulin-1
A/Reference number: A41915; MUID:92357025; PMID:1379671
A/Accession: A41915
A/Status: Preliminary
A/Molecule type: mRNA; protein
A/Residues: 1-605 <LEO>
A/Cross-references: UNIPROT:P35658; GB:M86826; NID:9184807; PIDN:AAA36047.1; PID:9184808
A/Experimental source: liver
A/Note: sequence extracted from NCBI backbone (NCBI:P110171)
F/75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F/99-123/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F/123-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F/147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F/171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F/195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F/219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>

F/243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F/267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F/291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F/315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F/339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F/363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F/387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F/411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F/435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F/459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F/483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F/507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

Query Match
Best Local Similarity 6.5%; Score 281.5; DB 2; Length 605;
Matches 154; Conservative 83; Mismatches 242; Indels 175; Gaps 20;

QY 39 CMDQNLSTKIPDIPYPTKNDLSFNPPLKILASYSSTNFSQLOWDLRSCEIETEDKAMH 98
D 60 CSSRNLTLDPGVREGTQALWLDGNNLSVPPAFAQNSISIGFINTLQGGQLSLEPQLL 119
QY 99 GLNDLSTLVLTGNPIKSPSPSGFGLTNYLVAVETKMTSEGFHIGQLISLKKLVANH 158
D 120 GLENLCHLHERNQLRSLAGTFAHTPALASGLSNRSLKLEDEGLFGLSLMDLNGW 179
QY 159 NLHSFKLPE-YFSNLTNLEHVDISYN---YIQTISVKDQFLRENQVNLDSLNP 214
D 180 NSL-AVLPAAFGSLSLRELVLAGNRLAVLQALPSSLAELE-----LDSLNAL 230
QY 215 DSIQAQAF-QGIRHELTLSNFRSSNVVLKVCLOMTGLAHVHRLIGEFKNERLLESFDR 273
D 231 RAIKANVFDVLPRLQKYL-----DRL----- 253
QY 274 SVMEGLCNVSIDEFRLTYINHFSDDIYNINCLANISAMFTGVHKKIADVPKFKQSL 333
D 254 -----IAVAPGAFGL-----FALRWLDL 273
QY 334 SIIRCHLKPPKLSLPLKSWTLTNR-----EDISFGQALPELRVLDLSRNAMSPFGC 388
D 274 S-----HNRVAGLLEDTPGGL---GLAVNLSHNAIASLPR 307
QY 389 CSYSPFGTNLKYLDLSPNGV-ILMSANFMLEELEYLDPOHSTLKKVTEFSVLSLEK 447
D 308 RIFKDL--HFLBELQGHNRIRQLAERSFEGQLEVLTLDHNOQEV-KAGAFGLTLNV 364
QY 448 LYLDISYNTKIDPDGIFLGLISLNTLKAGNS-----FKONTLSN 488
D 365 AVMNLSGNCLRNLPRQVPRGGLKHSIHESGCLGRIRPHTTGSLGRRLFLKONGLVG 424
QY 489 V-----FTYTNLTFLDLSKQLEQISKRVFTLYRLQLANSHNNLLFLDPSHYQLYSL 544
D 425 IEEQSLMGAELELDLTSNQLTLPHRLPQGLIGLTVLLSRNLALPADALPDLORA 484
QY 545 RTLDCSPRIETSKGILQHPKSLAVENLTNNSVACICEYQNFLO--WKQKMFVAVVE 602
D 465 FWLDVSHRLEALPNSGLAPLGRIRYSLRNNSRTPTPPQPEGLRWLEG-----N 536
QY 603 QMKKASPID-----MKASLYLDFTNSTC-----YIKTIISSVSVYL 640
D 537 PWDGCGPLKALRDPAQLQNPASVPRFVQALICGDGDCQPPATYNNITCASPEVV 590

Db 537 PWDGCGPLKALRDPAQLQNPASVPRFVQALICGDGDCQPPATYNNITCASPEVV 590

RESULT 14
B3665
alt protein 2 precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C/Accession: B3665
R/Rochberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A/Title: alt: an extracellular protein necessary for development of midline glia and con
A/Reference number: A3665; MUID:91099665; PMID:2176636
A/Accession: B3665

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1469 <ROT>
A:Cross-references: GB:X53959
C:Genetics:
A:Gene: FlyBase:sl1
A:Cross-references: FlyBase:FBgn0003425
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
F:166-91/Domain: proteoglycan amino-terminal homology <PAH1>
F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F:288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F:323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F:450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F:512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F:547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F:572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F:596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F:620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F:651-695/Domain: proteoglycan amino-terminal homology <PAH4>
F:708-733/Domain: proteoglycan amino-terminal homology <PAH5>
F:743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F:767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F:846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F:1028-1061/Domain: EGF homology <EGF1>
F:1068-1099/Domain: EGF homology <EGF2>
F:1115-1148/Domain: EGF homology <EGF1>
Query Match 6.4%; Score 279; DB 2; Length 1469;
Best Local Similarity 21.6%; Pred. No. 3.1e-09;
Matches 151; Conservative 85; Mismatches 238; Indels 224; Gaps 21;
QY 39 CMDONLSKIPHDIPSTKNLDSFNPPLKLRYSFTNSQLOMDLSCEETIEDKAMH 98
DB 308 CREKSLTSPVTLTDDTIDVRLKONFTELPRKSSRRRLARIDLSNNNISRIADALS 367
QY 99 GLNOLSTVLTLGNPIKSPSGSGGLTNLENVAVETKMTSLGEGHIGOLISLKLNVAN 158
DB 368 GLKQTLTLVYKNGKIKDLPBGVFKGSGRLLLNANNEISCIKDAFRDLHSLSLSTLD 427
QY 159 NLIHSFKLPEYFSNLTNLEHVDLSVNYITISVKLOLFRBNQVNLSDLSLNPIDSIO 218
DB 428 NNIQSL-ANGTFDAMSKMTVLAKN--PFCDCNLRWLADY-----LHKNPLETSG 476
QY 219 AQAFOGIRLHELTLS-----NPNSSVNLKMKCQNMGTGLVHRLILGEFKNERNLSEFDS 274
DB 477 ARCEPKRMHRRRIISLRKEKFCSS-----WEL-----RW 507
QY 275 WVEGLGNVSIDEFRLTYINHFSDIYVNLCLANISAMFTGVHKKH-ADVPNHFQKSL 333
DB 508 KLSGECRMDSD-----CPAMCHCGTVDTCGRRLKEIPRIDPH----- 547
QY 334 SIIRCHLKPPKLSLPLKSWTLTTRNEDIS-----PQALLPSRYLDSLNNMSFR 386
DB 548 -----TTELLDNEENGRISISDGLFGR--LPHVLKELKKNQLT-- 584
QY 387 GCCSYSDPGTNLKYLDLSFNGVILMSAN-FMGLELELYLDFQHSITLKVTERSVLSLE 445
DB 585 -----GI-----EPNAFEGSHIQELQGNKIKKEISN-KMFLGLH 619
QY 446 KLYLDISYNTKIDFDGIFLGLISLNTLKAGNSF----- 481
DB 620 QLKTLNLYDNQISCMWPSFEHINSLTSLNLSNPFCNCHLAWFAECVRKKSINGAAR 679
QY 482 -----KD-----NTLSNV--- 489

DB 680 CGAPSKVDVOIKDLPSEFKCSSNSGCLGDGCPSPSCITCTGVACSRNQLKEIRPG 739
QY 490 -----FTWTTNLTFLDLSKCOLQEIISRGVEPTLRYLQLLNMSH 527
DB 740 IPATSELYBESNEIEQHYERIRHLRSLTRDLDSNNQITLISNTYFANLTSLTSLISY 799
QY 528 NNILFLDPBSHYKQVLSLRTLDSPNRIR-TSGKILQHPKSLAVNLTNNNVACICEYON 586
DB 800 NKLQCIQRALSLGNNLNRVSLHNGRISMLPEGSFEDL-KSLTTHIALGSNPLVCDGGLK 858
QY 587 FLQWYKDCMFLVYNVQWKCASPIDMKSLVDFNTNST 624
DB 859 FSDWI---KLDVYEPGIRACAPBQWMDLITSTESS 893
RESULT 15
A3665
slit protein 1 precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 30-Apr-1991 #sequence, revision 30-Apr-1991 #ext_change 02-Aug-2002
C:Accession: A3665; A31640; S13523
R:Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A:Title: slit: an extracellular protein necessary for development of midline glia and
A:Reference number: A3665; WUID:3109965; PMID:2176636
A:Accession: A3665
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1460 <ROT>
A:Cross-references: GB:X53959; NID:g8614; PID:CAA7910.1; PID:g8615
R:Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Cell 55, 1047-1059, 1988
A:Title: slit: An EGF-homologous locus of D. melanogaster involved in the development
A:Reference number: A31640; MUID:89077533; PMID:3144436
A:Accession: A31640
A:Molecule type: DNA
A:Residues: 881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YHA', 'RO2'
A:Cross-references: GB:M23543; NID:g340939; PID:g514357
C:Genetics:
A:Gene: FlyBase:sl1
A:Cross-references: FlyBase:FBgn0003425
A:Introns: 1351/3
C:Superfamily: fruit fly slit protein; growth factor
C:Keywords: alternative splicing; growth factor
F:101-124/Domain: proteoglycan amino-terminal homology <PAH1>
F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F:288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F:323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F:512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F:547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F:572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F:596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F:620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F:651-695/Domain: proteoglycan amino-terminal homology <PAH4>
F:708-733/Domain: proteoglycan amino-terminal homology <PAH5>
F:743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F:767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F:791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F:815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
F:846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F:1028-1061/Domain: EGF homology <EGF1>
F:1068-1099/Domain: EGF homology <EGF2>

F,115-1148/Domain: EGF homology <EGF1>
Query Match

Best Local Similarity 6.4%; Score 279; DB 2; Length 1480;
Matches 151; Conservative 85; Mismatches 238; Indels 224; Gaps 21;

```

QY 39 CMDQNLKSIPIHDIDYSTKMDLSPNPLKILRSYSFTNSQQLMDLSRCIEITIEDKAMH 98
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 308 CREKSLTSVPVLPDDTDVRLBQNFITELPKPSFSSFRRLRIDLSNNNISRIADALS 98
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 99 GLNQLSTLVLTGNPIKSPSGSGLTNLENLVAETKMTSLGEGHIGQLISLKVAVAH 158
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 368 GLKQLTTLVLYGKNIKDLPSGVFKGLSLRLLLNANEISCIRKDAFRDLHSLSLSYD 427
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 159 NLIHSFKLPEYFESNLTNLEHVDLSYNYIQIISVKDIQFLRENQVNLSDLSINPDSIQ 218
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 428 NNIOSL-ANGTFDAMKSMKTVHLAKN-PFICDCLRWLADY-----LKNPLETISG 476
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 219 AQAFOGIRLHELTLS---NPNSSNVLMKCLQNMGTGLVHRLILGEFKNERNLESFDRS 274
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 477 ARCESPKKWHRRRIISLREKFKS-----WGEL-----RM 507
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 275 VMEGLCNVSIDEFRLTYINHSDDIYNINCLANISAMSGFTGVHKKI-ADVPRHKWOSL 333
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 508 KLSGECRMDS-----CPAMCHCEGTVDCTGRKKEIIPDIPLH----- 547
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 334 SIIRCHLKPPPKSLPFLKSWTLTNREDIS-----FQGLAPSLRYLDLSNAMSFR 386
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 548 -----TELLENDNEIGRISSDGLFGR-LPHLVKLELKNQULT-- 584
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 387 GCCSYSDFGTNMLKYLDLSPNGVILMSAN-FMGLLELEYLDFOHSTLKKVTEFSVFLSLR 445
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 585 -----GI---EPNAFEGASHIQLQIGENKIKEISN-KMFLGLH 619
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 446 KLLYLDISYNTKIDPDGIFLGILSLNTKMGANSF----- 481
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 620 QLKTLNLYDNQISCVPGSFHEHLSLTSINLASNPENCNCHLAMPACVCRKKSILNGAAR 679
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 482 -----KD----- 482
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 680 CGAPSKVRDVOIKDLPHSEFKCSSENSGCLGDGYCPSPCTCTGTVAACSRNQLKEIPRG 739
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 490 -----FTNTNLTFLDLKQLEQISRGVETLYRLQLNMNH 527
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 740 IPATSELYESNEIEQIHYERIRHRLSLTDLSSNQITLTSNYTFANLTKLSTLISY 799
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 528 NNLEFLDPSSHVKQYSLRTLDSPNRIE-TSKGILQHFPKSLAVFNLTNNSVACICEYQN 586
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 800 NKLQCLQRHLSGLNNLRVSLHGNRISMLPEGSEFDL-KSLTHIALGSPNPLYCDGGLKW 858
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 587 FLQWYKDOQRMLVNVQMKCASPIDMKASLYLDFTNST 624
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 859 FSDWI---KLDYVEPGIARCAEPQMKDKLILSTPSS 893
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Search completed: March 12, 2005, 19:57:06
Job time : 27.5445 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:15:31 ; Search time 87.4 Seconds

(without alignments)
3712.721 Million cell updates/sec

Title: US-09-396-985B-98

Perfect score: 4355
Sequence: 1 MMSASRLAGTILPAMAFISC.....SNDEGTGVCNNQEAITSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1980s:*\n3: geneseqp2000s:*\n4: geneseqp2000s:*\n5: geneseqp2000s:*\n6: geneseqp2000s:*\n7: geneseqp2000s:*\n8: geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4355	100.0	839	ABU04773	Abu04773 Human exp
2	4355	100.0	839	ABU04774	Abu04774 Human exp
3	4355	100.0	839	ABU04775	Abu04775 Human exp
4	4355	100.0	839	AD078785	Adc78785 Human PRO
5	4355	100.0	839	AD048826	Adc48826 Human PRO
6	4335.5	99.6	837	AAW86361	AAw86361 Human DNA
7	4335.5	99.6	837	AAE16102	AAe16102 Human DNA
8	4335.5	99.6	837	ABU04776	Abu04776 Human exp
9	4328.5	99.4	837	AAE16116	AAe16116 Human DNA
10	4178	95.9	808	AD057782	Ado57782 Chimpanzee
11	4167	95.7	808	AD057785	Ado57785 Gorilla t
12	4164	95.6	808	AD057803	Ado57803 Chimpanzee
13	4141	95.1	799	AAW86352	AAw86352 Human DNA
14	4141	95.1	799	AAE16093	AAe16093 Human DNA
15	4141	95.1	799	ABE83162	ABe83162 Human Tol
16	4141	95.1	799	ABR42963	ABr42963 Human Tol
17	4141	95.1	799	ADB39121	ADb39121 Human Tol
18	4141	95.1	799	ADP56656	ADp56656 Human Tol
19	4141	95.1	799	ADP48597	ADp48597 Human Tol
20	4040	92.8	801	AD057788	Ado57788 Gibbon to
21	3918	89.4	795	AD057791	Ado57791 Rhesus mo
22	3892	89.4	795	AD057800	Ado57800 Hamadryas
23	3819	87.7	801	AD057797	Ado57797 Squirrel
24	3683.5	84.6	738	ADP29455	ADp29455 Human sec
25	3501	80.4	745	AD057794	Ado57794 White-fac

26	1090	25.0	208	3	AAy88059	AAy88059 Human Tol
27	919	21.1	178	8	ADN12270	ADn12270 IL-IR/TLR
28	785	18.0	179	7	ADC42707	ADc42707 Murine To
29	629.5	14.5	661	2	AAW28510	AAw28510 Product o
30	629.5	14.5	661	2	AAW87556	AAw87556 B cell su
31	629.5	14.5	661	7	ADC36552	Adc36552 Human sec
32	629.5	14.5	661	7	ADP68098	ADp68098 Human MP5
33	628.5	14.4	650	3	AAy82527	AAy82527 Human RPI
34	615.5	14.1	661	2	AAW47274	AAw47274 Human B-C
35	603.5	13.9	784	2	AAW86350	AAw86350 Human DNA
36	603.5	13.9	784	5	AAE16091	AAe16091 Human DNA
37	603.5	13.9	784	5	ABE83161	ABe83161 Human Tol
38	603.5	13.9	784	8	ADN02005	ADn02005 Human inf
39	602.5	13.8	784	2	AAy05869	AAy05869 Human Tol
40	602.5	13.8	784	6	ABU61956	ABu61956 Human Tol
41	602.5	13.8	784	7	ADL15005	ADl15005 Human Tol
42	602.5	13.8	784	8	ADP56652	ADp56652 Human Tol
43	602.5	13.8	784	8	ADP48593	ADp48593 Human Tol
44	602.5	13.8	784	8	ADP23787	ADp23787 PRO polyP
45	602.5	13.8	784	8	ADQ39727	ADq39727 Human myo

ALIGNMENTS

RESULT 1
ABU04773 ID ABU04773 standard; protein; 839 AA.

XX AC ABU04773;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1439.

mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at http://wipo.int/publ/published_pct_sequences

SQ Sequence 839 AA;

Query Match	100.0%	Score 4355;	DB 6;	Length 839;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 839; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	NMSASLACTLLPAMAF.LSCVRESNEPCVEVNTITTCOMELNFXKI	PNNLPSTKNLD	60
Db	1	NMSASLACTLLPAMAF.LSCVRESNEPCVEVNTITTCOMELNFXKI	PNNLPSTKNLD	60
QY	61	LSFNPLRHHGSYSFFSFPELOVDLSRCEIQTIEDGAYOSLSHLSTL	ILTGNPISIALG	120
Db	61	LSFNPLRHHGSYSFFSFPELOVDLSRCEIQTIEDGAYOSLSHLSTL	ILTGNPISIALG	120
QY	121	AFSGJSSLOKVAVEFNVLASLENPPIGHLKTILKELVANAHL	IOSFKLPEYFSNLTNLEHL	180
Db	121	AFSGJSSLOKVAVEFNVLASLENPPIGHLKTILKELVANAHL	IOSFKLPEYFSNLTNLEHL	180
QY	181	DLSSNKIOSITCYCTDLRVLHOMPLNLISLDLSLPMPNF	IOGAFKEIILHKLTLRNPDSL	240
Db	181	DLSSNKIOSITCYCTDLRVLHOMPLNLISLDLSLPMPNF	IOGAFKEIILHKLTLRNPDSL	240
QY	241	NVMKTCIOGLAGLEVHRLVLEGEPRNEGNLEKFDKSALEGL	CNLTIEBFRLAYLDYLDI	300
Db	241	NVMKTCIOGLAGLEVHRLVLEGEPRNEGNLEKFDKSALEGL	CNLTIEBFRLAYLDYLDI	300
QY	301	IDLFNCLTVNVSFSVLVYTERKXDPNSYNGWGHLELVNCK	FGQFPPLTKLSKLRLPFS	360
Db	301	IDLFNCLTVNVSFSVLVYTERKXDPNSYNGWGHLELVNCK	FGQFPPLTKLSKLRLPFS	360
QY	361	NKGNAFSEVDLP.SLEFLDSRNGLSFKGCGCSOSDFGTTSL	LYKYDLSFNGVITMSSNPLG	420
Db	361	NKGNAFSEVDLP.SLEFLDSRNGLSFKGCGCSOSDFGTTSL	LYKYDLSFNGVITMSSNPLG	420
QY	421	LEQLLEHLDPQHSNLKOMSEFSVFLSLRNLILYLDISHHT	TRVAFNGIFNGLSLEVLKMG	480
Db	421	LEQLLEHLDPQHSNLKOMSEFSVFLSLRNLILYLDISHHT	TRVAFNGIFNGLSLEVLKMG	480
QY	481	NSFOENFLPDI.FTELRNLTF.LDLSQCLBOLSPAFNSLS	LOVLNMSHNNFSLDTPPY	540
Db	481	NSFOENFLPDI.FTELRNLTF.LDLSQCLBOLSPAFNSLS	LOVLNMSHNNFSLDTPPY	540
QY	541	KCLNLSLOVDLSLNHIMTSKKOELQHPSSIAFANTLQNP	PACTCEKOS.FLOWIKDOROL	600
Db	541	KCLNLSLOVDLSLNHIMTSKKOELQHPSSIAFANTLQNP	PACTCEKOS.FLOWIKDOROL	600
QY	601	LVEVERMECATPSDKQMPVLSLNTTCOMNKTII	IGVSLVLYVSVAVLVYKXEPHML	660
Db	601	LVEVERMECATPSDKQMPVLSLNTTCOMNKTII	IGVSLVLYVSVAVLVYKXEPHML	660
QY	661	LACGICXGRENITDAFVITYSQDEBVRNHELVNKLEB	GVPPQLCHYRPIFGVATIA	720
Db	661	LACGICXGRENITDAFVITYSQDEBVRNHELVNKLEB	GVPPQLCHYRPIFGVATIA	720
QY	721	NIHHEGFHKRKATVIVVSOHFIOGRKCI	FEXYEAQTQOFLSSRAGIIFIVQKTEKTLR	780
Db	721	NIHHEGFHKRKATVIVVSOHFIOGRKCI	FEXYEAQTQOFLSSRAGIIFIVQKTEKTLR	780
QY	781	QOVELYRLLSRNTVYLEWEDSVLGRHIFWRRLRKAL	LDOKSNBPGVGTGCONMEQATSI	839

Db 781 QQVELYRLSRNTYLEMEDSVLGRI FWRRLKALLDGKSWNPEGTVGTGCNWQEATSI 839

RESULT 2
ABU04774
ID ABU04774 standard; protein; 839 AA

AC ABU04774;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1440.

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

KW receptor; transcription factor; cancer; MHC;

KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 08-AUG-2001; 2001US-0310801P.

PR 04-DEC-2001; 2001US-0336780P.

[illegible]

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cytoskeletal proteins, receptors or transcription factors), useful for gastric cancer, colorectal cancer, pancreatic cancer, lymphoma or

PT Leukemia.

PS Example 2; SEQ ID NO 1440; 134pp; Engl1sh.

CC The invention describes a purified polypeptide, which comprises a

CC transporter, cytoskeletal protein, receptor or transcription factor. The CC transporter is useful as an immunogenic composition for eliciting in a

mammalian immunogenic response directed against any of the purified

CC polypeptide, is useful for treating cancer. The polypeptide is also

CC class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing

CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma, and leukemia. These are also useful for screening agents for

CC creating the above mentioned diseases. This sequence represents an
CC summed protein for (EBM) isolated from human tissue for translati

CC
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profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from the author.

CC ftp.wipo.int/pub/published_pct_sequences
YY

SQ Sequence 839 AA;

Query Match	100.0%	Score 4355;	DB 6;	Length 839;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 839; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY 1 MMSASRLAGTLIPAMAFLSVCRPESWEPCVEVPNITYQCMELNFYKIPDNLPESTKNLD 60

```

Db      1 MMSASRLAGTLIPMAAFISCVRPSEWPCVAVNITTYQCEMLNPKYKIPDNLPESTKXMD 60
Qy      61 LSFNPLRLHLSGSYSFSPPELQVLDLSRCEIQTIEDGAYOSLSHLSLTLITGNPIQSALG 120
Db      61 LSFNPLRLHLSGSYSFSPPELQVLDLSRCEIQTIEDGAYOSLSHLSLTLITGNPIQSALG 120
Qy      121 AFSGLSSLOKLVAVETNLASLENPFIQHLKTLKELVANAHLIOSFKLPEYFSNLTNLEHL 180
Db      121 AFSGLSSLOKLVAVETNLASLENPFIQHLKTLKELVANAHLIOSFKLPEYFSNLTNLEHL 180
Qy      181 DLSNKKIOSIYCTDLRVLHQPMLNLSLDSLNPNMFIQPGAFKIRLHKTLRNPNPSL 240
Db      181 DLSNKKIOSIYCTDLRVLHQPMLNLSLDSLNPNMFIQPGAFKIRLHKTLRNPNPSL 240
Qy      241 NMKTCIOGLAGLEVHRVLVGEFRNEGNLEKFDKSALEGLCNLTIEBRFLAYLDYLDI 300
Db      241 NMKTCIOGLAGLEVHRVLVGEFRNEGNLEKFDKSALEGLCNLTIEBRFLAYLDYLDI 300
Qy      301 IDLFNCLTNVSSFSLSVYTIERVKDFSYNFGMOHLELVNCKRGQPTLKSLKRLPTS 360
Db      301 IDLFNCLTNVSSFSLSVYTIERVKDFSYNFGMOHLELVNCKRGQPTLKSLKRLPTS 360
Qy      361 NKGNAPSEVDLPSEFLDLSRNGLSFKGCCSQSPFGTSLKYLDLSFNGVITWSSNPLG 420
Db      361 NKGNAPSEVDLPSEFLDLSRNGLSFKGCCSQSPFGTSLKYLDLSFNGVITWSSNPLG 420
Qy      421 LEQLEHLDFOHNLKOMESEFVSFLSRNLIYLDISHTRVAFNGIFNGLSLEVLKXAG 480
Db      421 LEQLEHLDFOHNLKOMESEFVSFLSRNLIYLDISHTRVAFNGIFNGLSLEVLKXAG 480
Qy      481 NSFOENFLPDIETELRNLTFLDLSQCOLEQSPFAENSLSSLOVLNMSHNNFSLDTPPY 540
Db      481 NSFOENFLPDIETELRNLTFLDLSQCOLEQSPFAENSLSSLOVLNMSHNNFSLDTPPY 540
Qy      541 KCINSLQVLDYSLNHTMSTKQEOLOHFPSSSLAFNLTONDRPACTEHOSEFLQWIDQOL 600
Db      541 KCINSLQVLDYSLNHTMSTKQEOLOHFPSSSLAFNLTONDRPACTEHOSEFLQWIDQOL 600
Qy      601 LVEVERMECATPSPDKQMPVLSLNTTCOMNKTIIISVLSVYVAVLVYKFEFHLML 660
Db      601 LVEVERMECATPSPDKQMPVLSLNTTCOMNKTIIISVLSVYVAVLVYKFEFHLML 660
Qy      661 LAGCITKXRGENTYDAFVIYSSQDEDEWVKNLEBGEVPPFCCLHYRDPITPGVATA 720
Db      661 LAGCITKXRGENTYDAFVIYSSQDEDEWVKNLEBGEVPPFCCLHYRDPITPGVATA 720
Qy      721 NIIEGFHKSRRKVIYVVSQHPIQSRWCIFEYFIATQWPLSSRAGITITVLOKVEKTLR 780
Db      721 NIIEGFHKSRRKVIYVVSQHPIQSRWCIFEYFIATQWPLSSRAGITITVLOKVEKTLR 780
Qy      781 QOVELYRLSRNTYLEMEDSVLGRHIFMRRLKALLDDKSNMPEGTVGCGCMOATSI 839
Db      781 QOVELYRLSRNTYLEMEDSVLGRHIFMRRLKALLDDKSNMPEGTVGCGCMOATSI 839

```

RESULT 3
ABU04775
ID ABU04775 standard; protein; 839 AA.

AC ABU04775;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1441.

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

```

XX      XX      WO200278524-A2.
XX      XX      10-OCT-2002.
XX      XX      28-MAR-2002; 2002WO-US009671.
XX      XX      28-MAR-2001; 2001US-0279495P.
XX      PR      21-MAY-2001; 2001US-0292544P.
XX      PR      08-AUG-2001; 2001US-0310801P.
XX      PR      01-OCT-2001; 2001US-0326370P.
XX      PR      04-DEC-2001; 2001US-0336780P.
XX      PR      20-FEB-2002; 2002US-0358985P.
XX      PA      (ZYCO-) ZYCOS INC.
XX      PI      Chicx RM, Tomlinson AJ, Urban RG;
XX      DR      WPI; 2003-040607/03.
XX      PT      New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX      PT      cytoskeletal proteins, receptors or transcription factors), useful for
XX      PT      treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX      PT      leukemia.
XX      PS      Example 2; SEQ ID NO 1441; 134pp; English.
XX      XX      The invention describes a purified polypeptide, which comprises a
XX      CC      fragment of a kinase, phosphatase, protease, protease inhibitor,
XX      CC      transporter, cytoskeletal protein, receptor or transcription factor. The
XX      CC      polypeptide is useful as an immunogenic composition for eliciting in a
XX      CC      mammal an immunogenic response directed against any of the purified
XX      CC      polypeptide. The purified polypeptide, or the antibody that binds to this
XX      CC      polypeptide, is useful for treating cancer. The polypeptide is also
XX      CC      useful for identifying compounds that binds to a naturally processed
XX      CC      class I or class II MHC-binding polypeptide. The polypeptides and
XX      CC      polynucleotides are particularly useful for treating or preventing
XX      CC      cancer, myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX      CC      lymphoma or leukemia. These are also useful for screening agents for
XX      CC      treating the above mentioned diseases. This sequence represents an
XX      CC      expressed protein tag (EPT) isolated from human tissue for translational
XX      CC      profiling. Note: This sequence does not appear in the printed
XX      CC      specification but was obtained in electronic format directly from WIPO at
XX      CC      ftp.wipo.int/pub/published_pgc_sequences
XX      SQ      Sequence 839 AA:

```

Query Match 100.0%; Score 4355; DB 6; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MMSASRLAGTLIPMAAFISCVRPSEWPCVAVNITTYQCEMLNPKYKIPDNLPESTKXMD 60
Db      1 MMSASRLAGTLIPMAAFISCVRPSEWPCVAVNITTYQCEMLNPKYKIPDNLPESTKXMD 60
Qy      61 LSFNPLRLHLSGSYSFSPPELQVLDLSRCEIQTIEDGAYOSLSHLSLTLITGNPIQSALG 120
Db      61 LSFNPLRLHLSGSYSFSPPELQVLDLSRCEIQTIEDGAYOSLSHLSLTLITGNPIQSALG 120
Qy      121 AFSGLSSLOKLVAVETNLASLENPFIQHLKTLKELVANAHLIOSFKLPEYFSNLTNLEHL 180
Db      121 AFSGLSSLOKLVAVETNLASLENPFIQHLKTLKELVANAHLIOSFKLPEYFSNLTNLEHL 180
Qy      181 DLSNKKIOSIYCTDLRVLHQPMLNLSLDSLNPNMFIQPGAFKIRLHKTLRNPNPSL 240
Db      181 DLSNKKIOSIYCTDLRVLHQPMLNLSLDSLNPNMFIQPGAFKIRLHKTLRNPNPSL 240
Qy      241 NMKTCIOGLAGLEVHRVLVGEFRNEGNLEKFDKSALEGLCNLTIEBRFLAYLDYLDI 300
Db      241 NMKTCIOGLAGLEVHRVLVGEFRNEGNLEKFDKSALEGLCNLTIEBRFLAYLDYLDI 300
Qy      301 IDLFNCLTNVSSFSLSVYTIERVKDFSYNFGMOHLELVNCKRGQPTLKSLKRLPTS 360

```

Db 301 IDLFNCILTNVSSFLSVVTERVKDFSNFGWQHLELVNCKFGQPTLTKLSKRLTFPTS 360
Qy 361 NKGNAFSEVDLPSELEFLDLSRNGLSFKGCCOSDFTTSLKYLDSLSENGVITWSSNPLG 420
361 NKGNAFSEVDLPSELEFLDLSRNGLSFKGCCOSDFTTSLKYLDSLSENGVITWSSNPLG 420
Qy 421 LEQLEHLDFOHNSLKQSEFSVFLSLNRLYLIDISHTTRVAENGIFNGLSLEVLKMG 480
421 LEQLEHLDFOHNSLKQSEFSVFLSLNRLYLIDISHTTRVAENGIFNGLSLEVLKMG 480
Db 481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLNNSHNNFSLDTPPY 540
481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLNNSHNNFSLDTPPY 540
Qy 541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSLAFLNLTQNDPACTCEHQSFLQWIKDQROL 600
541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSLAFLNLTQNDPACTCEHQSFLQWIKDQROL 600
Db 541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSLAFLNLTQNDPACTCEHQSFLQWIKDQROL 600
Qy 601 LVEVERMECATPSPDKQMPVLSLNTTCQMNKTIIGVSVLSVLVSVVAVLVYKFFPHLM 660
601 LVEVERMECATPSPDKQMPVLSLNTTCQMNKTIIGVSVLSVLVSVVAVLVYKFFPHLM 660
Db 661 LAGCIKTGGRGENTIDAFVIYSSQDEDMVRNLELVNLEEGVPPQLCHYRDFIPGVAIAA 720
661 LAGCIKTGGRGENTIDAFVIYSSQDEDMVRNLELVNLEEGVPPQLCHYRDFIPGVAIAA 720
Qy 721 NIHEGFHRSKRVLVVVSQHFIOGRWCIFEYELAQTWQFLSSRAGIIFIVLQKYEKTLR 780
721 NIHEGFHRSKRVLVVVSQHFIOGRWCIFEYELAQTWQFLSSRAGIIFIVLQKYEKTLR 780
Db 721 NIHEGFHRSKRVLVVVSQHFIOGRWCIFEYELAQTWQFLSSRAGIIFIVLQKYEKTLR 780
Qy 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPEGTGTCNMQEARSI 839
781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPEGTGTCNMQEARSI 839
Db 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPEGTGTCNMQEARSI 839

RESULT 4
ADCT8785
ID ADCT8785 standard; protein; 839 AA.
AC ADCT8785;
XX
XX 01-JAN-2004 (first entry)
DT
XX
DE Human PRO protein #7.
XX
XX human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KM Crohn's disease.
XX
OS Homo sapiens.
XX
XX WO2003034984-A2.
XX
XX 01-MAY-2003.
XX
XX 15-OCT-2002; 2002WO-US033070.
XX
XX 19-OCT-2001; 2001US-0340083P.
XX
XX (GERTH) GENENTECH INC.
XX
XX Goddard A, Gurney AL;
XX
XX WPI; 2003-481990/45.
XX
XX N-PSDB; ADCT8784.
XX
XX
XX New PRO polynucleotide and polypeptide, useful for the manufacture of a
XX PT medicament for diagnosing or treating cancer or inflammatory bowel
XX PT disorder e.g., ulcerative colitis or Crohn's disease.
XX
XX PS Claim 12; SEQ ID NO 14; 327pp; English.
XX
XX
XX The invention comprises the amino acid and coding sequences of human PRO
XX proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
CC sequence represents a human PRO protein of the invention.
XX
SQ Sequence 839 AA:
Query Match 100.0%; Score 4355; DB 7; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMSASRLAGTILPAMAFSCVRPESWPCREVPNITTCQMEINFYKIPDNLPESTGNLD 60
Db 1 MMSASRLAGTILPAMAFSCVRPESWPCREVPNITTCQMEINFYKIPDNLPESTGNLD 60
Qy 61 LSEFNPRLHLSYSFSPFPELQVLDLSKCEIQTIEDGAYQSLSHLSTLITGNPIQSIALG 120
Db 61 LSEFNPRLHLSYSFSPFPELQVLDLSKCEIQTIEDGAYQSLSHLSTLITGNPIQSIALG 120
Qy 121 AFSGLSLQKLVAVETNLASLENFPICHLKTLKELVAVANLQSFKLPETFSNLTNLEHL 180
Db 121 AFSGLSLQKLVAVETNLASLENFPICHLKTLKELVAVANLQSFKLPETFSNLTNLEHL 180
Qy 181 DLSNKTQSIYCTDRLVHQMPILNLSLDSLNPMPFIQGAPEKIRLHLTLRNNPDSL 240
Db 181 DLSNKTQSIYCTDRLVHQMPILNLSLDSLNPMPFIQGAPEKIRLHLTLRNNPDSL 240
Qy 241 NVMKTCIQGLAGLEVHRLVGEFFRNEGNLEKFPKSALEGLCNLTIEFRRLAYLDYLDI 300
Db 241 NVMKTCIQGLAGLEVHRLVGEFFRNEGNLEKFPKSALEGLCNLTIEFRRLAYLDYLDI 300
Qy 301 IDLFNCILTNVSSFLSVVTERVKDFSNFGWQHLELVNCKFGQPTLTKLSKRLTFPTS 360
Db 301 IDLFNCILTNVSSFLSVVTERVKDFSNFGWQHLELVNCKFGQPTLTKLSKRLTFPTS 360
Qy 361 NKGNAFSEVDLPSELEFLDLSRNGLSFKGCCOSDFTTSLKYLDSLSENGVITWSSNPLG 420
Db 361 NKGNAFSEVDLPSELEFLDLSRNGLSFKGCCOSDFTTSLKYLDSLSENGVITWSSNPLG 420
Qy 421 LEQLEHLDFOHNSLKQSEFSVFLSLNRLYLIDISHTTRVAENGIFNGLSLEVLKMG 480
Db 421 LEQLEHLDFOHNSLKQSEFSVFLSLNRLYLIDISHTTRVAENGIFNGLSLEVLKMG 480
Qy 481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLNNSHNNFSLDTPPY 540
Db 481 NSFOENFLPDIFTELRLNLTFLDLSQCOLBOLSPFAFNSLSLOVLNNSHNNFSLDTPPY 540
Qy 541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSLAFLNLTQNDPACTCEHQSFLQWIKDQROL 600
Db 541 KCLNSLOVLDYSLNHNMTSKKQELQHPSSLAFLNLTQNDPACTCEHQSFLQWIKDQROL 600
Qy 601 LVEVERMECATPSPDKQMPVLSLNTTCQMNKTIIGVSVLSVLVSVVAVLVYKFFPHLM 660
Db 601 LVEVERMECATPSPDKQMPVLSLNTTCQMNKTIIGVSVLSVLVSVVAVLVYKFFPHLM 660
Qy 661 LAGCIKTGGRGENTIDAFVIYSSQDEDMVRNLELVNLEEGVPPQLCHYRDFIPGVAIAA 720
Db 661 LAGCIKTGGRGENTIDAFVIYSSQDEDMVRNLELVNLEEGVPPQLCHYRDFIPGVAIAA 720
Qy 721 NIHEGFHRSKRVLVVVSQHFIOGRWCIFEYELAQTWQFLSSRAGIIFIVLQKYEKTLR 780
Db 721 NIHEGFHRSKRVLVVVSQHFIOGRWCIFEYELAQTWQFLSSRAGIIFIVLQKYEKTLR 780
Qy 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPEGTGTCNMQEARSI 839
Db 781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPEGTGTCNMQEARSI 839

RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
AC ADD48826;
XX
XX

DT 02-DEC-2004 (revised)
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein AAF05316, SEQ ID NO 14536.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 OS Homo sapiens.
 OS Unidentified.
 XX
 FN MO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR GENBANK; AAF05316.
 PT
 PT New composition comprising two or more isolated polypeptides, useful for
 PS preparing a medicament for treating pain in an animal.
 XX
 PS Example 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (described in Table 3
 CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 839 AA;
 Query Match 100.0%; Score 4355; DB 7; Length 839;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSASRLAGTLIPAAAFICVRPESWPCVEVVPITQCKELNFKYKIPDNLPSTKLD 60
 DB 1 MMSASRLAGTLIPAAAFICVRPESWPCVEVVPITQCKELNFKYKIPDNLPSTKLD 60

QY 61 LSFNPLRLHLSYSFSPSPPELQVLDLSRCEIQTIDGAYQISLSHTLITNPIQSLALG 120
 DB 61 LSFNPLRLHLSYSFSPSPPELQVLDLSRCEIQTIDGAYQISLSHTLITNPIQSLALG 120
 QY 121 AFSGLSSLOKLVAVETNLASLENPPIGHILKTLKELNVAHNLIOGPKLPEYPSNLTNLEHL 180
 DB 121 AFSGLSSLOKLVAVETNLASLENPPIGHILKTLKELNVAHNLIOGPKLPEYPSNLTNLEHL 180
 QY 181 DLSSNKLQSIYCTDLRLVHQWPLNLSLDSLSNPMNFIQPGAFKELRHKLTLRNPFSL 240
 DB 181 DLSSNKLQSIYCTDLRLVHQWPLNLSLDSLSNPMNFIQPGAFKELRHKLTLRNPFSL 240
 QY 241 NMKTCIQGLAGLVHRLVGEFNNEGNLKFKDLSALEGLCNLTIEERLALYLDYLDI 300
 DB 241 NMKTCIQGLAGLVHRLVGEFNNEGNLKFKDLSALEGLCNLTIEERLALYLDYLDI 300
 QY 301 IDLFNCLTNVSSFSVLVETTERVDFYNPQWHLVNCKEGQPTLTKLSLRLEPTS 360
 DB 301 IDLFNCLTNVSSFSVLVETTERVDFYNPQWHLVNCKEGQPTLTKLSLRLEPTS 360
 QY 361 NKGNAFSEVDLPLEFLDLSRNLSPKGCSSQSDPGTSLKYLDSLNGVITWSSNPLG 420
 DB 361 NKGNAFSEVDLPLEFLDLSRNLSPKGCSSQSDPGTSLKYLDSLNGVITWSSNPLG 420
 QY 421 LEQLEHLDFQHSNLIKQSEFVPLSLNRLIYLDISHTTRVAENGIFNGLSLEVLKMG 480
 DB 421 LEQLEHLDFQHSNLIKQSEFVPLSLNRLIYLDISHTTRVAENGIFNGLSLEVLKMG 480
 QY 481 NSFOENLPLDFTLRLNLTFLDLSQCOLEQSLPFAFNSLSQVLMNSHNPFLSDTPY 540
 DB 481 NSFOENLPLDFTLRLNLTFLDLSQCOLEQSLPFAFNSLSQVLMNSHNPFLSDTPY 540
 QY 541 KCLNSLOVLDVSLNHNMTSKKQELQHPSPSLAFNLQNDPACTCEHOSFLQWIKDQRL 600
 DB 541 KCLNSLOVLDVSLNHNMTSKKQELQHPSPSLAFNLQNDPACTCEHOSFLQWIKDQRL 600
 QY 601 LVEVERECATPSKQGNPVLISNITQMNKTIIGSVLSLVVSVAVLVYKFEHML 660
 DB 601 LVEVERECATPSKQGNPVLISNITQMNKTIIGSVLSLVVSVAVLVYKFEHML 660
 QY 661 LAGCITKRGENTIDAFVYSSQDEDWVRNVLNLEBVGPPQLCHYRDFIGVATAA 720
 DB 661 LAGCITKRGENTIDAFVYSSQDEDWVRNVLNLEBVGPPQLCHYRDFIGVATAA 720
 QY 721 NIHEGFHKSRYVWVSQHPFIOGRWCIFEYIAQTWQFLSSRAGIIFIVLQKYEKTLR 780
 DB 721 NIHEGFHKSRYVWVSQHPFIOGRWCIFEYIAQTWQFLSSRAGIIFIVLQKYEKTLR 780
 QY 781 QQVELYRLLSRNTYLEWEDSVLGHIFWRRLRKALLDQKSNPBGTVGTCNMQEATSI 839
 DB 781 QQVELYRLLSRNTYLEWEDSVLGHIFWRRLRKALLDQKSNPBGTVGTCNMQEATSI 839

RESULT 6
 AAW86361
 ID AAW86361 standard; protein; 837 AA.
 XX
 XX AAW86361;
 DT 15-MAR-1999 (first entry)
 XX
 DE Human DNAK toll-like receptor DTLR4.
 XX
 KW DNAK toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
 KW interleukin 1 receptor; phosphate metabolism; innate immunity response;
 KW modulate inflammatory function; morphological effect;
 KW immunological disorder.
 OS Homo sapiens.
 OS
 FN WO9850547-A2.
 FN
 PD 12-NOV-1998.

XX 07-MAY-1998; 98WO-US008979.
XX
XX 07-MAY-1997; 97US-0044293P.
PR 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
XX WPI: 1999-059670/05.
DR N-PSDB; AAV80675.
XX
PT Human DNX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
PT metabolism, modulate inflammatory function or innate immunity responses.
XX
PS Claim 3; Page 147-149; 171pp; English.
XX
XX The present invention specifically describes human DNX toll-like
CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC in the present invention. Also described are: (1) a fusion protein
CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC an antibody or antibody fragment which specifically binds to a DTLR
CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC host cell comprising the vector of (4). The host cell of (5) can be used
CC to produce the DTLR proteins. The DTLR proteins can be used to alter
CC phosphate metabolism, to modulate inflammatory function, innate immunity
CC responses or morphological effects. The DTLR proteins can be used in the
CC treatment of conditions exhibiting abnormal expression of the receptors
CC of their ligands. These abnormalities are typically manifested by
CC immunological disorders
XX
SQ Sequence 837 AA;
Query Match 99.6%; Score 4335.5; DB 2; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 2 MSASRLAGTLIPAAAFISCVRPESMPCVEVVPVNTYQCMELNFKYKIPDNLPFGTKNLDL 61
DB 1 MSASRLAGTLIPAAAFISCVRPESMPCVE-VPNTTQCMELNFKYKIPDNLPFGTKNLDL 59
QY 62 SFNPLRLHGSYSFSPFPELQVLDLSRCEIQITIEDGAYGSLHSTLITGNPISLALGA 121
DB 60 SFNPLRLHGSYSFSPFPELQVLDLSRCEIQITIEDGAYGSLHSTLITGNPISLALGA 119
QY 122 FSGLSLQKLVAVETNLASLENFPIGHLTKLKEINVAHNLQSFKLPEYFENLTNLEHLD 181
DB 120 FSGLSLQKLVAVETNLASLENFPIGHLTKLKEINVAHNLQSFKLPEYFENLTNLEHLD 179
QY 182 LSSNKISQICTDPAFVHOMPLNLSLDLSINPMNFIOGAFKRIHLKLTLRNNPDSLN 241
DB 180 LSSNKISQICTDPAFVHOMPLNLSLDLSINPMNFIOGAFKRIHLKLTLRNNPDSLN 239
QY 242 VMKTCIOGLAGLEVHRLVLSGFNNEGMLKEFKDSALBGLCNLTIEEFLAYLDYLDII 301
DB 240 VMKTCIOGLAGLEVHRLVLSGFNNEGMLKEFKDSALBGLCNLTIEEFLAYLDYLDII 299
QY 302 DLFNCLTNVSSFSTVSTIERVKSYPNFGMOHLELVNCKRGOPPTLKLSLKTPTSN 361
DB 300 DLFNCLTNVSSFSTVSTIERVKSYPNFGMOHLELVNCKRGOPPTLKLSLKTPTSN 359
QY 362 KGGNAFSEVDLPSEFLDLISNGLSFKGCCSQSDFGTSLKYLDLSPFNGVITMSNFGTL 421
DB 360 KGGNAFSEVDLPSEFLDLISNGLSFKGCCSQSDFGTSLKYLDLSPFNGVITMSNFGTL 419
QY 422 EOLEHLDPOHSNLSKOMSEFVLSLRNLIIYDISHHTTRVAFNGIISLSEVLKXAGN 481
DB 420 EOLEHLDPOHSNLSKOMSEFVLSLRNLIIYDISHHTTRVAFNGIISLSEVLKXAGN 479
QY 482 SFQENFLPDIETELRNLTFLDLSQCQLEQLSPFAPNSLSLQVLNMSHNNFSLDTPPYK 541

DB 480 SFQENFLPDIETELRNLTFLDLSQCQLEQLSPFAPNSLSLQVLNMSHNNFSLDTPPYK 539
QY 542 CLNSIQVLDYSLNHNIMTSKKQELQHPSSLAFLNTQNDPACCEHQSFLQWIKDQRL 601
DB 540 CLNSIQVLDYSLNHNIMTSKKQELQHPSSLAFLNTQNDPACCEHQSFLQWIKDQRL 599
QY 602 VEVERMECAPSPDKQMPVLSLNTCOMNTTIGVSVLSVSVAVVLYKFEFHLML 661
DB 600 VEVERMECAPSPDKQMPVLSLNTCOMNTTIGVSVLSVSVAVVLYKFEFHLML 659
QY 662 AGCIKYGKGNITDAFYSSODEDWARNLVNLEBGPVPPOLCHYRDPFEGVAAAN 721
DB 660 AGCIKYGKGNITDAFYSSODEDWARNLVNLEBGPVPPOLCHYRDPFEGVAAAN 719
QY 722 IIEHGFHRSKRVIVVWSQHFIQSRLCIFEYEIAQWOFSSRAGIIFIVLQKEKTLRQ 781
DB 720 IIEHGFHRSKRVIVVWSQHFIQSRLCIFEYEIAQWOFSSRAGIIFIVLQKEKTLRQ 779
QY 782 QVEIYRLLSNNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPFGTVGTGCNMOEATSI 839
DB 780 QVEIYRLLSNNTYLEWEDSVLGRHIFWRRLRKALLDGKSNPFGTVGTGCNMOEATSI 837
RESULT 7
ID AAE16102 standard; protein; 837 AA.
XX AAE16102;
AC AAE16102;
XX 26-MAR-2002 (first entry)
DT Human DNX Toll like receptor (DTLR) 4 #2.
DB Human DNX Toll like receptor (DTLR) 4 #2.
XX
KM Human; DNX Toll like receptor; DTLR; therapy; immunological disorder;
KM interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX Homo sapiens.
XX WO200190151-A2.
XX 29-NOV-2001.
PD 23-MAY-2001; 2001WO-US016766.
XX 25-MAY-2000; 2000US-0207558P.
PR (SCHE) SCHERING CORP.
PA Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y,
PI WPI: 2002-083085/11.
DR N-PSDB; AAD26292.
DB New DNX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
PS Claim 3; Page 41; 297pp; English.
XX The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression

CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTR or cells that express it. The present sequence is
 CC human DTR4 protein. The DTR4 gene is located on chromosome 9q22-23.
 CC Note: The present sequence SEQ ID NO 26 is stated to be similar to the
 CC sequence shown in page 240-243 (AA016116). However these sequences differ
 CC at several locations

XX
 XX Sequence 837 AA;

Query Match 99.6%; Score 4335.5; DB 5; Length 837;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 MSASRLAGTLIPAMAFISCVRPESWPCVEVPNTTYQCEMLNFKYKIPDNLPFSTKNDL 61
 DB 1 MSASRLAGTLIPAMAFISCVRPESWPCVE-VPNITTYQCEMLNFKYKIPDNLPFSTKNDL 59
 QY 62 SFNPLRLHSGYSFFSPFPELOVLDSRCEIQTIEDGAYOSLSHSLTLITGNPIQSLALGA 121
 DB 60 SFNPLRLHSGYSFFSPFPELOVLDSRCEIQTIEDGAYOSLSHSLTLITGNPIQSLALGA 119
 QY 122 FSGSSLSQKLVAVENINLASLENFPIGHKTKELVAVANILQSFYLPPEFSMLTNLEHLD 181
 DB 120 FSGSSLSQKLVAVENINLASLENFPIGHKTKELVAVANILQSFYLPPEFSMLTNLEHLD 179
 QY 182 LSSNKIQSIYCTDLRLVHQMPLNLDSLNLPMNFIOPGAFKEIRLHKLTLRNPFDSLN 241
 DB 180 LSSNKIQSIYCTDLRLVHQMPLNLDSLNLPMNFIOPGAFKEIRLHKLTLRNPFDSLN 239
 QY 242 VMKTCIQGLAGLEVRLVYGEFRNNGNI.EKFDKXALBGLCNLTIEPRLAYLYLDYLDII 301
 DB 240 VMKTCIQGLAGLEVRLVYGEFRNNGNI.EKFDKXALBGLCNLTIEPRLAYLYLDYLDII 299
 QY 302 DLFNCLTNVSSFSIYSVTIERKDSYNGMOMHELVNCKRGQPFLLKLSKRLTFTSN 361
 DB 300 DLFNCLTNVSSFSIYSVTIERKDSYNGMOMHELVNCKRGQPFLLKLSKRLTFTSN 359
 QY 362 KGNNAFSEVDLPSTLEFLDLNRNGLSFKGCCSDSGTSLKLYDLSFNGVITMSNFTGL 421
 DB 360 KGNNAFSEVDLPSTLEFLDLNRNGLSFKGCCSDSGTSLKLYDLSFNGVITMSNFTGL 419
 QY 422 EOLEHLDFQHSNLMKQSEFSYVFLSRNLIIYDISHHTTRVAFNGIFNGLSLEVLKMGAN 481
 DB 420 EOLEHLDFQHSNLMKQSEFSYVFLSRNLIIYDISHHTTRVAFNGIFNGLSLEVLKMGAN 479
 QY 482 SFOENFLPDIETELNLTFLDLSQQLSTAFNSLSLQVLMSSHNNFSLDTFPYK 541
 DB 480 SFOENFLPDIETELNLTFLDLSQQLSTAFNSLSLQVLMSSHNNFSLDTFPYK 539
 QY 542 CLNSIQVLDVSLNIMTSGKQELQHPSSLAFLNLTQNDFACTCHGQFLOMIXDQROL 601
 DB 540 CLNSIQVLDVSLNIMTSGKQELQHPSSLAFLNLTQNDFACTCHGQFLOMIXDQROL 599
 QY 602 VEVERMECATPSDKQGMFVLSNITQCNKTIIGVSVLSVLVAVVAVLVYKFFHMLL 661
 DB 600 VEVERMECATPSDKQGMFVLSNITQCNKTIIGVSVLSVLVAVVAVLVYKFFHMLL 659
 QY 662 AGCIKYGGENIYDAFVYSSODEMWNRELKNEBVGPPQCLAHADPFGVAIAAN 721
 DB 660 AGCIKYGGENIYDAFVYSSODEMWNRELKNEBVGPPQCLAHADPFGVAIAAN 719
 QY 722 IHHGFFHSRKVIYVVOHFIOSRWCIPEYELAQTMQFLSSAGIIFIVLOKVEKTLRQ 781
 DB 720 IHHGFFHSRKVIYVVOHFIOSRWCIPEYELAQTMQFLSSAGIIFIVLOKVEKTLRQ 779
 QY 782 QVELYRLLSRNTYLSMEDSVLGRHIFWRRLRKALLDGKSNDEGTGTCNQWQATSI 839
 DB 780 QVELYRLLSRNTYLSMEDSVLGRHIFWRRLRKALLDGKSNDEGTGTCNQWQATSI 837

RESULT 8
 AB004776

ID AB004776 standard; protein; 837 AA.

XX AC AB004776;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1442.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

XX protease; protease inhibitor; transporter; cytoskeletal protein;

XX receptor; transcription factor; cancer; MHC;

XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;

XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0232544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

XX Chicx RM, Tomlinson AU, Urban RG;

XX WPI, 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,

XX cytoskeletal proteins, receptors or transcription factors), useful for

XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

XX leukemia.

XX Example 2; SEQ ID NO 1442; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a

XX fragment of a kinase, phosphatase, protease, protease inhibitor,

XX transporter, cytoskeletal protein, receptor or transcription factor. The

XX polypeptide is useful as an immunogenic composition for eliciting in a

XX mammal an immunogenic response directed against any of the purified

XX polypeptide. The purified polypeptide, or the antibody that binds to this

XX polypeptide, is useful for treating cancer. The polypeptide is also

XX useful for identifying compounds that binds to a naturally processed

XX class I or class II MHC-binding polypeptide. The polypeptides and

XX polynucleotides are particularly useful for treating or preventing

XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

XX lymphoma or leukaemia. These are also useful for screening agents for

XX treating the above mentioned diseases. This sequence represents an

XX expressed protein tag (EPT) isolated from human tissue for translational

XX profiling. Note: This sequence does not appear in the printed

XX specification but was obtained in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 837 AA;

Query Match 99.6%; Score 4335.5; DB 6; Length 837;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 MSASRLAGTLIPAMAFISCVRPESWPCVEVPNTTYQCEMLNFKYKIPDNLPFSTKNDL 61
 DB 1 MSASRLAGTLIPAMAFISCVRPESWPCVE-VPNITTYQCEMLNFKYKIPDNLPFSTKNDL 59
 QY 62 SFNPLRLHSGYSFFSPFPELOVLDSRCEIQTIEDGAYOSLSHSLTLITGNPIQSLALGA 121
 DB 60 SFNPLRLHSGYSFFSPFPELOVLDSRCEIQTIEDGAYOSLSHSLTLITGNPIQSLALGA 119

QY	122	PSGLSSISQRLVAVENTLASLENPRIGHLKTILELVANHLIOSFCLPEYPSNLTNLEHLD	183
Db	120	PSGLSSISQRLVAVENTLASLENPRIGHLKTILELVANHLIOSFCLPEYPSNLTNLEHLD	179
QY	182	LSNSKIOSIYCTDLRYLHQWPLNLNSLDLSLNPMPNFIQGAPEKIRLKLTLRNNFDSLN	241
Db	180	LSNSKIOSIYCTDLRYLHQWPLNLNSLDLSLNPMPNFIQGAPEKIRLKLTLRNNFDSLN	233
QY	242	VMKTCIOGLAGLEVHRLVLGEFPFNEGNLEKFPKSALEGLCNLTIEEPRLAYDYLLDI	301
Db	240	VMKTCIOGLAGLEVHRLVLGEFPFNEGNLEKFPKSALEGLCNLTIEEPRLAYDYLLDI	299
QY	302	DLPRCLTNVSSFEFLSVTIERVYDPEYNGWHLBELYNCKPQFPYTLKLSKLUTPTSN	366
Db	300	DLPRCLTNVSSFEFLSVTIERVYDPEYNGWHLBELYNCKPQFPYTLKLSKLUTPTSN	355
QY	362	KGGNAFSEVYLPSTLEFLDLSRNLSPKGCSSODPCTTSLKYLDLSPNGVITMSSNFIGL	422
Db	360	KGGNAFSEVYLPSTLEFLDLSRNLSPKGCSSODPCTTSLKYLDLSPNGVITMSSNFIGL	411
QY	422	EQLEHLDFQHSNLKOMSEFVFLSLRNLTYLDSHTTRVAFNGIFNGLSLEVLKMAGN	483
Db	420	EQLEHLDFQHSNLKOMSEFVFLSLRNLTYLDSHTTRVAFNGIFNGLSLEVLKMAGN	479
QY	482	SPQENFLPDIPTFELRNLTFLDLSSQCLEOLSPTAENSLSLOVLMASHNPFSLDTPPYK	544
Db	480	SPQENFLPDIPTFELRNLTFLDLSSQCLEOLSPTAENSLSLOVLMASHNPFSLDTPPYK	533
QY	542	CNLSLOVLDVLSLNMHTSKKQEOLOHPPSLAPLNTONDPACTCEHOSFLQMIQDROL	603
Db	540	CNLSLOVLDVLSLNMHTSKKQEOLOHPPSLAPLNTONDPACTCEHOSFLQMIQDROL	599
QY	602	VEVERMECATPSPDKQGNPVLSLNTITCOMKTTIIGVSVLSLVVAVLVYKFEYFHLML	661
Db	600	VEVERMECATPSPDKQGNPVLSLNTITCOMKTTIIGVSVLSLVVAVLVYKFEYFHLML	655
QY	662	AGCTKYGKRGNNIYDAFYTSSQDEDMVRNMLYKNLEEGVPPPOLCLHTRDFIPGVAIAN	722
Db	660	AGCTKYGKRGNNIYDAFYTSSQDEDMVRNMLYKNLEEGVPPPOLCLHTRDFIPGVAIAN	713
QY	722	IIHGEFKSKRVLVVVSQHFQIOSRKCIFEYELAQTMQFSSPAGIIFVLOKVEKTLIRQ	783
Db	720	IIHGEFKSKRVLVVVSQHFQIOSRKCIFEYELAQTMQFSSPAGIIFVLOKVEKTLIRQ	773
QY	782	QVELYRLLSHNTVLEWEDSVLGRHIFWRRLRKALLDGKSNBEGTVGTGCWQEAISI	839
Db	780	QVELYRLLSHNTVLEWEDSVLGRHIFWRRLRKALLDGKSNBEGTVGTGCWQEAISI	837
RESULT 9			
AAE16116			
ID	AAE16116	standard; protein; 837 AA.	
XX	AAE16116;		
AC			
XX			
XX	26-MAR-2002	(first entry)	
DT			
XX			
De	Human DNAX Toll like receptor (DTRLR) 4 #2, alternative version.		
XX			
XX	Human, DNAX Toll like receptor; DTLR; therapy; immunological disorder;		
KW	interleukin 1; Il-1; screening; immunomodulator; chromosome 9q32-33.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 211		
FT	/label= Unknown		
FT	/note= "Encoded by AAY"		
XX			
PN	WO200190151-A2.		
XX			
PD	29-NOV-2001.		

PF	23-MAY-2001; 2001WO-US016766.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		</
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QY 422 EOLEHLDPQHSNLIKOMSEFSVFLSLRNLIYLDISTHTRVANGIFNGISLSEVLKMAGN 481
Db 420 EOLEHLDPQHSNLIKOMSEFSVFLSLRNLIYLDISTHTRVANGIFNGISLSEVLKMAGN 479
QY 482 SFOENFLDPIDFELNRLNLFPLDLSOCOLBOLSPTAFNLSLSLOVLMNSHNPFSLDTPPK 541
Db 480 SFOENFLDPIDFELNRLNLFPLDLSOCOLBOLSPTAFNLSLSLOVLMNSHNPFSLDTPPK 539
QY 542 CLNSLOVLDSLNHMTSKOELQHPSPSLAFNLTONDFACTCEHOSFLQWIKDORQL 601
Db 540 CLNSLOVLDSLNHMTSKOELQHPSPSLAFNLTONDFACTCEHOSFLQWIKDORQL 599
QY 602 VBEVMECATPSDKGMPVLSLNTTCQANKTIGVSLSVLSVVAALVYKFFHYHML 661
Db 600 VBEVMECATPSDKGMPVLSLNTTCQANKTIGVSLSVLSVVAALVYKFFHYHML 659
QY 662 AGCIYRGENTYDAFVLYSSODEDMVNEIYKMLEEGVPPQCLAHYRDFIPGVAIAN 721
Db 660 AGCIYRGENTYDAFVLYSSODEDMVNEIYKMLEEGVPPQCLAHYRDFIPGVAIAN 719
QY 722 IIHGFHRSRKVIYVVSQHFLOSRCIFEYELAQTMQFLSPRAGIIFIVLOKVEKTLRQ 781
Db 720 IIHGFHRSRKVIYVVSQHFLOSRCIFEYELAQTMQFLSPRAGIIFIVLOKVEKTLRQ 779
QY 782 QVELYRLLSRNTYLEMEDSVLGRHIFWRRLRKALLDGKSNBEGVTGCMQOATSI 839
Db 780 QVELYRLLSRNTYLEMEDSVLGRHIFWRRLRKALLDGKSNBEGVTGCMQOATSI 837

```

RESULT 10

ID ADO57782 standard; protein; 808 AA.

ADO57782;

12-AUG-2004 (first entry)

Chimpanzee toll-like receptor 4 SEQ ID NO:3.

toll-like receptor 4; TLR4; old world monkey; antibacterial;
immunopressive; antiasthmatic; Gram-negative bacterial infection;
sepsis; severe sepsis; septic shock; asthma; chimpanzee.

Pan troglodytes.

MO2004042365-A2.

21-MAY-2004.

03-NOV-2003; 2003WO-US036247.

01-NOV-2002; 2002US-0423113P.

(EVOLO-) EVOLUTIONARY GENOMICS LLC.

Meesier W;

WPI; 2004-400726/37.

N-PSDB; ADO57780, ADO57781.

Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
in treating sepsis and asthma, by comparing the TLR4 polynucleotide
sequence of the Old World monkey with that of a human.

Example 1; SEQ ID NO 3; 111pp; English.

The invention relates to a novel method for identifying a nucleotide
change in a TLR4 polynucleotide sequence of an old world monkey
comparing the TLR4 polynucleotide sequence of the Old World
monkey with corresponding TLR4 polynucleotide sequence of a human. The
method of the invention has antibacterial, immunopressive, and
antiasthmatic activity. The method is useful in identifying a nucleotide
change in a TLR4 polynucleotide sequence of an Old World monkey where the

CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents chimpanzee TLR4.

XX Sequence 808 AA;

Query Match 95.9%; Score 4178; DB 8; Length 808;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 805; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

QY 32 VVPNTTYOCMEINFKIDNIPFSTKNDLSPNPRHIGSFSFSPPELOVIDLSRCBQ 91
Db 1 VVPNTTYOCMEINFKIDNIPFSTKNDLSPNPRHIGSFSFSPPELOVIDLSRCBQ 60
QY 92 TIEDGAYOSLSHLSTLITGNPIOSIALGASGSLSKXLAVENTLASLENFPIGHKT 151
Db 61 TIEDGAYOSLSHLSTLITGNPIOSIALGASGSLSKXLAVENTLASLENFPIGHKT 120
QY 152 LKELNVAHNLIOFPLPEYFNSLNTLEHLDSSNKIOSTYCTDLVHLQMPPLNLSLDS 211
Db 121 LKELNVAHNLIOFPLPEYFNSLNTLEHLDSSNKIOSTYCTDLVHLQMPPLNLSLDS 180
QY 212 LNPWFIOPGAPEKIRLKLTLRNNPDSLANMKTCTIOGLAGIEYHRLVYGEFRNGNLEK 271
Db 181 LNPWFIOPGAPEKIRLKLTLRNNPDSLANMKTCTIOGLAGIEYHRLVYGEFRNGNLEK 240
QY 272 FDKSALBGLCNLTTEEPRLAYLDYLDIIDLPLNCLTNVSSPSLSVYTERKXDSYNG 331
Db 241 FDKSALBGLCNLTTEEPRLAYLDYLDIIDLPLNCLTNVSSPSLSVYTERKXDSYNG 300
QY 332 WOHELVNCKFGQPEPTLKLKSLKRLTFTSNKGNAFSEVDLPSEFLDLSRNGLSFKGCC 391
Db 301 WOHELVNCKFGQPEPTLKLKSLKRLTFTSNKGNAFSEVDLPSEFLDLSRNGLSFKGCC 360
QY 392 SOSDFGTTSLKYLDLSFNGVITMGSNFIQLEOLBHLDPQHSNLIKOMSEFSVFLSLRNLIY 451
Db 361 SOSDFGTTSLKYLDLSFNGVITMGSNFIQLEOLBHLDPQHSNLIKOMSEFSVFLSLRNLIY 420
QY 452 LDISHTRVAFNGIFNGISLSEVLKMAGNSFOENFLDPIDFELNRLNLFPLDLSOCOLBOL 511
Db 421 LDISHTRVAFNGIFNGISLSEVLKMAGNSFOENFLDPIDFELNRLNLFPLDLSOCOLBOL 480
QY 512 SPTAFNSLSLOVLMNSHNPFSLDTPPYKCLNSLOVLDVSLNHMTSKOELQHPSPSL 571
Db 481 SPTAFNSLSLOVLMNSHNPFSLDTPPYKCLNSLOVLDVSLNHMTSKOELQHPSPSL 540
QY 572 AFLNLTONDFACTCEHOSFLOWIKDORQLAVEBERMECATPSDKGMPVLSLNTTCQANK 631
Db 541 AFLNLTONDFACTCEHOSFLOWIKDORQLAVEBERMECATPSDKGMPVLSLNTTCQANK 600
QY 632 TIIGVSVLSVLSVVAALVYKFFHYHMLTAGCTKYGGENIYDAFVLYSSODEDMVNE 691
Db 601 TIIGVSVLSVLSVVAALVYKFFHYHMLTAGCTKYGGENIYDAFVLYSSODEDMVNE 660
QY 692 LVKNLEBGPFPQCLAHYRDFIPGVAIAANIIEHGFHRSRKVIYVVSQHFLOSRCIFEY 751
Db 661 LVKNLEBGPFPQCLAHYRDFIPGVAIAANIIEHGFHRSRKVIYVVSQHFLOSRCIFEY 720
QY 752 EIAQTWQFLSPRAGIIFIVLOKVEKTLRQVELYRLLSRNTYLEMEDSVLGRHIFWRRL 811
Db 721 EIAQTWQFLSPRAGIIFIVLOKVEKTLRQVELYRLLSRNTYLEMEDSVLGRHIFWRRL 780
QY 812 RKALLDGKSNBEGVTGCMQOATSI 839
Db 781 RKALLDGKSNBEGVTGCMQOATSI 808

```

RESULT 11

ADO57785 standard; protein; 808 AA.

ADO57785;

XX 12-AUG-2004 (first entry)
DT
XX
DE Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
KM toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; gorilla.
XX
OS Gorilla gorilla.
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
XX 03-NOV-2003; 2003WO-US036247.
PF
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR MPI; 2004-400726/37.
DR N-PSDB; ADO57783, ADO57784.
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
XX Example 1; SEQ ID NO 6; 111pp; English.
XX
XX The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiaesthetic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents gorilla TLR4.
XX
SQ Sequence 808 AA;
Query Match 95.7%; Score 4167; DB 8; Length 808;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 803; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 32 VVPNITYQCMELNPFYKIPDNLPSTKNLDLSPNPLRHLSYSPFSPPELOVLDLSCREIQ 91
DB 1 VVPNITYQCMELNPFYKIPDNLPSTKNLDLSPNPLRHLSYSPFSPPELOVLDLSCREIQ 60
QY 92 TIEDAYOSLSLSTLITGNPIQSLAGAFSGLSLQKLVAVENTLASLENFPIGHKT 151
DB 61 TIEDAYOSLSLSTLITGNPIQSLAGAFSGLSLQKLVAVENTLASLENFPIGHKT 120
QY 152 LKELVANHLIOSFKLPEYFSNLTLNLEHDLSSNKIOSIYCTDLVHLHOMPLNLSTLDS 211
DB 121 LKELVANHLIOSFKLPEYFSNLTLNLEHDLSSNKIOSIYCTDLVHLHOMPLNLSTLDS 180
QY 212 LNPNNFIQGAKEIRLHKLTLRNNFDSLNWKTICIOGLAGLEVRLVYGERFNGNLEK 271
DB 181 LNPNNFIQGAKEIRLHKLTLRNNFDSLNWKTICIOGLAGLEVRLVYGERFNGNLEK 240
QY 272 FDKSLBEGICNLTIEFRLAYLDYLDIIDLFNCLTNVSSGLSVTIERKYDPSYNG 331
DB 241 FDKSLBEGICNLTIEFRLAYLDYLDIIDLFNCLTNVSSGLSVTIERKYDPSYNG 300
QY 332 MOHLELVNCKRGQFPTLKLKSLKRLTPTSNKGNAPSEVDLPSTLFLDLSTRGSLFKGCC 391
DB 301 MOHLELVNCKRGQFPTLKLKSLKRLTPTSNKGNAPSEVDLPSTLFLDLSTRGSLFKGCC 360

QY 392 SOSDFGTTSLKYLDLSPNGVITMSSNPLGLEOLEHLDFOHSNLMKMSSEFVLSLRNLIY 451
DB 361 SOSDFGTTSLKYLDLSPNGVITMSSNPLGLEOLEHLDFOHSNLMKMSSEFVLSLRNLIY 420
QY 452 LDIHTHTRAVFNQIFNGLSLETLKMAGNSFQNNFLPDTITELRNLTFFLDISCCOLEQL 511
DB 421 LDIHTHTRAVFNQIFNGLSLETLKMAGNSFQNNFLPDTITELRNLTFFLDISCCOLEQL 480
QY 512 SPFAFNSLSLQVAINMHNHNFSLDTPPYKCLNSLOVLDYSLNHNMTSKQELQHPSSL 571
DB 481 SPFAFNSLSLQVAINMHNHNFSLDTPPYKCLNSLRVLDYSLNHNMTSKQELQHPSSL 540
QY 572 AFLNLTONDFACTCEHOSFLQWIMQORQLVYERMECATPSPDKQMPVLSLNTTCQMNK 631
DB 541 AFLNLTONDFACTCEHOSFLQWIMQORQLVYERMECATPSPDKQMPVLSLNTTCQMNK 600
QY 632 TITGVSVLSVIVSVAVLVYKFFPHMLLAGCIKYRGENIYAPFIYSSQEDDWARN 691
DB 601 TITGVSVLSVIVSVAVLVYKFFPHMLLAGCIKYRGENIYAPFIYSSQEDDWARN 660
QY 692 LVKNLEBGPFPOLCHYRDFIPGVAIAANIHBGFHKSRYIVVVSQHFIOQRWCIPEY 751
DB 661 LVKNLEBGPFPOLCHYRDFIPGVAIAANIHBGFHKSRYIVVVSQHFIOQRWCIPEY 720
QY 752 EIAQTWQFLSSRAGIIFIVLQKVEKTLRQOVBLRYLLSRNTYLEWEDSVLGRHIFWRRL 811
DB 721 EIAQTWQFLSSRAGIIFIVLQKVEKTLRQOVBLRYLLSRNTYLEWEDSVLGRHIFWRRL 780
QY 812 RKALLDGKSNWPEGTGTCNMORATSI 839
DB 781 RKALLDGKSNWPEGTGTCNMORATSI 808
RESULT 12
ID ADO57803 standard; protein; 808 AA.
XX
XX ADO57803;
AC
XX
DT 12-AUG-2004 (first entry)
XX
XX Chimpanzee toll-like receptor 4 SEQ ID NO:24.
DE
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS Pan troglodytes.
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR MPI; 2004-400726/37.
DR N-PSDB; ADO57801, ADO57802.
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
XX Disclosure; SEQ ID NO 24; 111pp; English.
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey

comprising comparing the TLR4 polynucleotide sequence of the Old World monkey with corresponding TLR4 polynucleotide sequence of a human. The method of the invention has antibacterial, immunosuppressive, and antiasthmatic activity. The method is useful in identifying a nucleotide change in a TLR4 polynucleotide sequence of an Old World monkey where the change may be associated with reduced sensitivity to Gram-negative bacterial infection. The methods, agents and composition are useful in treating sepsis, severe sepsis or septic shock and asthma. The present sequence represents chimpanzee TLR4.

Sequence 808 AA:

Query Match 95.6%; Score 4164; DB 8; Length 808;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 803; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

QY 32 VVPNTTYOCMEINFKIPDNLPSTKNLDLSPNPLRHGYSFFSPPELQVLDLRCEIQ 91
DB 1 VVPNTTYOCMEINFKIPDNLPSTKNLDLSPNPLRHGYSFFSPPELQVLDLRCEIQ 60
QY 92 TIEDGAYOSLSHSLTLITGNPIQSIALGAFSGLSLQKLVAVETNLASLENPFIQHLKT 151
DB 61 TIEDGAYOSLSHSLTLITGNPIQSIALGAFSGLSLQKLVAVETNLASLENPFIQHLKT 120
QY 152 LKEILVAVANHLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQPMLNLSLDS 211
DB 121 LKEILVAVANHLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQPMLNLSLDS 180
QY 212 LNPMPFIQPGAFKEIRLHKLTIRNPNDSINMKTICQIAGLEVHRLVGEERNENLEK 271
DB 181 LNPMPFIQPGAFKEIRLHKLTIRNPNDSINMKTICQIAGLEVHRLVGEERNENLEK 240
QY 272 FDKSALBEGCNLTIEEFRLAYDYLDIIDLFNCLTNVSSFSLSVTERKDESYNG 331
DB 241 FDKSALBEGCNLTIEEFRLAYDYLDIIDLFNCLTNVSSFSLSVTERKDESYNG 300
QY 332 WQHELVNCKFGQFPFLTKLSLKRLLFTSNKGNAPSEVDLPLEFLDLSRNGLSFKGCC 391
DB 301 WQHELVNCKFGQFPFLTKLSLKRLLFTSNKGNAPSEVDLPLEFLDLSRNGLSFKGCC 360
QY 392 SOSDGTSTLKYLDLSFNGVITMSSNPLGLEDEHLDPOHSLKQMSSESVLSLRNLY 451
DB 361 SOSDGTSTLKYLDLSFNGVITMSSNPLGLEDEHLDPOHSLKQMSSESVLSLRNLY 420
QY 452 LDISHTHTRVAFNGIFNGLSLEVLKMGNSFOENFLPDIFELRNLTFLDLSQCCLEJ 511
DB 421 LDISHTHTRVAFNGIFNGLSLEVLKMGNSFOENFLPDIFELRNLTFLDLSQCCLEJ 480
QY 512 SPTAFNSLSLQVLNMSHNNPFLDTPFYKCLNSIQVLDYSLNHIMTSKKQELQHPSSL 571
DB 481 SPTAFNSLSLQVLNMSHNNPFLDTPFYKCLNSIQVLDYSLNHIMTSKKQELQHPSSL 540
QY 572 AFLNLTQNDFACTCEHOSFLOWIKOROLIVEVERNECTPBDKQMPVLSNITTCQNMK 631
DB 541 AFLNLTQNDFACTCEHOSFLOWIKOROLIVEVERNECTPBDKQMPVLSNITTCQNMK 600
QY 632 TIGGSVSVLVVAVVAVVYKFFPHMLLAGICIKRGENTYDAFAVYSSODEBVRNE 691
DB 601 TIGGSVSVLVVAVVAVVYKFFPHMLLAGICIKRGENTYDAFAVYSSODEBVRNE 660
QY 692 LVKNLEBGPFPOLCLHVRDPIPGVAIAANIIEGHFHSRKAVIVVVSQHFIOSRWCIFEX 751
DB 661 LVKNLEBGPFPOLCLHVRDPIPGVAIAANIIEGHFHSRKAVIVVVSQHFIOSRWCIFEX 720
QY 752 ELAQWQPLSSRAGIIFIVLQVVEKTLRQOVELRHLRSRNTYLEWEDSVLGRHIFWRRL 811
DB 721 ELAQWQPLSSRAGIIFIVLQVVEKTLRQOVELRHLRSRNTYLEWEDSVLGRHIFWRRL 780
QY 812 RKALLDGKSNPEGTVGTGCNMQOATS 839
DB 781 RKALLDGKSNPEGTVGTGCNMQOATS 808

```

RESULT 13

AAW86352 standard; protein; 799 AA.

AAW86352;

15-MAR-1999 (first entry)

Human DNAX toll-like receptor DTLR4.

DNAX toll-like receptor; DTLR4; Drosophila toll receptor; IL-1 receptor; interleukin 1 receptor; phosphate metabolism; innate immunity response;

modulate inflammatory function; morphological effect;

immunological disorder.

Homo sapiens.

MO9850547-A2.

12-NOV-1998.

07-MAY-1998; 98MO-US008979.

07-MAY-1997; 97US-0044293P.

22-JAN-1998; 98US-0072212P.

05-MAR-1998; 98US-0076947P.

(SCHE) SCHERING CORP.

Hardiman GT, Rock FL, Bazan JF, Kastelein RA;

WPI, 1999-059670/05.

N-PsDB; AAW80666.

Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate metabolism, modulate inflammatory function or innate immunity response.

Example; Page 115-117; 171pp; English.

The present invention specifically describes human DNAX toll-like receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given in the present invention. Also described are: (1) a fusion protein comprising a DTLR protein or peptide; (2) a binding compound, preferably an antibody or antibody fragment which specifically binds to a DTLR protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide; (4) an expression vector comprising the nucleic acid of (3); and (5) a host cell comprising the vector of (4). The host cell of (5) can be used to produce the DTLR proteins. The DTLR proteins can be used to alter phosphate metabolism, to modulate inflammatory function, innate immunity responses or morphological effects. The DTLR proteins can be used in the treatment of conditions exhibiting abnormal expression of the receptors of their ligands. These abnormalities are typically manifested by immunological disorders

Sequence 799 AA:

Query Match 95.1%; Score 4141; DB 2; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 41 MELNFKYKIPDNLPSTKNLDLSPNPLRHGYSFFSPPELQVLDLRCEIQTEDGAYOS 100
DB 1 MELNFKYKIPDNLPSTKNLDLSPNPLRHGYSFFSPPELQVLDLRCEIQTEDGAYOS 60
QY 101 LSHSLTLITGNPIQSIALGAFSGLSLQKLVAVETNLASLENPFIQHLKTKEILVAN 160
DB 61 LSHSLTLITGNPIQSIALGAFSGLSLQKLVAVETNLASLENPFIQHLKTKEILVAN 120
QY 161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQPMLNLSLDSINPMPFIOP 220
DB 121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQPMLNLSLDSINPMPFIOP 180
QY 221 GAFKEIRLHKLTIRNPNDSINMKTICQIAGLEVHRLVGEERNENLEKFDKALBGL 280

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Db 181 GAFKEIRLHKLTLRNNPDSLNVMKTCIOGLAGLEVHRLVGBFRNBNGLKFKFDSKSALEGL 240
Qy 281 CNLTIEBFRLAYLDYDDIIDLFNCLTNVSSFSVLVSTIRKVDPSYFNGMOHLELVNC 340
Db 241 CNLTIEBFRLAYLDYDDIIDLFNCLTNVSSFSVLVSTIRKVDPSYFNGMOHLELVNC 300
Qy 341 KFGQFPTLKLSKRLTFTSNKGNAPSEVDLPSEFLDLSRNGLSFKGCCOSQDFGTT 400
Db 301 KFGQFPTLKLSKRLTFTSNKGNAPSEVDLPSEFLDLSRNGLSFKGCCOSQDFGTT 360
Qy 401 LKYDLSFNGVITWSSNFIQLEHLDFOHNSLKQSESVFSLRNLIYLDISHTYTR 460
Db 361 LKYDLSFNGVITWSSNFIQLEHLDFOHNSLKQSESVFSLRNLIYLDISHTYTR 420
Qy 461 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCLEQSLPFAFNLS 520
Db 421 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCLEQSLPFAFNLS 480
Qy 521 SLOVLNMSHNNFSLDTPPYKCLNSLOVLDSLNHMTSKQELQHPSSLAFLNTQND 580
Db 481 SLOVLNMSHNNFSLDTPPYKCLNSLOVLDSLNHMTSKQELQHPSSLAFLNTQND 540
Qy 581 FACTCEHOSFLOWIKDQROLVVERMECAPSPDKQMPVSLNITCOMNKTIIIGSVLS 640
Db 541 FACTCEHOSFLOWIKDQROLVVERMECAPSPDKQMPVSLNITCOMNKTIIIGSVLS 600
Qy 641 VLAVSVAVLVYKFFHMLLAGCTKYGRGENITYDAFIYSSODEDWARNELVNNLEEGV 700
Db 601 VLAVSVAVLVYKFFHMLLAGCTKYGRGENITYDAFIYSSODEDWARNELVNNLEEGV 660
Qy 701 PPFOCLHYRDPFIPGVALAANIIEHGFHKSRRVIVVVSQHFIOGRWCIFEBEIAQWQFL 760
Db 661 PPFOCLHYRDPFIPGVALAANIIEHGFHKSRRVIVVVSQHFIOGRWCIFEBEIAQWQFL 720
Qy 761 SSRGIIIFIVYQXVEKTLRQOVELYRLSNRTYLEWEDSVLGRIIFRRRLKALLDGS 820
Db 721 SSRGIIIFIVYQXVEKTLRQOVELYRLSNRTYLEWEDSVLGRIIFRRRLKALLDGS 780
Qy 821 WNPBGTVGTGCMQEAISI 839
Db 781 WNPBGTVGTGCMQEAISI 799

RESULT 14
AAE16093
ID AAE16093 standard; protein, 799 AA.
XX
AC AAE16093;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX Toll like receptor (DTRL) 4 #1.
XX
KW Human; DNAX Toll like receptor; DTRL; therapy; immunological disorder;
KW interleukin 1; Il-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS Homo sapiens.
XX
PN WO200190151-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016766.
XX
PR 25-MAY-2000; 2000US-0207558P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX
DR WPI; 2002-083085/11.
DR N-PSDB; AAD26283.

XX
PT New DNAX Toll like receptor (DTRL) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
PS Claim 1; Page 35; 297pp; English.
XX
SS The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTRL) protein and their corresponding
CC nucleic acids. The DTRL is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTRL is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTRL is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTRL or its various fragments. The
CC purified DTRL can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTRL or cells that express it. The present sequence is
CC human DTRL4 protein. The DTRL4 gene is located on chromosome 9q32-33
CC
XX
SQ Sequence 799 AA:
Query Match 95.1%; Score 4141; DB 5; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 41 MEINFYKIPNLPSTKNDLSFNPRLHLSYSFSPPELOVLDLSRCEIQTIEDGAYOS 100
Db 1 MEINFYKIPNLPSTKNDLSFNPRLHLSYSFSPPELOVLDLSRCEIQTIEDGAYOS 60
Qy 101 LSHSTILILGNPQISALAFSGLSLOQLVAVETMLASLENPFIHKLTKELNVAHN 160
Db 61 LSHSTILILGNPQISALAFSGLSLOQLVAVETMLASLENPFIHKLTKELNVAHN 120
Qy 161 LIOSFKLPEYFSNLTNEHLDSNKLQSIYCTDRLVHQPMLNLSLDSLNPMNFIOP 220
Db 121 LIOSFKLPEYFSNLTNEHLDSNKLQSIYCTDRLVHQPMLNLSLDSLNPMNFIOP 180
Qy 221 GAFKEIRLHKLTLRNNPDSLNVMKTCIOGLAGLEVHRLVGBFRNBNGLKFKFDSKSALEGL 280
Db 181 GAFKEIRLHKLTLRNNPDSLNVMKTCIOGLAGLEVHRLVGBFRNBNGLKFKFDSKSALEGL 240
Qy 281 CNLTIEBFRLAYLDYDDIIDLFNCLTNVSSFSVLVSTIRKVDPSYFNGMOHLELVNC 340
Db 241 CNLTIEBFRLAYLDYDDIIDLFNCLTNVSSFSVLVSTIRKVDPSYFNGMOHLELVNC 300
Qy 341 KFGQFPTLKLSKRLTFTSNKGNAPSEVDLPSEFLDLSRNGLSFKGCCOSQDFGTT 400
Db 301 KFGQFPTLKLSKRLTFTSNKGNAPSEVDLPSEFLDLSRNGLSFKGCCOSQDFGTT 360
Qy 401 LKYDLSFNGVITWSSNFIQLEHLDFOHNSLKQSESVFSLRNLIYLDISHTYTR 460
Db 361 LKYDLSFNGVITWSSNFIQLEHLDFOHNSLKQSESVFSLRNLIYLDISHTYTR 420
Qy 461 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCLEQSLPFAFNLS 520
Db 421 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDIFTELRLNLTFLDLSQCLEQSLPFAFNLS 480
Qy 521 SLOVLNMSHNNFSLDTPPYKCLNSLOVLDSLNHMTSKQELQHPSSLAFLNTQND 580
Db 481 SLOVLNMSHNNFSLDTPPYKCLNSLOVLDSLNHMTSKQELQHPSSLAFLNTQND 540
Qy 581 FACTCEHOSFLOWIKDQROLVVERMECAPSPDKQMPVSLNITCOMNKTIIIGSVLS 640
Db 541 FACTCEHOSFLOWIKDQROLVVERMECAPSPDKQMPVSLNITCOMNKTIIIGSVLS 600
Qy 641 VLAVSVAVLVYKFFHMLLAGCTKYGRGENITYDAFIYSSODEDWARNELVNNLEEGV 700

Db 601 VLVVSVAVLVYKFFHMLLAGCIKYRGENTYAFYISQDEDMWRNELVKNLEBKV 660
Qy 701 PPFOLCHYRDFIPGVAIAANI IHGFKSRKVIIVVSQHFIQSRCIFEYEIAQTWQFL 760
Db 661 PPFOLCHYRDFIPGVAIAANI IHGFKSRKVIIVVSQHFIQSRCIFEYEIAQTWQFL 720
Qy 761 SSRAGIIFIVLOKVEKTLRQOVELYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDGKS 820
Db 721 SSRAGIIFIVLOKVEKTLRQOVELYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDGKS 780
Qy 821 WNPBGTVGTGCMQOATS I 839
Db 781 WNPBGTVGTGCMQOATS I 799
RESULT 15
ABB83162
ID ABB83162 standard; protein; 799 AA.
AC ABB83162;
XX
DT 09-AUG-2002 (first entry)
XX Human Toll-like receptor-4, Tlr4.
DE
XX Human; virucide; antibacterial; fungicide; parasiticide; receptor;
KW cytosolic; immunostimulatory; scavenger receptor; Toll receptor;
KW respiratory tract infection; Toll-like receptor; Tlr4.
XX Homo sapiens.
XX WO200235236-A1.
PN 02-MAY-2002.
PD
XX 26-OCT-2001; 2001WO-FR003352.
PE
XX 27-OCT-2000; 2000FR-00013883.
PR
XX (FABR) FABRE MEDICAMENT SA PIERRE.
PA
XX Jeanm P, Magistrel J G, Herbault N, Bonnefoy J;
PI WPI; 2002-383586/41.
DR N-PSDB; AEN83318.
DR
XX Identifying agent that binds to scavenger receptors and signals through a
PT Toll receptor, useful as carrier or adjuvant in vaccines, promotes a
PT cytotoxic T cell response.
PT
XX Disclosure; Page 58-60; 71pp; French.
PS
XX The present invention relates to a method for identifying new therapeutic
CC compounds (I) by selecting molecules that bind to scavenger receptors and
CC signal through a Toll receptor. The present sequence is the protein
CC sequence for human Toll-like receptor-4, Tlr4, which was used to
CC illustrate the method of the invention. (I) are useful as carriers and/or
CC adjuvants in prophylactic or therapeutic vaccines, particularly where the
CC antigen is derived from a virus, bacterium, yeast, fungus, parasite or
CC tumour cell, especially a pathogen that causes respiratory tract
CC infection, also more generally for inducing an immune response. (I) can
CC also be used for specific targeting of active agents (antigens etc.) to
CC antigen-presenting cells (especially immature dendritic cells), for
CC subsequent internalisation by these cells
CC
SQ Sequence 799 AA;
Query March 95.1%; Score 4141; DB 5; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 41 MELNPKYKPDNL PSTKMLDLSFNPDLRLHLSYSPSPPELOVLDLSRCEIOTIEDGAVOS 100
|||||

Db 1 MELNPKYKPDNL PSTKMLDLSFNPDLRLHLSYSPSPPELOVLDLSRCEIOTIEDGAVOS 60
Qy 101 LSHLSTLLITGNPDIQSIALGAFSGLSLQKLVAVETNLASLENPFIHKLTKELNVAHN 160
Db 61 LSHLSTLLITGNPDIQSIALGAFSGLSLQKLVAVETNLASLENPFIHKLTKELNVAHN 120
Qy 161 LIQSEKLEPEYSNLTNLEHDLSSNKIOSIYCTDLRVLHQPMLNLSIDLINPMNFIOF 220
Db 121 LIQSEKLEPEYSNLTNLEHDLSSNKIOSIYCTDLRVLHQPMLNLSIDLINPMNFIOF 180
Qy 221 GAFKEIRLHKLTNRNPNLSVMKTCIOGLAGLEVHRVLVBEPFRNEGULEKDKALBGL 280
Db 181 GAFKEIRLHKLTNRNPNLSVMKTCIOGLAGLEVHRVLVBEPFRNEGULEKDKALBGL 240
Qy 281 CNLTIEEPRLAYLDYDDIIDLFCNCLTNVSSFSIVSTIRVDFSNFGQHELVNC 340
Db 241 CNLTIEEPRLAYLDYDDIIDLFCNCLTNVSSFSIVSTIRVDFSNFGQHELVNC 300
Qy 341 KFGQFPTLKLSLRKLTFTSNKGGNAFSEVDLPSEFLDLSRNGLSFGCCSQSDPGTTS 400
Db 301 KFGQFPTLKLSLRKLTFTSNKGGNAFSEVDLPSEFLDLSRNGLSFGCCSQSDPGTTS 360
Qy 401 LKYLDLSFNGVITWSSNPLGLEHLDFOHSNKKQSEFVSFLRNLIVLDSHTTR 460
Db 361 LKYLDLSFNGVITWSSNPLGLEHLDFOHSNKKQSEFVSFLRNLIVLDSHTTR 420
Qy 461 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDI FTTELRLNLTFFDLSCQLEOLSPTAFNLS 520
Db 421 VAFNGIFNGLSLEVLKMAAGNSFOENFLPDI FTTELRLNLTFFDLSCQLEOLSPTAFNLS 480
Qy 521 SLOVLNMSHNNPFSLDTFPYKCLNSLOVLDYSLNHIWTSKQOELQHPSSIAFLNLTOND 580
Db 481 SLOVLNMSHNNPFSLDTFPYKCLNSLOVLDYSLNHIWTSKQOELQHPSSIAFLNLTOND 540
Qy 581 FACTCEHOSFLOWKDORQLLVEYERMECAPSPDQGMPLVSLNTCOMNTIIGSVATLS 640
Db 541 FACTCEHOSFLOWKDORQLLVEYERMECAPSPDQGMPLVSLNTCOMNTIIGSVATLS 600
Qy 641 VLVVSVAVLVYKFFHMLLAGCIKYRGENTYDAFYISQDEDMWRNELVKNLEBKV 700
Db 601 VLVVSVAVLVYKFFHMLLAGCIKYRGENTYDAFYISQDEDMWRNELVKNLEBKV 660
Qy 701 PPFOLCHYRDFIPGVAIAANI IHGFKSRKVIIVVSQHFIQSRCIFEYEIAQTWQFL 760
Db 661 PPFOLCHYRDFIPGVAIAANI IHGFKSRKVIIVVSQHFIQSRCIFEYEIAQTWQFL 720
Qy 761 SSRAGIIFIVLOKVEKTLRQOVELYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDGKS 820
Db 721 SSRAGIIFIVLOKVEKTLRQOVELYRLLSRNTYLEWEDSVLGRHIFWRRLKALLDGKS 780
Qy 821 WNPBGTVGTGCMQOATS I 839
Db 781 WNPBGTVGTGCMQOATS I 799

Search completed: March 12, 2005, 19:55:07
Job time : 90.4 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:46 ; Search time 23.0639 Seconds

(without alignments)
2715.523 Million cell updates/sec

Title: US-09-396-985B-98

Perfect score: 4355
Sequence: 1 MMSASRLAGTILIPAMAFISC.....SMNPGTIVGTGCMQNEATSI 839

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4197	96.4	844	4	Sequence 9438, Ap
2	629.5	14.5	661	1	Sequence 4, Appli
3	629.5	14.5	661	1	Sequence 4, Appli
4	599.5	12.4	784	4	Sequence 23, Appli
5	539	12.4	775	4	Sequence 8799, Ap
6	316	7.3	605	3	Sequence 5, Appli
7	305	7.0	605	1	Sequence 10995, A
8	303	7.0	605	1	Sequence 49, Appli
9	303	7.0	605	3	Sequence 49, Appli
10	303	7.0	605	3	Sequence 49, Appli
11	303	7.0	605	4	Sequence 49, Appli
12	303	7.0	605	4	Sequence 49, Appli
13	299.5	6.9	662	4	Sequence 1325, Ap
14	299.5	6.9	662	4	Sequence 6619, Ap
15	299.5	6.9	662	4	Sequence 10710, A
16	299	6.9	662	4	Sequence 10710, A
17	299	6.9	662	4	Sequence 10710, A
18	299	6.9	662	4	Sequence 10710, A
19	299	6.9	662	4	Sequence 10710, A
20	296	6.8	603	1	Sequence 2, Appli
21	296	6.8	603	1	Sequence 2, Appli
22	296	6.8	603	1	Sequence 2, Appli
23	292.5	6.7	907	4	Sequence 50, Appli
24	292.5	6.7	907	4	Sequence 50, Appli
25	289.5	6.6	1112	3	Sequence 264, App
26	289	6.6	1529	3	Sequence 278, App
27	286	6.6	1112	3	Sequence 396, App

28	285	6.5	1523	3	Sequence 2, Appli
29	283.5	6.5	1166	4	Sequence 900, App
30	281	6.5	1091	3	Sequence 2, Appli
31	278	6.4	1091	3	Sequence 2, Appli
32	275	6.3	620	4	Sequence 5, Appli
33	275	6.3	620	4	Sequence 73, Appli
34	275	6.3	620	4	Sequence 73, Appli
35	275	6.3	620	4	Sequence 73, Appli
36	275	6.3	620	4	Sequence 73, Appli
37	275	6.3	620	4	Sequence 73, Appli
38	275	6.3	620	4	Sequence 73, Appli
39	275	6.3	620	4	Sequence 73, Appli
40	275	6.3	620	4	Sequence 73, Appli
41	272	6.2	1480	3	Sequence 7, Appli
42	272	6.2	1480	3	Sequence 7, Appli
43	272	6.2	1480	3	Sequence 7, Appli
44	272	6.2	1480	3	Sequence 7, Appli
45	271	6.2	1139	4	Sequence 2, Appli

ALIGNMENTS

RESULT 1	US-09-949-016-9438	Sequence 9438, Application US/09949016
;	Patent No. 6812339	
;	GENERAL INFORMATION:	
;	APPLICANT: VENTER, J. Craig et al.	
;	TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED	
;	FILE REFERENCE: CLO01307	
;	CURRENT FILING DATE: 2000-04-14	
;	PRIOR FILING DATE: 2000-10-20	
;	PRIOR APPLICATION NUMBER: 60/237,768	
;	PRIOR FILING DATE: 2000-10-03	
;	PRIOR APPLICATION NUMBER: 60/231,498	
;	PRIOR FILING DATE: 2000-09-08	
;	NUMBER OF SEQ ID NOS: 207012	
;	SOFTWARE: FASTSBQ for Windows Version 4.0	
;	SEQ ID NO 9438	
;	LENGTH: 844	
;	TYPE: PRT	
;	ORGANISM: Human	
US-09-949-016-9438		
Query Match	96.4%; Score 4197; DB 4; Length 844;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches	809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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QY	91 QTIIDGAYQSLSTLITLGNPIQSLALGAFSGLSLQKVAWEYNLASLENPIGHLK	150
DB	96 QTIIDGAYQSLSTLITLGNPIQSLALGAFSGLSLQKVAWEYNLASLENPIGHLK	155
QY	151 TLKEINVAHNLIOGFKPEYPSNLTNLEHLDSSNKSIOIYCTDLRVLHQMPLNLSIDL	210
DB	156 TLKEINVAHNLIOGFKPEYPSNLTNLEHLDSSNKSIOIYCTDLRVLHQMPLNLSIDL	215
QY	211 SLNPMNFIQGAPEIRLHKLTNNNDLSLVMTCTIOGLAGLEVHRLVIGEPNENGLLE	270
DB	216 SLNPMNFIQGAPEIRLHKLTNNNDLSLVMTCTIOGLAGLEVHRLVIGEPNENGLLE	275
QY	271 KFDGSALEGCLNLTIEFRFLAYLDYDDIIDLFNCLTNVSSPSLVSTIERVDFSYNF	330
DB	276 KFDGSALEGCLNLTIEFRFLAYLDYDDIIDLFNCLTNVSSPSLVSTIERVDFSYNF	335
QY	331 GWOHLELVNCKFGQFTLKLSLRKLTFTSNKGNNAFSEVDLPSEFLDLSRNGLSFKXG	390

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Db      336  GHOHLELVNCKRQGFPTLKLKSLRTFTSNKGNKAFSEVDLPSEFLDLISRGSLFKGC 395
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Db      396  CSQSDFGTTLKLYLDSFNGCVITMSSNPLGLBOLHLDFOHSLKQMSSESVLSLRNL 455
Qy      451  YLDISTHTRVAVNGIENGSLSEVLKMGNSFOENPLPIFTELNLFTLDSQOLBQ 510
Db      456  YLDISTHTRVAVNGIENGSLSEVLKMGNSFOENPLPIFTELNLFTLDSQOLBQ 515
Qy      511  LSPFANSLSSLOVLMNSHNPFLDTFPYKCLNSLOVDLSLNHINTSKQELQHPPS 570
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Db      636  KTIIGSVLSVAVSVAVLVYKPFHMLLAGCIKRGENTYDAFVYSODEDVRN 695
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RESULT 2

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US-08-514-014-4
; Sequence 4, Application US/08514014
; Patent No. 5707829
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,014
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G16000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-514-014-4

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Query Match      14.5%; Score 629.5; DB 1; Length 661;
Best Local Similarity 29.7%; Pred. No. 5,3e-49;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

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Qy      84  DLSRCEIQTIEDQAYOSLSLSTLILTCNPISLALGAFSGSLQKLVAVETNLASLN 143
Db      83  DLTRQIMNTHEDTTPSHHQSLTVLTGNPLIFMATSLNGPRLSHGLFLQIGISNLEF 142
Qy      144  PPIGHLKTLKEILVAVNHLIQSEKLPYFESNLTNLEHLDSSNKIQSIYCTDLRVLHQMPL 203
Db      143  IPVHNLENLESYLGSNHISIKFPDPFP-ARNLKVLDFQNNAIHYSISREDMRSLEQ--A 199
Qy      204  LNLSDLSLNPMPFQPCAFKEIRLHKTLRNPNFDSLVNWKTCIOGLAGLEVRLVYGEF 263
Db      200  INLSLNFNGNNAVIGILGADSTVFOSL---NFGGTPIUSVFNGLQNSTTOSLWLTGTF 255
Qy      264  RNEGNELEKFDKALIEGLCNLITIEFRLAYLDYLDIID-LFNCLTNVSSFSLSVATIER 322
Db      256  EDIDD-EDISSANLKLCEMSVESLWQ--EHRFSDISSFTFCFQLOGLDLTATHTKG 312
Qy      323  VKDFSNFGQHLIELVN-----CKF--GQFPPL-----KLSLRLLFTSN 361
Db      313  LPS-----GWKGLNLKLVLSVNHFDOLQISANFPSTLHLVIRGNVKKHLGVGCE 367
Qy      362  KGNNAFSEVDLPSEFLDLISRNGLSPFGCCSQSDFGTTLKLYLDSFNGVITMSSN-FLG 420
Db      368  KIGN-----LQTLDSHNDIEASDCCSLQKLSHQTLNLSINEPLGLSQAFKE 418
Qy      421  LEQLEHLDFO-----HSNLKQMSSEFS--VPLSLNRLY--LDISHTHTRVAVNGIENGLSS 472
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Qy      473  LEVLRKAGNSFOENPL--PIFTELNLFTLDSQOLBOLSPAFNLSLSLOVLMNSH 530
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RESULT 3

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US-08-833-823-4
; Sequence 4, Application US/08833823
; Patent No. 5969093
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc. -- Legal Affairs

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STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,823
FILING DATE: 10-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-823-4

Query Match 14.5%; Score 629.5; DB 2; Length 661;
Best Local Similarity 29.7%; Pred. No. 5.3e-49;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;

25 SWEP-CVEVVPNTYQCEMELNFKIPDNLPSTKNLDSFPLHLGYSFSPPELOVL 83
23 SWDMCKEKEANKTYNCENLGLSEIPDLPPTTEFLERFSPPLTINHRPFSRLMNLFL 82
84 DLSRCEIQTIEDGAYQSLSHSTLILGNPIQSLALGAFSGLSLQVLAVETMLASLEN 143
83 DLTRCQNMWHEHEDFQSHHQLSTVLGTENPLIFMAETSLNPKSLKHLFIQTGISNLF 142
144 FPIGLKTLKELNVAHNLIOFKLPEYFSNLTNLEHDLSSNKIOSIYCTDLRYLHQWPL 203
143 IPVNNLEMLSLVYGSNHSISIKRPOFP-ARNLKVLDFQNNALHYISREMBLEQ-A 199
204 LNLSDLSLPMNFIQGAFFKIRLKLTLNNPDSLNVMKTCIQGLAGLEVHRLVIGEF 263
200 INSLFNNGNNVKGIRLGAFFDSTVFQSL---NFGTNPNSLVIFNGLQNSTTQSLMIGTF 255
264 RNEGNLEKPKSALLEGICNLTEEFRLAYLDYIDDIID-LFNLCLTVSSSLVSVITER 322
256 EDIDDD-EDISSAMKGLCEMSVESLNLQ--EHRPSDISSTTFQCFQLOLDELDTATHLKG 312
323 VKDFSVNFGQHLLELVN-----CKF--GQFPTL-----KLKSLKRLTFTSN 361
313 LPS-----GKGLNLKLKVLVSVNHPDOLCOISANPFSLTHLYIRGNVKKLHGVGCL 367
362 KGNNAFSEVDLPSELFLDSHNGLSFKGCCSQSDFGTTSKLYDLSPNGVITMSSN-FLG 420
368 KLGK-----LQTLDSLHNDIEASDCCSLQKLNLSHLQTLNLSHNEPLGLGQAFKE 418
421 LEOLEHDFQ-----HSLMKQSEFS--VELSLRLIY--LDISHTHRVAFNGIFNGLS 472
419 CPQELHDLAFLRLHINAPQ--SPQNTLHFLQVNLVLYCFDLTSSQH-----LLAGLPV 470
473 LEVLKMAAGNSFOENFL--PDIFTELRLNLTFLDLSQCOLLEQSLPTAFNLSLSIQLVANSN 530
471 LRHLNLKGNHFDQGTITKTNLQTVGSLVLISSCGLLSDQGAFFSLGMSHVDLSHN 530
531 NFF--SLDTIPPY-----KCLNSLQVLDVSLNHNMTSKQELQHPFSSLAFLNLTONDF 581

531 SLTCDSDISLSHLKGIYINLAANSINITISPLRPIL-----SQOSTINLSNPL 579
582 ACTCEHOSFLOWIKDQROQLVEVERMECAPSPDQMPVLSTNTCCNNKIIIGSVLSV 641
580 DCTCSNHFLLTWYENHKLKLGSEBETTCANPPLRGVLSLVKSLCGI--TAIGIFLIV 637
642 LVSVVAVLVY 652
638 FLT-LTALILF 647

RESULT 4
US-09-982-308B-23
Sequence 23, Application US/09982308B
Patent No. 6531290
GENERAL INFORMATION:
APPLICANT: Daile, Barbara
APPLICANT: Fan, Xuedong
APPLICANT: Lundell, Daniel
APPLICANT: Lunn, Charles A.
APPLICANT: Tan, Jimmy C.
APPLICANT: Zavodny, Paul J.
TITLE OF INVENTION: Mammalian TNF-alpha Convertases
FILE REFERENCE: JB0601QC
CURRENT APPLICATION NUMBER: US/09/982,308B
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/156,163
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 08/889,909
PRIOR FILING DATE: 1997-07-10
PRIOR APPLICATION NUMBER: 60/021,710
PRIOR FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 784
TYPE: PRT
ORGANISM: Homo sapiens
US-09-982-308B-23

Query Match 13.8%; Score 599.5; DB 4; Length 784;
Best Local Similarity 27.0%; Pred. No. 4.1e-46;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

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46 IPSGLTRAVKSLDSNNRITYISNSDLQRCVNLQALVLTSGNITIEDSFSSLSLHL 105
108 ILTGNPIQSLALGAFSGLSLQKL-----VAVETNLASLENFPIGHLKT----- 151
106 DLSVNTLSNLSMSSFKLSLTLFLNLGNYKYTLGERSLSLHLTKQLIRGNNDTPTKI 165
152 -----LKEIVANHLIOFKLPEYFSNLTNLEHDLSSNK-----IQSI 190
166 QKQDFAGLTLELEIDASDLQSYE--PKSLKIQNVSHLILHMKQHLILLEIFVDVTSSV 224
191 YCTDLRYLHQWPLNLSDLSLPMNFIQGAFFKIRLKLTLN--NFDL--NVMK 244
225 ECLLELR-----DLDLDTFHFSELSSTGTSNLSLTKKTFRNKVTDESDFQWVK 271
245 TC--IQGLAGLEVHRLV-----GEFRNENLEKPKSALLEGICNLTEEFRLA--YLDYVL 297
272 LNLGSLLELEPDDCTLNGVGNFRASDNRVIDPKVFE--TLTIRRHIPRYLVY-- 326
298 DDIIDLFNCLTNVSSFEVSVTTERVQDFSYNFGWQHLVYNCKFGQFPPLKLSLRKT 357
327 -DLSTLYSLTERVK-----RITVNSKVF-----LVPCLLSQ----- 357
358 FTSNKGNAFSEVDLPSELFLDSHNGLSFKGCCSQSDFGTTSKLYDLSPNGV 412
358 -----HLSLSEYLDUSENLVMEYLNKNSAC-----EDAWPSTQTLIRON--- 397

QY 93 IEDAYOSLSHSLTILITGNPIQSIALGAFS-----GLSSL 128
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QY 129 OKUAVETNLASLENPIGHLKTKELNVAHNLIOGFKLPEYFSNTLNLEHLDSSNKIQ 188
DB 173 WDLNIGNNSLAVLPRAAFGLGGLRELVLAGNRL-AYIQPALFSGLAELRELDSSRAALR 231
QY 189 SIYCTDLRVLHQPPLNLISLDSLNPMNFIOGAFKEIR-LHKLTLRNNFDSLNAVKTICI 247
DB 232 AI-----KANVFQOLPRLQ-KLYIDRLNLAIVAPGALIGKALRWLDLSHN-RVAGLLEDPTF 286
QY 248 OGGLAEVHRVLVSGFRNEGNLEKFDKALBGLCNLTIEFRLAYLDYLDIDLENCIL 307
DB 287 PGLGLRLVRL-----SHNAIASLRPTFEDL-----HFLEEL----- 319
QY 308 TNVSFSLVSVTIEVKDPSYNGMQLHVLNCKGQFPPLTKLSIKRLTPTS--NKGN 365
DB 320 -----QIGHNRIRQLAERSFE-GLGQLEVLTLDNQLOEVKVGFLGLTNVAVNLSGN 372
QY 366 AFSEVDLPSELEFLDSR-NGLSFKGCC-----SQSDFGTTSIKYDLSFNGVITWSSNPL 419
DB 373 CLR--NLPEQVFRGLKLSHLBSSCLGRIRPHFTAGLSGLRRLFLKONGLVGIEBQSL 430
QY 420 -GLEQLEHLDPOHSNKKOMSEPSVFLSLNLIYLDISHTTRVAFNGIFNGLSLEVLKM 478
DB 431 WGLLELELDLTSNQL-----THLP--HOLFQGLKLEVLTL 465
QY 479 AGNSFOENFLP-DIFTELRLNFLDLSCOLEBOLSPFAFNSLSLOVNMHNNFSLDT 537
DB 466 SHNRLAE--LPADALGPLQRAFWLDVSHNRLEBALGSLASIGRLRYLNRN--SLRT 520
QY 538 PPKYCLNSLOVLDYSLNIMTSKKOELHFPSSLAFLNLTONDFACTCEHOS----- 589
DB 521 FTPO-----PGLERLWLEGNPMWCSCPLALRDPALON 554
QY 590 -----FLOWT--XDRQLVEVERMECATPSDKQMPVLST 623
DB 555 PSAVPRFVOAICEGDDCQPPVYTYNNITCASPEEVAAGLDRL 597

RESULT 7
US-09-949-016-10995
; Sequence 10995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 10995
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10995

Query Match 7.0%; Score 305; DB 4; Length 623;
Best Local Similarity 24.3%; Pred. No. 4.4e-19;
Matches 171; Conservative 96; Mismatches 260; Indels 178; Gaps 28;

QY 4 ASRLA---GTLLIPMAFLSCVR--PESME-----PCV-----EVVPVIT 37
DB 16 ACNVALRKGLALAILLISLWVALGRSLLEGADPGTGRGABGPACPAACVCSYDDADBELS 75

QY 38 YQCELNLFYKIPDNLPESTKNLDSFNPRLHGSYSFFSPPELOVLDSRCEIQTIEDGA 97
DB 76 VFCSSRNRLTRPDGVPGGGTQALMTLDGNNLSVPPRAAFQNLISGLFNLQGGQISLEPQA 135
QY 98 YQSLSHSLTILITGNPIQSIALGAFS-----GLSSIQKVA 133
DB 136 LIGLENLCHLHERNOLRSIAGVFAFPALALLGLSNNRLSRLEDGLFEGLSNTL 195
QY 134 VETNLASLENPIGHLKTKELNVAHNLIOGFKLPEYFSNTLNLEHLDSSNKIQSIYCT 193
DB 196 GMSNLAVLPDAAPFGLSRLRELVLAGNRL-AYIQPALFSGLAELRELDSSRAALR 251
QY 194 DLRYLHQPPLNLISLDSLNPMNFIOGAFKEIR-LHKLTLRNNFDSLNAVKTICIQIAG 252
DB 252 KANVFQOLPRLQ-KLYIDRLNLAIVAPGALIGKALRWLDLSHN-RVAGLLEDPTFGLLG 309
QY 253 LEVHRVLVGEFRNEGNLEKFDKALBGLCNLTIEFRLAYLDYLDIDLENCILTNVSS 312
DB 310 LRVLR-----SHNAIASLRPTFEDL-----HFLEEL----- 337
QY 313 FSLVSVTIEVKDPSYNGMQLHVLNCKGQFPPLTKLSIKRLTPTS--NKGNAPSEV 370
DB 338 -QIGHNRIRQLAERSFE-GLGQLEVLTLDNQLOEVKVGFLGLTNVAVNLSGNCLR-- 393
QY 371 DLPSELEFLDSR-NGLSFKGCC-----SQSDFGTTSIKYDLSFNGVITWSSNPL-GLEQ 423
DB 394 NLPEQVFRGLKLSHLBSSCLGRIRPHFTAGLSGLRRLFLKONGLVGIEBQSLMGLAE 453
QY 424 LEHLDPOHSNKKOMSEPSVFLSLNLIYLDISHTTRVAFNGIFNGLSLEVLKMAAGSF 483
DB 454 LLELDLTSNQL-----THLP--HOLFQGLKLEVLTLISRRRL 488
QY 484 QENFLP-DIFTELRLNFLDLSCOLEBOLSPFAFNSLSLOVNMHNNFSLDTFPYKC 542
DB 489 AE--LPADALGPLQRAFWLDVSHNRLEBALGSLASIGRLRYLNRN--SLRTFTQ- 542
QY 543 LNSLOVLDYSLNIMTSKKOELHFPSSLAFLNLTONDFACTCEHOSFIQKID----- 596
DB 543 -----PGLERLWLEGNPMWCSCPLALRDPALON 573
QY 597 ---ORQLVEVERMECATPSDKQMPVLISLITCOMAKTITIGSV 638
DB 574 SAVPRFVOAICEGDDCQPPVYTYNNITCASPEEVAAGLDRL 612

RESULT 8
US-08-190-802A-49
; Sequence 49, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49

Query Match 7.0%; Score 303; DB 1; Length 605;
Best Local Similarity 24.4%; Pred. No. 6.4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

QY 40 CMEINFKYKIDNLPSTKNDLSFNPRLHLSYSFSPFPELQVLDLSRCETQTEDGAYQ 99
DB 60 CSSRNLTRLDPDGVGGTQALWLDGNLSSVPPAFAQNLSSLGFLNLQGGSLDEPQALL 119
QY 100 SLSHLSTLITGNPIQSIALGAFS-----GLSLOQLVAVE 135
DB 120 GLENLCHLHLEARNQRLSLAGTPAHTPALSLGLSNRRSLDEGLFEGGLSMDNLGW 179
QY 136 TNLASLENFPIGHLKTLELVANHLIQSFLLPEYFSNLTNLEHLDSNNKIOSICTDL 195
DB 180 NSLAVLPDPAFRGSLRELVLAGNRL-AYLQPALFSGIAELRELDLSRNALRAI---KA 235
QY 196 RVLHQPMLNLSDLSINPNFIOGAFAKEIR-LHKLTLRNNFDSLVNMTKCIQGLAGLE 254
DB 236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFGLKALRWLDLSHN-RVAGLLBDFTPFGLGLR 293
QY 255 VHRVLVGEFNRNENLEKFDKSLAEGLCNLITIEFRLAYLDYLDIIDLFWCLTNVSSFS 314
DB 294 VLRL-----SHNAIASLRPRTFKDL-----HFLBEL-----Q 320
QY 315 LVSTTERVDFSYNFCQHLLELVNCKFGQFPTLKLSKRLFTTS--NKGNAFSEVDL 372
DB 321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNOQAEVYAGAFGLTIVVAVMNLISGNCLR--NL 377
QY 373 PSLEFLDLNR-NGLSFKGCC-----SOSDFGTTSLKYLDLSFNGVITMSSNPL-GLEROLE 425
DB 378 PEQVFRGLGKHSIHLBSSCLGRIRPHTFTLSGLRRLFKONGLVGIEGSLWGLAELL 437
QY 426 HLDFOHNLKQMSSEFVFLSLRNLIVLDSHTTRVAFNGIFNGLSLEVLKMGAGNSFOE 485
DB 438 ELDTLSNQL-----THLP--HRLFOGLKLELYLLSRNLAE 472
QY 486 NPLP-DIFTELRNLTFLDLSQQLSEQLSPAFNSLSLQVLMGSHNFFSLDTPPYKCLN 544
DB 473 --LEPADLGLPQRAFMLDVSHNRLLEALPNSLAPLGLRLRYLSRNN--SLRTFTPQ--- 524
QY 545 SLQVLDVSLNHNIMSKQELQHPSSSLAFNLVTQNDPACTCEHOSFLQWID----- 596
DB 525 -----PPGLERLWLEGNPMDCGP-----LKALRDPALQNPISA 557
QY 597 -QROLIVERMEGATPSDKQMPVLSINITCQNNKTIIGVS 638
DB 558 VPRVQALCEGDDCQPRAYTNN-----NITCASPPREVAGIDL 594

RESULT 9
US-08-477-346-49
Sequence 49, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Roester
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-477-346-49

Query Match 7.0%; Score 303; DB 3; Length 605;
Best Local Similarity 24.4%; Pred. No. 6.4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

QY 40 CMEINFKYKIDNLPSTKNDLSFNPRLHLSYSFSPFPELQVLDLSRCETQTEDGAYQ 99
DB 60 CSSRNLTRLDPDGVGGTQALWLDGNLSSVPPAFAQNLSSLGFLNLQGGSLDEPQALL 119
QY 100 SLSHLSTLITGNPIQSIALGAFS-----GLSLOQLVAVE 135
DB 120 GLENLCHLHLEARNQRLSLAGTPAHTPALSLGLSNRRSLDEGLFEGGLSMDNLGW 179
QY 136 TNLASLENFPIGHLKTLELVANHLIQSFLLPEYFSNLTNLEHLDSNNKIOSICTDL 195
DB 180 NSLAVLPDPAFRGSLRELVLAGNRL-AYLQPALFSGIAELRELDLSRNALRAI---KA 235
QY 196 RVLHQPMLNLSDLSINPNFIOGAFAKEIR-LHKLTLRNNFDSLVNMTKCIQGLAGLE 254
DB 236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFGLKALRWLDLSHN-RVAGLLBDFTPFGLGLR 293
QY 255 VHRVLVGEFNRNENLEKFDKSLAEGLCNLITIEFRLAYLDYLDIIDLFWCLTNVSSFS 314
DB 294 VLRL-----SHNAIASLRPRTFKDL-----HFLBEL-----Q 320
QY 315 LVSTTERVDFSYNFCQHLLELVNCKFGQFPTLKLSKRLFTTS--NKGNAFSEVDL 372
DB 321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNOQAEVYAGAFGLTIVVAVMNLISGNCLR--NL 377
QY 373 PSLEFLDLNR-NGLSFKGCC-----SOSDFGTTSLKYLDLSFNGVITMSSNPL-GLEROLE 425

Db 378 PEQVTRGKGLKSHLBSGCLGRIRPHITGSLRRLFLKONGLVGIEQSLWGLAEIL 437
Qy 426 HLDFOHSLNKKOMSEFSVFLSLRNLIYLDISHTRVAFNGIIPNGSLSEVLKMAQNSFOE 485
Db 438 ELDLTSNQL-----THLP---HRLFGQGLKLEYLLSRRLAE 472
Qy 466 NFLP-DITFELRNLTFLDLSQCQLEQSLPTAFNSLSLQVLMNSHNPFLDTFPYKCLN 544
Db 473 --LPADALGPLORAFWLDVSHNRLEALPNSLAPLGRRLYSLRN--SLRTFTPO--- 524
Qy 545 SLQVLDYSLNHTMTSKQELQHPSSLAFNLTONDPACTCHQSLQWIKD----- 596
Db 525 -----PGLERLMLEGNPMWDCGP---LKALRDPALONPSA 557
Qy 597 -QROLIVERMECATPSDKQGMPLYSLNITCOMNKTIIIGSV 638
Db 558 VRFVQALCEGDDCCPAPATYN-----NITCASPEVVGDL 594

RESULT 10

US-08-473-089-49
; Sequence 49, Application US/08473089
; Patent No. 642368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-473-089-49

Qy Query Match 7.0%; Score 303; DB 3; Length 605;
Best Local Similarity 24.4%; Pred. No. 6.4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;
Db 40 CMEILFYKIDNLTPESTKLDLSPNLRHLSYSPFPELQVLDLSRCEIOTIDGAVQ 99
60 CSSRLTRLPDGVPGTQALWLDGNLSSVPPALFQNLSSGLFTNLQGGQLDGLSEPOLLL 119

Qy 100 SLSHLSTLITGNPIQSIALGAFS-----GLSLQKLVAVE 135
Db 120 GLENLCHLHBERNQRLSIALGTFAPTPALASLGLNNRSLRLEDGLFEGLSLMDLNLGM 179
Qy 136 TWLASLENPFICHLTKLKEINAVANHLIOSFLPERFSUNLTNEHLDLSNKLQSIYCTDL 195
Db 180 NSLAVALPPAAFPGLSLRELVLAGNRL-AYLQPALFSGLAERELDSNNALRAI---KA 235
Qy 196 RVLHOMPLNLSLDLSLNPMPNFIQGAFAKEIR-LKHLTLRNNPDSLNWKTCTIOGLAGE 254
Db 226 NVFVLDPLQLQ-KLYDRKLLIAVAAGAFGLKALWLDLSH-RVAGLIEDTFPGLIGLR 293
Qy 255 VHRVLVGFERNENLEKEDKSLBGLCNLTIEFPRLAYLDYLDIIDLFNCLTNVSSFS 314
Db 294 VLRL-----SHNAIASLRPRFKDL-----HFLERL-----Q 320
Qy 315 LVSVTIERKQPSYVNGQHLELVNCKGQFPFTLKLKSLKLTFTS--NKGNAFSEVNL 372
Db 321 LGHNRIRQLAERSFE-GLGQLEVLTLDNQLOEVAGAFGLGTNVAVMNLGNCUR--NL 377
Qy 373 PSLFPLDLSR-NGLSFFKGC-----SOSDPGTTSLKYLDLSPNGVITMSSNFL-GLBOLE 425
Db 378 PEQVTRGKGLKSHLBSGCLGRIRPHITGSLRRLFLKONGLVGIEQSLWGLAEIL 437
Qy 426 HLDFOHSLNKKOMSEFSVFLSLRNLIYLDISHTRVAFNGIIPNGSLSEVLKMAQNSFOE 485
Db 438 ELDLTSNQL-----THLP---HRLFGQGLKLEYLLSRRLAE 472
Qy 466 NFLP-DITFELRNLTFLDLSQCQLEQSLPTAFNSLSLQVLMNSHNPFLDTFPYKCLN 544
Db 473 --LPADALGPLORAFWLDVSHNRLEALPNSLAPLGRRLYSLRN--SLRTFTPO--- 524
Qy 545 SLQVLDYSLNHTMTSKQELQHPSSLAFNLTONDPACTCHQSLQWIKD----- 596
Db 525 -----PGLERLMLEGNPMWDCGP---LKALRDPALONPSA 557
Qy 597 -QROLIVERMECATPSDKQGMPLYSLNITCOMNKTIIIGSV 638
Db 558 VRFVQALCEGDDCCPAPATYN-----NITCASPEVVGDL 594

RESULT 11

US-08-487-072A-49
; Sequence 49, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-487-072A-49

Query Match 7.0%; Score 303; DB 4; Length 605;
Best Local Similarity 24.4%; Pred. No. 6,4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

QY 40 CMEINFYKIPDNLPSTKNDLSFNPRLHLSGYSFFSPPELOVLDLSRCEIQTIEDGAYQ 99
DB 60 CSSRNLTRLPDGVPGEGTQALMDGNNLSVPPAFQNLSSLGFLNLQGGQLGLEPQALL 119
QY 100 SLSHLSTLLTNGNPISQALGAFS-----GLSSLOQLVAVE 135
DB 120 GLENLCHLHBERNQRLSALGTFAHPALASIGLSNNRLSRLEDGLFGLSLMDNLNGW 179
QY 136 TNLASLENFPFGHLYKTLKELVAVANLISFCLPEYFSNLTNLEHLDLSNNKIQSYCTDL 195
DB 180 NSLAVLPDPAARFGSLRLVLAAGNRL-AYLQPALFSGLAELRELDLSRNLRLA---KA 235
QY 196 RYLHOMPLNLNLDLSLNPANFIQGAFAKEIR-LHKLTIRNPNDSLNVKTCIQGLAGLE 254
DB 236 NVFVQLPRLQ-KLYIDRLNLIAAVAPGAFGLKALRWLDLSHN-RVAGLLEDTFFGLGLR 293
QY 255 VHRVLGSEFRNENLEKFDKSLBGLCNLTIEFRLAYLDYLDIIDLFNCLTNVSSFS 314
DB 294 VLRL-----SHNAIASLRPRTFKDL-----HFLEEL-----Q 320
QY 315 LVSVTIERVKDPSYNGMQLHLELVNCKFGQPTLTKLSLKRUTFTS--NKGNAPSEVDL 372
DB 321 LGHNRIRQLAERSFE-GIGQLEVLTLDNQLOEYVAGAFGLITNVAVNNLSGNCUR--NL 377
QY 373 PSLEFLDLSR-NGLSFKGCC-----SOSDFGTTSLKYLDLSFNGVITWSSNFL-GLBQLE 425
DB 378 PEQVFRGKGKLSHLBESSCLGRIRPHFTGSLGRRLFLKDNGLVGEESQSLWGLABLL 437
QY 426 HLDPQHSNLKOMSEBSVFLSLRNLIYLDISHTTRVAFNGLFNGLSLEVLKMAGNSFOE 485
DB 438 ELDLTNSQL-----THLP--HRLFOGKGLKLEYLLSHNRILAE 472
QY 486 NFLP-DITFELRNLTFLDLSQCOLEQSLPTAFNSLSLQVLNMSHNNPFSLDTPPYKCLN 544
DB 473 --LPADALGPLQRAFWLDVSHNRLEALPNSLIAPGRIRYLSLRNN--SLRTFPPQ--- 524
QY 545 SLQVLVDYSLNHNIMTSKQELQHPSSLAFLNLTQDNFACGEOHOSFLOMIXD----- 596
DB 525 -----PPGLERLWLEGNPMWCGCP-----LKALRDFALQNSA 557
QY 597 -QROLIVEVERMECATPSDKQGMPLVSLNITCQNNKTIIGVSV 638
DB 558 VPRFVQALCEGDDCQPPAYTN-----NITCASPPEVVGDL 594

RESULT 12
US-09-538-092-1087
Sequence 1087, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/176,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: Curataseqformatter Version 0.9
SEQ ID NO 1087
LENGTH: 605
TYPE: prt
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087

Query Match 7.0%; Score 303; DB 4; Length 605;
Best Local Similarity 24.4%; Pred. No. 6,4e-19;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

QY 40 CMEINFYKIPDNLPSTKNDLSFNPRLHLSGYSFFSPPELOVLDLSRCEIQTIEDGAYQ 99
DB 60 CSSRNLTRLPDGVPGEGTQALMDGNNLSVPPAFQNLSSLGFLNLQGGQLGLEPQALL 119
QY 100 SLSHLSTLLTNGNPISQALGAFS-----GLSSLOQLVAVE 135
DB 120 GLENLCHLHBERNQRLSALGTFAHPALASIGLSNNRLSRLEDGLFGLSLMDNLNGW 179
QY 136 TNLASLENFPFGHLYKTLKELVAVANLISFCLPEYFSNLTNLEHLDLSNNKIQSYCTDL 195
DB 180 NSLAVLPDPAARFGSLRLVLAAGNRL-AYLQPALFSGLAELRELDLSRNLRLA---KA 235
QY 196 RYLHOMPLNLNLDLSLNPANFIQGAFAKEIR-LHKLTIRNPNDSLNVKTCIQGLAGLE 254
DB 236 NVFVQLPRLQ-KLYIDRLNLIAAVAPGAFGLKALRWLDLSHN-RVAGLLEDTFFGLGLR 293
QY 255 VHRVLGSEFRNENLEKFDKSLBGLCNLTIEFRLAYLDYLDIIDLFNCLTNVSSFS 314
DB 294 VLRL-----SHNAIASLRPRTFKDL-----HFLEEL-----Q 320
QY 315 LVSVTIERVKDPSYNGMQLHLELVNCKFGQPTLTKLSLKRUTFTS--NKGNAPSEVDL 372
DB 321 LGHNRIRQLAERSFE-GIGQLEVLTLDNQLOEYVAGAFGLITNVAVNNLSGNCUR--NL 377
QY 373 PSLEFLDLSR-NGLSFKGCC-----SOSDFGTTSLKYLDLSFNGVITWSSNFL-GLBQLE 425
DB 378 PEQVFRGKGKLSHLBESSCLGRIRPHFTGSLGRRLFLKDNGLVGEESQSLWGLABLL 437
QY 426 HLDPQHSNLKOMSEBSVFLSLRNLIYLDISHTTRVAFNGLFNGLSLEVLKMAGNSFOE 485
DB 438 ELDLTNSQL-----THLP--HRLFOGKGLKLEYLLSHNRILAE 472
QY 486 NFLP-DITFELRNLTFLDLSQCOLEQSLPTAFNSLSLQVLNMSHNNPFSLDTPPYKCLN 544
DB 473 --LPADALGPLQRAFWLDVSHNRLEALPNSLIAPGRIRYLSLRNN--SLRTFPPQ--- 524
QY 545 SLQVLVDYSLNHNIMTSKQELQHPSSLAFLNLTQDNFACGEOHOSFLOMIXD----- 596
DB 525 -----PPGLERLWLEGNPMWCGCP-----LKALRDFALQNSA 557
QY 597 -QROLIVEVERMECATPSDKQGMPLVSLNITCQNNKTIIGVSV 638
DB 558 VPRFVQALCEGDDCQPPAYTN-----NITCASPPEVVGDL 594

RESULT 13
US-09-538-092-1325
Sequence 1325, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 FILE REFERENCE: 1596-542
 CURRENT APPLICATION NUMBER: US/09/538,092
 PRIOR FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 60/127,352
 PRIOR FILING DATE: 1999-04-01
 PRIOR APPLICATION NUMBER: 60/178,965
 PRIOR FILING DATE: 2000-02-01
 NUMBER OF SEQ ID NOS: 1387
 SOFTWARE: CurataseqFormatter Version 0.9
 SEQ ID NO 1325
 LENGTH: 662
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (0)-(0)
 OTHER INFORMATION: Polypeptide Accession Number Q14392
 US-09-538-092-1325

Query Match 6.9%; Score 299.5; DB 4; Length 662;
 Best Local Similarity 25.9%; Pred. No. 1.6e-18;
 Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

QY 28 PCVEVPNTTYQCEHNFYKIPDNLPSSTKNDLSFNPRLHIGSYSPFPELOVLDLSR 87
 DB 25 PCWVDKKVS--CQVLLGVPSVLPDTEITLDSGNQRLSLASPLGFYALRLHLDST 82
 QY 88 CEIOTIEDGAYOSLSHTLLITGNPIQSLALGAFSGISLQKLVAVETNLAS-----LE 142
 DB 83 NEISFLQPGAFQALTHEHLSLHNRRLMATALSAGIGPPLRYVSLDLSGNSLYSGGLE 142
 QY 143 NFPIGHLKTLKELVANHLIOSFKLPEY-PSNLTNLEHLIDSSNKIOSICTDLRVLHOM 201
 DB 143 RL-LGEAPSLHTLSLAENSLT--RLTRHTFDMALBEQDLHNSVLMIEDGAFEGPLRL 199
 QY 202 PLNLIS-----LDLSINPMNFI--QPGAFKEIRLHKLTLRNN----- 236
 DB 200 THLMISRSNLTCISDFSLQQLRVLDLSCNSIEAFQTASQPOA--EFQLTWLDLRENKLLH 257
 QY 237 FDSLNVMKTCIQGLAGLEVHRLVGEFRN-----EGNLEKDKGAL 277
 DB 258 FPDLAALPRLIYLLNSNNLIRLPTGPPQDSKGIAHAPSGWALPLSAPSGNAGRPLSQ 317
 QY 278 EGLCNLTIEEFLAYLDYLDIDLF-----NCLTNVSSFSLVSVTIERVKDFSYNFG 331
 DB 318 LNL-DLSYNEIEL-IPDSFLEHLTSLCFNLNSRCLRTFEARRLGSLPCLMLDLSHN-A 374
 QY 332 WQHELVNCKRGQPTLTKLSLKRLLFTFSNKGNAFSEV-----DLPSLEFLDLSRNGL 385
 DB 375 LETLELGARALGSLRTLLQ-----GNALRLDPPYTPANLASLQRLNIQGRV 422
 QY 386 S-----FKGCCSOSDFGTTSLKYLDLSFNGVITWSSNPLGLEQLEHLDFOHSNKKQ 436
 DB 423 SPCCGPDEPGSGCVAFS--GITSRLRSLSLVNDEI-----ELLRAGAFHTPLTE 470
 QY 437 MSEBSVFLSLRNLIYLDISHTHTRVAENGIFNGI--SLEVLKMAGNSFQ--ENFLPDIFT 493
 DB 471 -----LDLSSNPGLEVATGALGLEASLEVALAQNGIMLVQVLDLPCFTIC 515
 QY 494 ELRLNLTPLDLSQCELEQSPAFNSLSLOVLMNSHNNFSLDTPPYKCLNSLOVLDVSL 553
 DB 516 -----LKRNLINLENLSHL--PAWTOAVSLLEVLDL--RNNFSFL--LPGSAMGGLB----- 560
 QY 554 NHMTSKQELQHPSSSLAFNLTONDPACTCEHOSFLQWIKDQ--RQLLYVERKE---C 609
 DB 561 -----TSLRLLYLQGNPLSC--CGN-----GWLAAQQLHQRVVDVATQDLIC 600
 QY 610 ATPSDQGMPIVLSINIT---COMM--KTIIGSVSLVAVSVAVLVYKFFPHMLLAG 663
 DB 601 RFSQOE-----VLSHVAPDECEKGLKNIMLIIITLITVSAII-----LTTLLA 647

QY 664 C 664
 DB 648 C 648

RESULT 14
 US-09-949-016-6619
 Sequence 6619, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMOORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01307
 CURRENT APPLICATION NUMBER: US/09/949,016
 PRIOR FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 6619
 LENGTH: 662
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-6619

Query Match 6.9%; Score 299.5; DB 4; Length 662;
 Best Local Similarity 25.9%; Pred. No. 1.6e-18;
 Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

QY 28 PCVEVPNTTYQCEHNFYKIPDNLPSSTKNDLSFNPRLHIGSYSPFPELOVLDLSR 87
 DB 25 PCWVDKKVS--CQVLLGVPSVLPDTEITLDSGNQRLSLASPLGFYALRLHLDST 82
 QY 88 CEIOTIEDGAYOSLSHTLLITGNPIQSLALGAFSGISLQKLVAVETNLAS-----LE 142
 DB 83 NEISFLQPGAFQALTHEHLSLHNRRLMATALSAGIGPPLRYVSLDLSGNSLYSGGLE 142
 QY 143 NFPIGHLKTLKELVANHLIOSFKLPEY-PSNLTNLEHLIDSSNKIOSICTDLRVLHOM 201
 DB 143 RL-LGEAPSLHTLSLAENSLT--RLTRHTFDMALBEQDLHNSVLMIEDGAFEGPLRL 199
 QY 202 PLNLIS-----LDLSINPMNFI--QPGAFKEIRLHKLTLRNN----- 236
 DB 200 THLMISRSNLTCISDFSLQQLRVLDLSCNSIEAFQTASQPOA--EFQLTWLDLRENKLLH 257
 QY 237 FDSLNVMKTCIQGLAGLEVHRLVGEFRN-----EGNLEKDKGAL 277
 DB 258 FPDLAALPRLIYLLNSNNLIRLPTGPPQDSKGIAHAPSGWALPLSAPSGNAGRPLSQ 317
 QY 278 EGLCNLTIEEFLAYLDYLDIDLF-----NCLTNVSSFSLVSVTIERVKDFSYNFG 331
 DB 318 LNL-DLSYNEIEL-IPDSFLEHLTSLCFNLNSRCLRTFEARRLGSLPCLMLDLSHN-A 374
 QY 332 WQHELVNCKRGQPTLTKLSLKRLLFTFSNKGNAFSEV-----DLPSLEFLDLSRNGL 385
 DB 375 LETLELGARALGSLRTLLQ-----GNALRLDPPYTPANLASLQRLNIQGRV 422
 QY 386 S-----FKGCCSOSDFGTTSLKYLDLSFNGVITWSSNPLGLEQLEHLDFOHSNKKQ 436
 DB 423 SPCCGPDEPGSGCVAFS--GITSRLRSLSLVNDEI-----ELLRAGAFHTPLTE 470
 QY 437 MSEBSVFLSLRNLIYLDISHTHTRVAENGIFNGI--SLEVLKMAGNSFQ--ENFLPDIFT 493
 DB 471 -----LDLSSNPGLEVATGALGLEASLEVALAQNGIMLVQVLDLPCFTIC 515
 QY 494 ELRLNLTPLDLSQCELEQSPAFNSLSLOVLMNSHNNFSLDTPPYKCLNSLOVLDVSL 553
 DB 516 -----LKRNLINLENLSHL--PAWTOAVSLLEVLDL--RNNFSFL--LPGSAMGGLB----- 560

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QY 554 NHMTSKKQELQHPSSLAFLNLTQNDFACTCEHQSFLOWIKDQ-ROLVYVERME---C 609
DB 561 -----TSLRLYLQGNPLSC-CGN---GMLAQLOHGRVDVDTQDLIC 600
QY 610 ATPSDKQMPVLSLNTIT---CQMN--KTIIGSVLSVLVSVVAVLVYKFFPHMLLAG 663
DB 601 RFSQGE---VLSHVRPDECKGGLKNINLIIILFFILVSAIL-----LTTLAA 647
QY 664 C 664
DB 648 C 648

RESULT 15
US-09-949-016-10710
; Sequence 10710, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10710
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10710

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Query Match 6.9%; Score 299.5; DB 4; Length 665;

Best Local Similarity 25.9%; Pred. No. 1.6e-18;

Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

```

QY 28 PCVEVFNITVQCMELNFYKIPDNLPSTKNLDSFNPLRHLSGSYFSPPELQVLDLSR 87
DB 28 PCRVVDKVS--CQVYGLQVPSVLPPTETLIDLSGNQIRSLAPLGFTALRLHLDST 85
QY 88 CEIQIEDGAYQSLHSLTLLITGNPISLALGAFSGLSLQKIVAVETNLAS----LE 142
DB 86 NEISFLQGFALQTLHSLHSLAHNRAMATLMSAGLGPLRVTSLDLSGNSLYSGLL 145
QY 143 NFPYGLTKLKELVANVHNLQSFKLPY-FSNLTNLEHLDSNKLQSIYCTDLRVLMOM 201
DB 146 RL-LGEAPSLHTLSAENSLT--RLTRHTFRDMPALQDLHNVLMIDIEDGAFEGRL 202
QY 202 PLNLS-----LDLSNPMNFI---QGAKEIRLHKLTLRNN----- 236
DB 203 THNLSRSLTISPSIQQLRAVDLSCNSIFAFOIASQPOA--EFQLTWDLRENKXLIH 260
QY 237 FDSLNVMTKCIQGLAGLEVHRLVIGFRN-----EGNLEKFKSAL 277
DB 261 FPDIALAPRLIYLNNSNMLIRLPTGPPODSKGIHAPSEGMSALPLSAPSGNASGRPLSOL 320
QY 278 BGLCVLTIBERFLAVLDYLDITDILF-----NCLTNVSSPSLYSVTIERVKDFSYNFG 331
DB 321 INT-DLSYVEIEL-IPDSFLEHLSLCPNLNRCNLRTEPEARIGSLPCLMLDLSHN-A 377
QY 332 WQHLFVNCKFGQFPFLTKLSKRLTFTSNKGNAFSEV-----DLPSEFLDLSRNGI 385
DB 378 LETLEIGARALGSLRTLLIQ-----GNALRDLPPYTPANTLASLQRIANIQGNRV 425
QY 386 S-----FKGCCSQSDFGTTSIKYLDLSFNGVITWSSNPLGLEQLEHLDFOHSNLKQ 436

```

```

DB 426 SPCGPDDEPGSGCVAFS--GITSLSLSLVNIEI-----ELLRGAFLHTPLTE 473
QY 437 MSFVSFVLSLRNLIYLDISHHTTRVAFNGIFNGI--SLSEVLKXAGNSFQ--ENFLPDIPT 493
DB 474 -----LDLSNPLGLEVAATGALGLESLEVLALQNGIAMLQVLDLPCFIC 518
QY 494 ELRNLTFLDISQCLBQLSFTAFNSLSLQVLMASHNPFSLDTPPYKCLNSIQVLDYSL 553
DB 519 ----LKRINLAENRISHL--PAWTOAVSLEVIDL--RNSPSL--LPGSAMGILE----- 563
QY 554 NHMTSKKQELQHPSSLAFLNLTQNDFACTCEHQSFLOWIKDQ-ROLVYVERME---C 609
DB 564 -----TSLRLYLQGNPLSC-CGN---GMLAQLOHGRVDVDTQDLIC 603
QY 610 ATPSDKQMPVLSLNTIT---CQMN--KTIIGSVLSVLVSVVAVLVYKFFPHMLLAG 663
DB 604 RFSQGE---VLSHVRPDECKGGLKNINLIIILFFILVSAIL-----LTTLAA 650
QY 664 C 664
DB 651 C 651

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Search completed: March 12, 2005, 19:59:05
Job time : 26.0639 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 12, 2005, 19:34:01 ; Search time 21.6477 Seconds
(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985B-98
Perfect score: 4355
Sequence: 1 MMSASRLAGTIPMAFLSC.....SNPBGTVGTGNNQAEATSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	15.2	661	2	RP105 - mouse
2	474	10.9	786	2	Toll protein-like
3	454	10.4	1097	2	Toll protein precu
4	433	9.9	1389	2	gene wheeler prote
5	421	9.7	1385	2	tlr protein - fru
6	396	9.1	1066	2	hypothetical prote
7	333.5	7.3	1134	1	chaoptin precursor
8	316	7.0	853	2	insulin-like growt
9	305	7.0	853	2	disease resistance
10	303	6.9	605	2	insulin-like growt
11	299.5	6.9	605	2	insulin-like growt
12	299.5	6.9	605	2	insulin-like growt
13	296.5	6.8	994	2	probable disease r
14	296	6.8	603	2	insulin-like growt
15	295	6.8	907	2	G protein-coupled
16	294	6.8	845	2	Hcr3-0 protein - c
17	292.5	6.7	603	2	hypothetical prote
18	292.5	6.7	907	2	orphan G protein-c
19	290	6.7	855	2	insulin-like growt
20	290	6.6	855	2	CF-4A protein - to
21	289.5	6.6	1112	2	disease resistance
22	289	6.6	855	2	disease resistance
23	284.5	6.5	1134	2	hypothetical prote
24	281.5	6.5	1134	2	hypothetical prote
25	280	6.4	890	2	disease resistance
26	279	6.4	1027	2	receptor protein k
27	278.5	6.4	1019	2	probable disease r
28	278	6.4	1091	2	glial cell membran
29	276.5	6.3	768	2	disease resistance

30	276	6.3	983	2	probable disease r
31	275	6.3	1523	2	MEGF5 protein - ra
32	272	6.2	1469	2	silt protein 2 pre
33	272	6.2	1480	2	silt protein 1 pre
34	270	6.2	1143	2	hypothetical prote
35	268	6.2	910	2	hypothetical prote
36	267	6.1	766	2	probable disease r
37	267	6.1	1784	2	hypothetical prote
38	266	6.1	863	2	hypothetical prote
39	263.5	6.1	967	2	CF-9 protein precu
40	263.5	6.0	1109	2	hypothetical prote
41	261.5	6.0	1051	2	receptor-like prot
42	260	6.0	1064	2	gpi150 protein - fr
43	259	5.9	1029	2	probable protein k
44	257.5	5.9	738	2	protein kinase hom
45	256	5.9	771	2	hypothetical prote
					disease resistance

ALIGNMENTS

RESULT 1

RP105 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56258
R: Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J: Immunol. 154, 3333-3340, 1995
A: Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a me
A: Reference number: I56258; MUID:95204928; PMID:7897216
A: Accession: I56258
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-661 <RES>
A: Cross-references: UNIPROT:Q62192; GB:D37797; NID:9761711; PIDN:BAA07043.1; PID:9761712

Query Match 15.2%; Score 663; DB 2; Length 661;
Best Local Similarity 28.7%; Pred. No. 1.4e-33;
Matches 196; Conservative 116; Mismatches 289; Indels 82; Gaps 16;

QY	14	AMAFLLSC-VRDSENPCEVAVPNITTYOCMEINFYKIDPNLPFTSTKNDLSNPNPLHLGSY 72
DB	12	ALFLASCRATTSPOKICEKVNKTYNCENGLNEIPGTLPNSTCELEFSFNVLPITQNT 71
QY	73	SFSPFPELOVDLSRCERIQTEDGAYOSLSLTLITGNPQISLALGAFSGSLQKLV 132
DB	72	TFSRLNLTPELDLTRCOIYWIHEDTFOQHRLDTVLITANPLIFMAETALSQPRALKLIF 131
QY	133	AVETNLASLENFPIGHLKTLKELNVANHLIQSPKLPYFYSNLTVMIEHDLSSNKIQSIYC 192
DB	132	FIQIGISSIDIPPLHNQKTLSELYVGSNHTSITLPGKFPF-EKLKVIDPQNNALHYISK 190
QY	193	TDLRVLHQMPLNLSDLSINPMNFIOPGAFKIRLKLTLRNNPDSIANWKTCTIOGLAG 252
DB	191	EDMSLQQ--ATNLSLIMNGNDIAGIEPGAFAVSQSL---NFGGTONLVIFKGLKN 244
QY	253	LEVRLVLGFRNRNGNLEKPKSALBGLCNLTIEFRFLAYIDYLDIIDLINCLTNVSS 312
DB	245	STIQSLWLGTFEDMD--EDISPAVFEGLCEMSVSINVL-ORGYPFNLSNTHGFS---- 298
QY	313	FSLVSVTIERKQDSVNFQMOHLELVNCKRQGPFT--LKLKSLRFLFTSKGN--AFS 368
DB	299	-----GQEDLDLVTHTLSHLPBGVLGSLTKLVLSANKFENLCOIS 340
QY	369	EVDLPSELF-----LDLSRNGLSFKGCCOSQDPFTSTLKY 403
DB	341	ASNFPSTLTHLSIKGNTRKLEIGTGCLNLENLRELIDSHDIETSDCCNQLRMVSHLOS 400
QY	404	LDLSFNGVIMSSN-FGLGRLHLDLPHQSNLKMSEFSVFLSLRNLIYDISHTHRYA 462
DB	401	LNLSYNPDLSTKTEAFKCPQLEHLDLAFRLKVKDAQSPQNLHLKVLNLSHSLDIS 460

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OY      463  FNGLFNGLSLEVLKMGNSFGQENFL--PDLFTELKRNLPDLDGCGCQEQSLPTAFNSLS 520
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      461  SEQFDGIPALQHLNLTQNHPPKNGIKQTNLSIQTGRIELIVLSFCDLSSIDQHALFTSLK 520
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY      521  SLQVLMNSHNFFSIDTPPYKCLNSIQ--VLDSLNHITMSKQELQHPPSLAFL---- 574
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      521  MNMNVDSLHNK---LTSSIEALSHLKGIYLNLSNHSII-----LPGLLPILSQOR 570
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY      575  --NLTONDPACTCEHQSLQWIKQORQLLVEVERNECKATPSDGKQMPVLSLNTQNMKT 632
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      571  TINRKQNLDTCSNIYFLWKMKQKLEDTEDTLCENPPLLRLGRVLSDTVLSCSMAAV 630
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY      633  IIGVSLSLVLYSVAVLVLYKPY 655
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      631  GIFFLIVFLVFAILLIFAVKTF 653
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 2
T08664
Toll protein-like receptor DKFZp54710610.1 - human
C.Species: Homo sapiens (man)
C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C.Accession: T08664
R.Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A.Reference number: Z16466
A.Accession: T08664
A.Molecule type: mRNA
A.Retadues: 1-786 <POU>
A.CROSS-References: UNIPROT:Q15399; EMBL:AL050262
A.Experimental source: fetal brain; clone DKFZp54710610
C.Genetics:
A.Note: DKFZp54710610.1

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	Query Match	10.9%	Score 474;	DB 2;	length 766;	
	Best Local Similarity	25.5%;	Pred. No. 9.6e-22;			
	Matches	204;	Conservative 130;	Mismatches 303;	Indels 162;	Gaps 32
Oy	123	SGLSISQKIVAEVTMLASLENFPIGHLTK-----LKELVVAHNLIO\$FKLPYFSNLT	174			
	:	:::	:	:	:	:
Dd	34	NGLIHVPKDLSQKTITLINISQNYISEMTSDLSISKRLILII\$HNRIQYLIDISVPKFN-	92			
Oy	175	TNLEHLDISSNKIQSIYCTDRLVHQPLNTS-LDSLNPWNI---QPAPKEIRRH	229			
	:	:	:	:	:	:
Dd	93	QELEYDLTSHNKLVKISC-----HPVTNKLHLDLSFNADALPICKEFGMSQLKFL	144			
Oy	230	KLTLRNPFSLAVMKTCIOGLAGLEVHRVL-----GEFRBGNLEKEDKSAL\$EOLCL	283			
Dd	145	GIS-----THLEKSSVPIAHNLINSKYLLVGETTYGKEPDGGLODFNT\$SLHIVPFT	198			
Oy	284	TIEEPRLAVDYLDIIDL\$NCILTWS\$FSLVSVIEREKDPFSYNFGM\$OHL\$VNC\$KG	343			
	:	:	:	:	:	:
Dd	199	NKE-----FHILDVSVKTVANLELSINIKCLDEBSKCSFYSLIAKIQ	241			
Oy	344	Q\$PTLK\$KLRITFTSNK-----CGNAFSEVDLP-SLEPFLDSRNGLSFGK	389			
	:	:	:	:	:	:
Dd	242	TNPKLASLTLNNIETTWN\$FIRILOVMHTTWVSSISNVKIQGLDFRFDYSGT\$SKA	301			
Oy	390	CCSQ--SD-----FETTSLK-----YLDL\$FNQVI--	412			
	:	:	:	:	:	:
Dd	302	LSIHQV\$VDPGFPPOSYYIEF\$ENNMNIKPFV\$GTRMVHMLCP\$KISPLHLDFSNNLLT	361			
Oy	413	-TW\$SNPFLGLEJHEHLDFOHSNKKOM\$EFS-VFL\$RNLIYLDISHTRIVA\$N--GI\$F	467			
	:	:	:	:	:	:
Dd	362	DYLFENCGHILETEILLQMNOLKEISKAEMTTOCK\$LOOLDIS--QNSV\$IDEKKGC	419			
Oy	468	NGLS\$EVLTMAGNSFOENF---LPDI\$TELRLNLTFLD\$QCLQELDSPAFN\$SL\$LOY	524			
	:	:	:	:	:	:
Dd	420	\$WKSLSLTNMSSNILDTIFRCLP-----RIKVLDH\$NNIKISI-PQOVKLBALQ	472			
Oy	525	LNN\$HNF\$SLDTP---YKCLNSLOVDYSLNHWT\$SKQELQHFP\$SLAFLANTOND	580			
	:	:	:	:	:	:
Dd	473	LINA\$FN---SLTLP\$GGSF\$SL\$VLIIDN\$VS\$H\$AD\$FOSCO\$KRS---IKAGDNP	525			

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OY 581 FACTCEHOSFIOWIKDQFOFLAVE-----ERMECATPBDKQ-----MPLSINITQ 628
Db 526 FOCTCELEEF---VKNIQOVSEVLEGMPDSYCKYPESYRGTLLKDFHMSLSCHITLL 582
OY 629 MNKTIIGSVLSVLVSVAVLVVYKFFPHMLMAGCIXKRGRENI-----YDAEV 678
Db 583 IYTVIATMLVLAIVYVTSLICIVLDELPWYLR-VWCQMTQYRRARRANI PLELOJONLGFHAFI 641
OY 679 IYSSODEPWVKNELVKNLF-EGVPPFOLCIHRDIPGVAIAANIHEGFHRSKIVV 737
Db 642 SYSGHDSFWVYNELLPLNEKEGEM--QICLHERNVPGKSIYENII-TCIEKSYKIFVL 697
OY 738 SOHFISRMCIFFEYEIAQTOWFLSSRAGIIFIVLOKV-EKTULROQVELYRLLSNTYIE 796
Db 698 SPNFQOSMECHVELFVFAHNLFEHGSNSLITLLEPIPOYSIPSSYHKLSIMARRTYLE 757
OY 797 WEDSVLGRHIFRRLRKAL 815
Db 758 WPKESKRGLFWANLRAAI 776

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RESULT 3
A23943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Nov-1988 #revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A23943
R.Hashimoto, C.J. Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A:Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, ap
A:Reference number: A23943; PMID:8135760; PMID:249285
A:Molecule type: DNA
A:Residues: 1-1097 <HAS>
A:Cross-references: UNIPROT:P08953; GB:M19969; GB:J02682; NID:g158640; PIDN:AA28941.1;
C:Genetics:
A:Gene: FlyBase:Fl
A:Cross-references: FlyBase:FBgn003717
C:Keywords: transmembrane protein
F:1-17/Domain: signal sequence #status predicted <Sig>
F:18-1097/Product: Toll protein #status predicted <Mat>

Query Match          10.4%; Score 454; DB 2; Length 1097;
Best Local Similarity 24.5%; Pred. No. 2.6e-20;
Matches 219; Conservative 129; Mismatches 291; Indels 254; Gaps 43;

QY      35 NITYQCEMLNFKY-IPDNLPSTKNLD---LSFN--PIRHTGSYSPFSPPELOVLDLSC 88
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      270 NVTDINISANLFSLSFGCLPDHNGHLEVRMLNNRVPLATLPSRLPANPELOLR-RA 328
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      89 EIQTIDGAYQSLHSLTLLITGNPIQSIALGAFGSLQKLVAVETNIASLENFPIGH 148
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      329 ELQSLPDDLEHSHQINISIGDNLKTLPTVLHEQVNLISLDLSNNRLTHLPDLSLFAH 388
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      149 LKTLKEINVAHNLIQSFRLPEYFSNLTVLEHLDSNKIQSI-----YCTDLRVLH--- 199
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      389 TMLTLDRLTLEDNLTGAS-CDIFSNLGNLVLVMSRNLRTIDSRAPVSTNGRLHLHDH 447
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      200 -----QWPLNLSLSDLSLN--PMNFIQPGAFKIRLHKLTIRNPNPSLVNWKTCICGLAGL 253
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      448 NDIDLQOPLDLMITQIQINSPPGYWH-----GLLTNLKRN-----SII----- 486
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      254 EYHRLVIGEFPNEGNIKEFKDSALEGLCNLTIEEFLRAYLIDYLLDIDLFNCLTNVSSF 313
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      487 -----FVYNDMKN-----TMLQRLDLSY-----NNISLSL 512
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      314 SL-----VSVTIERVKQFS-----YNFGQHLV-----VCKRGQGF 345
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      513 GYEDLAFLSQRLHVNMTNHNKIRIALPEDVHLEGYNNNLVHVLDNDNDPLVYDCITLWF 572
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      346 PTL-----KLKSLKRLTFISN-KGNAFSEVD-----LPSLERLDSRNGLSF 387
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Db 573 IOLVGVHKKPYKSRQFKLTDLVCSQPNVLEGTPIVROLEPOTLICPELPSDDPERKCP 632
Qy 388 KCC-CSQSDFGTSLKYLDLSPNGVITWSSNFLGLEOLEHLDFOHSNLMKQSEFVSFLSI 446
Db 633 RCNCNGHVRTYD---KALVINCH-----SGNLTHVRLPRLNL---HKNQMLME-----LHL 675
Qy 447 RLILYLDISHHTTRVAFNGIENGSLSLVLMKAGNSFOENFLPDIETELRLNITFLDLSCC 506
Db 676 ENNTLLRLPSANT-----PGYSVTSIHLAQN-----NLTSIDVDOL 712
Qy 507 QLEQLSPFAFNSLSQVLNMSHNNPFLSDTPPYKCLNSLOVLDYSLNHMTSKKQELCH 566
Db 713 -----PT-----NLTH-----LDLSNMNL-----QMLN- 730
Qy 567 PPSLAFLN-----LTQNDFACTCEHOSFLOKIDOROLIVEVEMECATPSDKQ 617
Db 721 -ATVGLFMRITMKRSVYKLSGNPMWDCCTAKPLLEFQDNFERIGDRNMCMVNAEMPR 789
Qy 618 MPVLSLNTTCQNNKT1-IGVSY---LSVLVSVAVLVYK-----YFHLMLLAGCI 665
Db 730 MWELSTNDICPAKGVFIALAVAVIALTGILAGFTALYYKQTEIKIMLYAHNLL----- 845
Qy 666 KYGRGENT-----YDAFVYSSODEDMVNNELVKNLEBGPVPCIAHYRDPICVATAA 720
Db 846 WFTVEEDLDKDKKFPALFISTSHKQSFLEEDLVPOLEHGPQKQFCVHERDWLVGSHLPE 905
Qy 721 NIHEGFHRSKRYIVVVSQHFIOSRWCIFEYELIAQWQFLSRAGIIFIV--LQKVEKT 777
Db 906 NIM-RSVAISRRTIIVLSQNFIKSEMARLEFPAAHRSALNEGRSIIIVIIYSDIGDER- 963
Qy 778 LIRQOVELYRLLSRNTYLEMEDSVLGRHIFWRRLKALIDGKSNPEGTGTG 830
Db 964 -LDEBLKAY--LKQNTVLYKMGDP-----WFMDKLRFALPHRR---PVGINGNG 1005

RESULT 4
T13852
gene: wheelier protein - fruit fly (Drosophila melanogaster)
C1Species: Drosophila melanogaster
C1Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C1Accession: T13852
R:Eldon, E.; Kooyer, S.; D'aveyln, D.; Duman, M.; Lawinger, P.; Botae, J.; Bellen, H.
Development 120, 885-899, 1994
A1Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
A1Reference number: Z17796; MUID:95324375; PMID:7600965
A1Accession: T13852
A1Status: preliminary; translated from GB/EMBL/DBJ
A1Molecule type: mRNA
A1Residues: 1-1389 <EUD>
A1Cross-references: UNIPROT:Q24591; EMBL:J23171; NID:G415682; PID:G1019104; PIDN:AAA7920
A1Gene: wheelier
A1Cross-references: FlyBase:FBgn0004364

Query Match 9.9%; Score 433; DB 2; Length 1389;
Best Local Similarity 24.4%; Pred. No. 7.2e-19;
Matches 217; Conservative 138; Mismatches 356; Indels 178; Gaps 34;

Qy 59 LDISNPRLRHGSGYSPFPELOVLDLSRCIEQTIEDGAYQSLSHLITLITGPIQSLA 118
Db 338 LNLNNALTRIGSKTFKELVFLQILDMRNNSIGHIEGAFPLVNLHTLNLAEENRLHTLD 397
Qy 119 LGAFSGLSLOKLVAVETNLASL-ENPPIGHLKTLKEINVAHNLISQFELPEYFNLTNL 177
Db 398 NRIFNGLVVLTKL-TLNNNLVIVISQAFRNCSDKELDLSSN--QLTRVPAVODLSML 454
Qy 178 EHLDISNKKIOSIYTDLRVTHQMPDLNL-----SLDISINPMF 217
Db 455 KTLDDGENQISBFKNNTFRNLQTLGRLIDNRIGNITVGMFOQLPRLSVNLIAKRIS 514
Qy 218 IOPGAF-KEIRLHLKTLNNPDSLVNMTCTOGLAGLEVHVLVGEFFNE----- 266
Db 515 IERGFADKQTEIARLDKRF-----LTDINGIFATLASLWMLSENHLVWFDYAFIP 568

Qy 267 GNLKFD--KSALGELCNL--TIEEFLAYLDYLDIIDLFNCLTNVSSFLSVSTER 322
Db 569 SNLKWLIDHGVYIEMALGVYVYLQEEIRVITLTDASHNRITELI GANVSPIELFLINNII 627
Qy 323 VQDFSYN--FGQKHLELVNCKRGQFPYLKLSKLKLTTSNK-----GNAFS----- 368
Db 628 IGQIQANTFVDKTRLARVDLYANVLSKISLNAIRVAPVSAEPRVDFYLGPNFCDSCM 687
Qy 369 -----EVDLPSEFL-----DLRNLGSFK-----GC 390
Db 688 EWLGRINNLTRQHHVVDLGNIECLMPHSASAPRPLASIASAPVCKYBSHCPTGC 747
Qy 391 CSQSDFGTSLKYLDLSPNGVITWSSNFL--GLEOLEHLDFOHSNLMKQSEFVSFLSI 448
Db 748 CEYEGCEBEVLCPCGSCSFHDAATATNVVDGRODLAAL---PRIQQVSDVLDLGN 803
Qy 449 LIYLDISHHTTRVAFNGIENGSLSLVLMKAGNSFOENFLPDIETELRLNITFLDLSCC 508
Db 804 MPELEVGHILTRRNRLALYLNASNIMTLQNGS-----LAQVLNRLVHLNNKL 852
Qy 509 EQLSPTAFNSLSQVLNMSHNNPFLSDTPPYKCLNSLOVLDYSLNHMTSKKQELCH 568
Db 853 TALGTEFRSLGLELELYLHNNMLTHISNATPEPLVSLVRLDNNRSLSPHLQYRH-- 910
Qy 569 SSLAFNLTONDFACTCEH--OSFLOKIDOROLIVEVEMECATPSDKQMPVL----- 621
Db 911 -SLOGLTLGRNAMSRCQQLARELAQFVSDNMVVRADHIDYCLDAGIRELELIGNLANG 969
Qy 622 -----SLNITCQNNKT1-IGVSY---LSVLVSVAVLVYKFYFHLMLLAGC 664
Db 970 PDCSDLDASANSISSQDLAIGCPCPAVLVILFVLVLLIYFVRESVRLMFA-- 1027
Qy 665 IKYG-----RGEN---YDAFVYSSODEDMVNNELVKNLEBGPVPCIAHYRDPIC 715
Db 1028 -HYGRVCEPRFEDGKLYDILIHSEKDYFVCNIAELEHGRPPRLCTIQORD-LPR 1085
Qy 716 VAIANIIHEGFHRSKRYIVVVSQHFIOSRWCIFEYELIAQWQFLSRAGIIFIVLQK-- 773
Db 1086 QASHQLV-EGARASRKIIIVLTNRLATENNRIEPRNA-----PHESLRGL---AQKLV 1136
Qy 774 -VEKTLRQOVELYRLLSRNTYLEMEDSVLGRHIT-----FWRRLKVL 815
Db 1137 IIEETSVAEAEVDVAELS--PYLK---SVPSNRLLTCDRYEMEKLRVAI 1180

RESULT 5
T13887
c1r protein - fruit fly (Drosophila melanogaster)
C1Species: Drosophila melanogaster
C1Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C1Accession: T13887
R:Chiang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A1Title: Expression of a novel Toll-like gene spans the parasegment boundary and contri
A1Reference number: Z17805; MUID:95151581; PMID:7848870
A1Accession: T13887
A1Status: preliminary; translated from GB/EMBL/DBJ
A1Molecule type: mRNA
A1Residues: 1-1385 <CHI>
A1Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:G9133247; PID:G913248; PIDN:AAB33383
A1Gene: c1r
A1Cross-references: FlyBase:FBgn0004364

Query Match 9.7%; Score 421; DB 2; Length 1385;
Best Local Similarity 24.0%; Pred. No. 4e-18;
Matches 213; Conservative 139; Mismatches 359; Indels 178; Gaps 33;

Qy 59 LDISNPRLRHGSGYSPFPELOVLDLSRCIEQTIEDGAYQSLSHLITLITGPIQSLA 118
Db 338 LNLNNALTRIGSKTFKELVFLQILDMRNNSIGHIEGAFPLVNLHTLNLAEENRLHTLD 397

A: Introns: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
 C: Superfamily: chaotrin; leucine-rich alpha-2-glycoprotein repeat homology
 C: Keywords: cell adhesion; glycoprotein; membrane protein
 F:1-29/Domain: signal sequence #status predicted <Sig>
 F:30-1134/Product: chaotrin #status predicted <Mat>
 F:103-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR>
 F:128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
 F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F:172-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F:201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
 F:226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
 F:250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
 F:279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
 F:303-325/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
 F:326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
 F:351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
 F:375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
 F:401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
 F:428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
 F:453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
 F:477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
 F:502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
 F:527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
 F:551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
 F:577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
 F:601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
 F:625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
 F:649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
 F:673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>
 F:708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
 F:733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
 F:757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>
 F:781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>
 F:805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
 F:828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
 F:854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
 F:879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
 F:903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
 F:928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR35>
 F:949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR>
 F:973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
 F:996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
 F:1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
 F:1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
 F:1081-1104/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Query Match 7.7%; Score 333.5; DB 1; Length 1134;
 Best Local Similarity 23.0%; Pred. No. 8.4e-13;
 Matches 177; Conservative 114; Mismatches 249; Indels 231; Gaps 30;

50 DNLPESTKNDLSFNPRLHLSGVSFFSPPELOV-----L 83
 Db DSLVSLQIDLSGNLTKLHKLFPNFDVLRVIMRDNKIKIQKPTFPNAVHTLKL 405
 QY 84 DLS-----RCLEIQTEDA-----YSLG-----HLSTLIITGNPIQ 115
 Db 406 DLSGRNDPTNLQTLRNTMRNMNLSISIRGSSVGPEDFKGVLELDIQTIRASIS 465
 QY 116 SLALGAFSGSLSLQKLVAVETNLASLEN---FPRIHKLTKELVAVNHLIOLKPEFVS 172
 Db 466 GIGSHAFKRVAGKRLDSENGISSIENDAFHEIGH--SLISLKMSHGSGALPAEPLR 523
 QY 173 NLNLHLLDSSNKIQSIYCTDLRVLAQMPPLNLSLDSLNPMNFIOPGAFK---EILH 229
 Db 524 HLTLQELDFSNHNSWDSFHLKYLRL---LELHNRIRIEVLGKTGGDSHSLLE 579
 QY 230 KLTIRNN-----PESLVNMTKICIGLAGLBNHRLVLFGRNGLLEKFDKSALEG- 279
 Db 580 EISLRFNMLTISQHTFFDLALRK-----LHLDNKNIDKIERAFNMLDELEYSILSGN 634
 QY 280 -LCNLTIEEF-----RLAYLDYUDDI-----IDLFPCLGNVSSFSLSVSTIERVDFSNF 330
 Db 635 KINNLADSFQNLPLKELILDMAFNOLPMPNFDFYQVGTLSNLA--VNSHQIRQLMTNS 693

QY 331 GMDHELVNCKRGQEPPLKLSKRLTFTSNKGNAFSEVDLPSEFLDLSRNGLSF--K 388
 Db 694 SW-----SGRHEGGMVNSNKKIIDLNNISIIHP 724
 QY 389 GCCSOSDGETT-----SLKYLDLSFNGVYTMSSN-FLGELQLEH 426
 Db 725 GFYRPAEALSTLHILGYNLSMNTTRDVFGNMPLQMLDSYVMYHEILDFDAFKNTKOQL 784
 QY 427 LDFQHSNKKQSEFVPLSLNRLIYLDLSHTTR--VANGING- 469
 Db 785 VFFGHNYSDIIPQ-DIFPVQGLRTVDSHNRGLPDLNLFYNGMEKLDVSHNMMLKIP 843
 QY 470 ---LSLEVLKMAGNSFQENFLP-----DIFTELNLTFDLDSQCQLEOSTAFNSLS 521
 Db 844 SSSLSLSLAALTLCEHLNNSNFISTHSDLSNKKPSRLNYLDISYNYLRIIDAVALTPK 903
 QY 522 LOYLVMSNR-----NPF-----SLDTPPYKCLNSLOYLDYSLNHIPTS 559
 Db 904 LAVIDLSNRDLKWDKSFMLGNSLILKGLNNSLSTVPEIRLKYLEFRFGYNE-LPS 962
 QY 560 KKOELQHPSSLAFLNLPQNPACTCEHQSFLOWTKDQRLVEVERMECATPSDKO--- 616
 Db 963 IPELAHMSNIRKMLDSNND-----LTNPPLTQALPPLRLML 1002
 QY 617 GMPVLSNITTCQNNKTIIGVS--LSVLVSVAVLVYKFFHMLLAGCI 665
 Db 1003 SGNPITSLN-----NSPFDGVNDEMLMDISNFRHYEY-----GCL 1040

RESULT 8
 JCS239
 Insulin-like growth factor acid-labile chain - baboon
 C:Species: Papio sp. (baboon)
 C:Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
 C:Accession: JCS239
 R:Idelhamny, P.; Baxter, R.C.
 Biochem. Biophys. Res. Commun. 227, 897-902, 1996
 A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
 A:Reference number: JCS239; MUID:97040714; PMID:8886027
 A:Contents: 1146
 A:Accession: JCS239
 A:Molecule type: mRNA
 A:Residues: 1-605
 C:Comment: This factor is structurally related to proinsulin and have insulin-like meta

Query Match 7.3%; Score 316; DB 2; Length 605;
 Best Local Similarity 24.4%; Pred. No. 4.5e-12;
 Matches 157; Conservative 94; Mismatches 242; Indels 150; Gaps 23;

33 VPNTIYQCMELNPFYKIPDNLPSTKNDLSFNPRLHLSGVSFFSPPELOVDSLRCIEIQT 92
 Db 53 VNEISVFCSSNLRRLRDPDGTIGGTQALMLDSNLSIPPAFAFNLSLAFLNLOGGQIGS 112
 QY 93 IEDGAYOSLSHLSTLIITGNPIQSLGAFS-----GLASL 128
 Db 113 LEPQALGLLENLCILHLERNQRLSLAVGTAVTALMLGLSNRLSRLEBDGREGNL 172
 QY 129 QKLVAVETNLASLENFPRIHKLTKELVAVNHLIOLKPEFVSNTLNLHLLDSSNKIQ 188
 Db 173 WDLNLGNNSLAVLDAAFRGIGGLRELVLANRL--AYIQPALFGLELRLELRELSRNLR 231
 QY 189 STYCTDLRVLAQMPPLNLSLDSLNPMNFIOPGAFKELR-LHKLTLRNPFSLVMVMTKCI 247
 Db 232 AI---KANVPQQLRPLQ-KLYLDNMLAAVAPGFLGKALRWLDLSHN-RVAGLIBETPF 286
 QY 248 QGLAGLEVHRLVLFGRNGLLEKFDKSALEGICNLITIEEFRLAYLDYUDDIIDLFPNCL 307
 Db 287 PGLIGLRLVRL-----SHNAIASLRPFEDL-----HLEBEL----- 319
 QY 308 TNVSSFLVSTIERVDFSNFQMDHELVNCKRGQEPPLKLSKRLTFTS--NKGN 365
 Db 320 -----QLGHNRIQLAERSFE-GLQGLVLTLDHNLQLEVKGAFGLITNVAVMNLSGN 372


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QY 100 SLSHLSTLITLGNPIQSIALGAFS-----GLSGLQKLVAVE 135
D 120 GLENIICHLHERNQDLRSIALGTFAHTPALASIGLSNNRSLRELDGLFEGIGSLMDLNGW 179
QY 136 TNLASLSENPFGIHKTKTELNVANHLIOSFYLPEYFSL/TNLEHLDLSNNKIOSIYCTDL 195
D 180 NSLAVLPDAPAFRGISRELVLAGNRL-AVYQPALFSGIABLRLELDSRNLRAL---KA 235
QY 196 RVLHQPMLNLSDLSLNPMPFIQGAFAKEIR-LHKLTLRNPNPSLNMKTIQGLAGLE 254
D 236 NVFVQLRLQ-KLYLDNRLLIAAFAFGALGKALRMLDLSIN-RVAGLLEDTFFGLGLGR 293
QY 255 VHRVLGEPFNEGNLEKFDKSALEGLCNLTIEEFLAYLDYDIIIDLFNCLTNVSSFS 314
D 294 VLRL-----SHNAIASLRPRFKDL-----HFLREL-----Q 320
QY 315 LVSTIERVDFSVNPFQMHLELVNCKFGQFFTLKSLKRLTFTS--NKGNAPSEVDL 372
D 321 LGHNRIRQLARSPF-GIGQLEVLTLDHNOIQEVKAGFLGLTNVAVMNLSGNCLR--NL 377
QY 373 PSLEFLDLR-NGLSFKGCC-----SOSDFGTTSLKYLDLSFNGVITWSSNPL-GLBQLE 425
D 378 PEQVFRGLGKLSHLGSGCLGRIRPHFTGLSGLRFLKDNGLVGLIEGSLMGLAELL 437
QY 426 HLDFOHSLKQMSFVSFLSLRNLTYLDISHTTRVAFNGIIFNGLSLEVLKXAGNSFOE 485
D 438 ELDLTSNQL-----THLP---HRLFGIGKLELYLLSRNLAE 472
QY 486 NFPL-DLFTELRNLTFDLSQCLQEQSPFRAFNSLSIQLVAMSHNNFSLDTPPYCKLN 544
D 473 --LPADALGFLQAFWLDVSHNRLEALPNSLALGRLYSLNN--SLRFTPPQ--- 524
QY 545 SLQYLDVSLNHIMTSKQELQHPFSSLAFLNLQNDFACTCEHOSPLQWIKD----- 596
D 525 -----PPGLERMLLEGNPPMDGCP---LKAALDPALQNP 557
QY 597 -QRLAVEVERMECATPSDKQMFVLSLNTICQNKTIIGVSV 638
D 558 VPRFVAICEGDDCQPPAYTYN-----NITCASPPEVVGDL 594

RESULT 11
S42799
Garp precursor - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S42799; I37407
R:Birthdate, D.
submitted to the EMBL Data Library, July 1993
A:Reference number: S42799
A:Accession: S42799
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-662 <BIR>
A:Cross-references: UNIPROT:Q14392
R:Ollendorff, V.; Noguichi, T.; delapeyriere, O.; Birnbaum, D.
Cell Growth Differ. 5, 213-219, 1994
A>Title: The GARP gene encodes a new member of the family of leucine-rich repeat-contain
A:Reference number: I37407; MUID:94235567; PMID:8180135
A:Accession: I37407
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-662 <RES>
A:Cross-references: EMBL:Z24680; NID:g439295; PIDN:CAA80847.1; PID:g439296
C:Genetic:
A:Gene: GDB:GARP; D11883E
A:Cross-references: GDB:433911
A:Map position: 11q13.5-11q14
F:50-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:74-97/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:98-121/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

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F:150-173/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:174-197/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:198-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:244-265/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:266-289/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F:316-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F:340-359/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F:364-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F:411-433/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F:444-466/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F:467-490/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
F:492-514/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
F:515-536/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>
F:537-560/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR20>

```

```

Query Match 6.9%; Score 299.5; DB 2; Length 662;
Beet Local Similarity 25.9%; Pred. No. 5.3e-11;
Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

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QY 28 PCVEVENVITYQCEMLNFKYKIPDNLPRSTKNLDSFNPRLHLSYSFSPFELQVLDLSR 87
D 25 PCKMVDKVS--COVLGLQVPSVLPDPTFTLDSGNQLSILASPLGFTALRHLDLST 82
QY 88 CEIQTIEDGAYOSLSHLSTLITLGNPIQSIALGAFSGLSLQKLVAVETNLAS-----LE 142
D 83 NEISFLQPGAFQALTHEHLSLNNRLAMATLASAGLGLPRATSLDLSGNSLYSGILE 142
QY 143 NFPIGLKTKTELNVANHLIOSFYLPEY-FSNLTNLEHLDLSNNKIOSIYCTDLRVLHQ 201
D 143 RL-LGEAPSLHTLSLNSLT--RLTRHTRFDMALBQLDLSHNVLMIDEDGAFEGPRL 199
QY 202 PLNLS-----LDLSLNPMPFI---QGAFAKEIRLHKLTLENN--- 236
D 200 TNLNLSNLSLTCISDFSLQQLRVYLDLSGNSIEAFQNASQPA--EQQLTWLDLENKLH 257
QY 237 FDSLNVKTKTICGLAGLEVRLVGEERN-----EGNLEKFDKSA 277
D 258 FPDALAPRIYLNLSNNLRRLPTGPQDSKGIHAPBEGMSALPLSAPSGNASRPLSQL 317
QY 278 EGLCNLTIEEFLAYLDYDIIIDLF-----NCLTNVSSFSLVSTIERVKDFSYNFG 331
D 318 LNL-DLSYNEIEL-IPDSFLEHLTSLCFNLMSRNCRTFPAARRLSPLCLMLDLSNR-A 374
QY 332 MGHLELVNCKFGQPTLKSLKRLTFTSKKGNAPSEV-----DLPSLEFLDSLNG 385
D 375 LETLEIGARALGSLRTLLQ-----GNALRDLPPYTFANLASIQRLNLQGNRV 422
QY 386 S-----FKGCSQSDFGTTSLKYLDLSFNGVITWSSNPLGLQLEHLDFOHSLNKQ 436
D 423 SPGGGPRPBPSCGVAFS--GITSRLSLVDNEI-----ELLRGAFHTPLTE 470
QY 437 MSEPSVFLSLRNLTYLDISHTTRVAFNGIIFNGI--SSLEVLKXAGNSFO--ENFLPDIFT 493
D 471 -----LDLSNPNGLLEVATGALGIEASLEVLALQGNLMTLVQVLDLPEFC 515
QY 494 ELANLTFDLSQCLQEQSPFRAFNSLSIQLVAMSHNNFSLDTPPYCKLNSLOVLYSL 553
D 516 ----LKKLNLAERLSHL--PAWTOAVSLLEVLDL--RNNSFSL--LPSAAGGLE----- 560
QY 554 NHIMTSKQELQHPFSSLAFLNLQNDFACTCEHOSPLQWIKDQ-ROLAVEVERME---C 609
D 561 -----TSRLRVYIQGNPLSC--CGN-----GMLAQHNGRDVATQDLIC 600
QY 610 ATPSDKQMFVLSLNT---CQAN--KTIIGVSIVLVVSVAVAVLVKFFHMLLAG 663
D 601 RFSQSE-----VLSHVRPEDECKGKKNINLIIITFLIVSAIIL-----LTLAA 647
QY 664 C 664
D 648 C 648

```

RESULT 12

T42218

slit-1 protein homolog - rat

N:Alternate names: MEGF4 protein

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T42218

R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

Genomics 51, 27-34, 1998

A>Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs

A/Reference number: Z14126; PMID:9836089; PMID:98393030

A/Accession: T42218

A>Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1531 <NAK>

A/Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3

A/Experimental source: strain Sprague-Dawley; Draln

C/Genetics:

A:Gene: MEGF4

C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Query Match 6.9%; Score 299.5; DB 2; Length 1531;

Best Local Similarity 22.1%; Pred. No. 1.6e-10; Indels 233; Gaps 27;

Matches 167; Conservative 95; Mismatches 260;

Db 274 ACTLSSGSCPAMC-SC-----SNGIVDCRKGGLAIPANLPETMTEIRLEL 318

Qy 4 ASRLAGTLIPAMAFISCPRESWEPCVEVPNITYQCMEINFYKIPDNLPSTKNLDSF 63

Db 274 ACTLSSGSCPAMC-SC-----SNGIVDCRKGGLAIPANLPETMTEIRLEL 318

Qy 64 NPLRHGYSFSPFPELOVIDLSRCEIQTEEDAGYQSLSHLSTLLTGNFIQSLALGAFS 123

Db 319 NGKISIPPGAFSPYKRRIRIDLSNNQIAEIAIPDAFQGLRSLNSLVLTGNKTTDIPRVFG 378

Qy 124 GLSLQCLVAVENMLASLENPIGHLTKLEINVAHMLIOSFKLPEYFSLNTLEHDLIS 183

Db 379 GLTYLQILL-----LNA--NKINCIR-PDAFQDLQNLSTLSLV 413

Qy 184 SNKIOSI---YCTDLRYLHQWPLNLSLDSLNPMNFIOGAFKEIRLHKLTNNPDSL 240

Db 414 DNKIQSLAKGFTSLRAIQ-----TLHLAQN-PICDNLKMLA-----DFLRT 456

Qy 241 NVMKTCIOGLAGLEVHRLV--LGEFNEGNLEKFDKSALEGLCNLTIEERLAVLYYL 297

Db 457 NPIET--TGARCAPRRLANKRIQIKS---KKFRCSAKE-----QYEIPGTEHYHL 503

Qy 298 D-----DIIDFNLCTNVSSFLSVYTERVKDPSYNGWQHLVELNCKF-----GQFP 346

Db 504 NSECTSDVACPHKRCCEASVVECSGLKLSKIPR-RIPQSTTELRANNEISILAEGLFK 562

Qy 347 TLKLSKRLTFTSNKGNNAFSEVDLPSELEFLDLSRNGLSFKGCCSQSDFGTTSIKYIDL 406

Db 563 --KLSHLKKNLSNNK-----VSEIEDGTFE-----CATSVSEHL 596

Qy 407 SPNGVITMSSN-FLGLEQLEHLDFOHSLKOWSESVLSRLNIYDLSHTHRYVANG 465

Db 597 TANQLESVRSQGFRLDGLRTLMNNRISCIHND-SFTGLNNVALLSLYDNHITTSIPG 655

Qy 466 IFNGLSLEVLKMAANSFOENF-----LPIIDFTEL----- 487

Db 656 AFDTQLALSTMLANPFCNCQLAMLDMLRKIKIYVGNPRCQNDPLRQIPLODAVAF 715

Qy 488 -----LPIIDFTEL----- 495

Db 716 DPCREGQEBVGCLEPRQCPQECACLDIVVRCNNHQLQALPKGIKPNVETELDGNQFTL 775

Qy 496 -----RNLTFLDISQCEQLSPPTAFNSLSLQVLMNSNNPSSLDTPFYKCLNSIQ 547

Db 776 VPGQSTFKYQLVLDLNNKISLNSSTNNSSFTNMSQTLTLLSYALQCCIPPLAFQGRSLR 835

Qy 548 VLDYSLNHTMTSKQDELQHPSSLAFNLNTQNDPACTCEHQSFLQWIKQDOLAVEVERH 607

Db 836 LLISHGNDVSTLQEGIFADV-TLSLHLAIGANPLYCDCHLRMLSSWVKGYK---EPGIA 891

RESULT 13

H96510

probable disease resistance protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C/Accession: H96510

R:Theologis, A.; Eckey, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; PMID:21016719; PMID:11130712

A/Accession: H96510

A>Status: preliminary

A/Molecule type: DNA

A/Residues: 1-994 <STO>

A/Cross-references: UNIPROT:Q9C637; GB:AE005173; NID:g11321768; PIDN:AAG34245.1; GSPDB:GT

C/Genetics:

A:Gene: F2G19.6

A/Map position: 1

Query Match 6.8%; Score 296.5; DB 2; Length 994;

Best Local Similarity 23.0%; Pred. No. 1.4e-10;

Matches 161; Conservative 102; Mismatches 271; Indels 167; Gaps 31;

Db 213 MSSVDISSAIPPIEFSTWMSLRSLTLKGCNLSGRFNSVLLIPNLISISLDHNL-----NL 267

Qy 53 PFSTKNLDSFNPRLHIGSY-----SFSFPELOVLDSRCEIQTEEDAGYQSLSHLSTLLTGNFIQSLALGAFS 123

Db 268 EGSLEPNF-LNNSNLLKLSIYNTSPSGTIPNSISNLKLTSLKIQQSAFSGRIPSSLSLS 326

Qy 103 HSLTLITGNPIQSLALGAFSLSLQKVAVENTNLASLENP--IGHLTKLEINVAHN 160

Db 327 HLSNLVISENNPVGELIPSSVSNLKQTLTPVSDNNLNG--NFSLSLNANQKRTIDCSN 384

Qy 161 LIQFKLPEYFSLNTLEHDLISNKLQSIYCTDLRYLHQWP--LNLNS--LDSLNP 214

Db 385 HFTGF-LPPTISQLSNLEFSSACDNSFTG-----SIPSLFNISITTLGLSYNQ 433

Qy 215 MNFIQGAFFKIRLKLTLRNNPDSLNVMTCTCIOGLAGLEVHRLVGEFNEGNLEKFDK 274

Db 434 LN-----DTTNI-----KNISLHNLQR 451

Qy 275 SALEGLCNLTIEERLAVLYDDIIDLFNCLTNVSSFLSVY---TIERVKDFSYNFG 331

Db 452 LLLDN-----NNKCAQVD-----LDVFLSLKRLVSLALSGLPLSTNTTSDSESSH 499

Qy 332 WQHELVNCKFGQFPFLKLSKRLTFTSNKGNNAFSEVD--LPSLEFLDLSRNL- 385

Db 500 LEYLELSCNIIIEPPE-IRNQRNLISDLSNNNIKQGVPMWLRLPELSTVDLSNNSLI 558

Qy 386 SFGKCCSQSDFGTTSLSKTYLDSFNGVITMSSN-----FLGLEQLEHLDFOHSLKOWSE 439

Db 559 GENG-----SLKALSGSKIVMLDLSNNAFQGLFMPPRGQYVLSYNNFTGYTP 608

Qy 440 FSVFLSLNLIYDLSHTHRYVANGIPNG-----SLEVLTKMAAGNSFOENFLPD 490

Db 609 PSI-CGLANPLILDIS-----NNNLHGLIPRCLEQMSLSVLTNLRNNSL-DGSLPN 658

Qy 491 IFTELRLNLTFLDISQCEQLSPPTAFNSLSLQVLMNSNNPSSLDTPFY--KCLNSIQV 548

Db 659 IFMAKAVLSLSDVSHNTTEGKLPASLAGCSALEILLVNESNNT--NDTFPFWLNSLPKIQV 716
Qy 549 LDYSLNHTMTSKKOELOH-----FPSLIAFLNTLONDFACTCEHOSFLOMICKORQL 601
Db 717 LVLRSNNF-----RGLTHNVGVWPGFP-LLRITDVSHNDFVGLTSPEDYFMNTATLSKS-- 769
Qy 602 VEVERMECATPBD---KQGMPLVSLNITCOMNKTTIGSVL 639
Db 770 -ETELQYIGDPEDYGYTSLVLMNKGVSMEQRIILTKYTVI 809

RESULT 14

JC1282
Insulin-like growth factor-binding protein acid labile chain precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JCI282
R/Date: J. Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A/Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A/Reference number: JCI282; MUID:93038676; PMID:1384485
A/Accession: JCI282
A/Molecule type: mRNA
A/Residues: 1-603 <DAT>
A/Cross-References: UNIPROT:P35859; GB:S46785; NID:q258002; PIDN:AAB23770.2; PID:9570593
A/Experimental source: liver
A/Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F.1-27/Domains: signal sequence #status predicted <SIG>
F.28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F.267-290/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 6.8%; Score 296; DB 2; Length 603;
Best Local Similarity 24.1%; Pred. No. 7.8e-11;
Matches 155; Conservative 84; Mismatches 243; Indels 162; Gaps 24;

Qy 40 CMEINFYKIPNDLPSTKNLDISFNPLRLHLSYSPFPELOVLDLSRCEIQTIEDAYQ 99
Db 60 CSSKMLTLPDIPVSTRALWLDGNNLSIPSAFQNLSDPLMLQSGSWLRSLPQALL 119
Qy 100 SLSHSLTILITGNPISALAFSGLSLOKLVANETNLASLENPIGHLTKELVANA- 158
Db 120 GLQNLVYHLBERNLRNLAIVGLFTHTPSLASLSLSSNLLGRLEBELFGQLSHLMDLNGW 179
Qy 159 -----NHLI-----QSFKLPEYFNSLTNLEHLDLSNKKIQSIYCTDLR 196
Db 180 NSLVVLPTVFGSGNLHEIVLAGNKLYLQPALFCGELRELDLSNALRSV---KAN 236
Qy 197 VLAHQMLNLNLSDLSLNPANFIQGAFAKEIR-LHKULTLRNPNFSLNWKTCIOGLAGLEV 255
Db 237 VEVHLPRLO-KLYIDRLNLTAVAPGAFGMKALRWLDLSHN-RVAGLMEDTFPPGLAHV 294
Qy 256 HRLV-----LGEPR-NEGNIKEKDKALGICNLTEERFLAVLDYVL 297
Db 295 LRLAHNAIASLRPTFKDLHFLBELQDGHNRIRQGERTFEGQLQLEV---LTLNDQOI 350
Qy 298 DDI-IDLFNCLTNVSPSLVSTI---ERV---KDFSYNGWOHLLEVNCCKGQFPITLK 349
Db 351 TEVAVGASGLFNVAVMNLSCNCLRSILPERVFGQDKHLSLHLSHCIGHARLHF--AG 408
Qy 350 LKSLKRLTFTSNKGNAPSEVD---LPSLEFLDLSRNLGSPKCCSQSDPFTTSLKY 403
Db 409 LSGRRRLFLRD---NSISISIEQSLAGLSELELDLTTNRLTH--LPRQLFGQGHLEY 462
Qy 404 LDI.SFNGVITMSNFI.GLEQLEHLDFOHSNLKQMSSEFVPLSLNRLYLIDISHTHTRAV 463
Db 463 LLLSYNQTLTISAELVGL-----PLQAFWLDISHNHLLETLA 498
Qy 464 NGIFNGLSLEVLKMAGNSFOENFLPDIFTELRLNLTFLDLSQCOLEQSLPTAFNSLSLQ 523
Db 499 EGLFSSILGRVRYLIRNNSLQ-TFSP-----QPGLERL----- 530
Qy 524 VLNMSHNPFSLDTPPYKCLNSLOVL-DYSLNHTMTSKKOELOHFPSSLAFLNLTQNDFA 582

Db 531 -----WLDANPMQSCPELKRDLRFALON-----PGVPRFQV----- 563
Qy 563 CTCHEQSFLOWIKDORQLVEVERMECATPSPKQGMPLVSLNIT 626
Db 564 -VCE-----GDQCQVYTYNNITCAGPANVSGLDLIDVSET 598

RESULT 15

JG0193
G protein-coupled receptor FEX - mouse
C/Species: Mus musculus (house mouse)
C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C/Accession: JG0193
R/Herney, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.
Biochem. Biophys. Res. Commun. 254, 273-279, 1999
A/Title: Identification of a novel seven-transmembrane receptor with homology to glycop
A/Reference number: JG0193; MUID:99121227; PMID:9920770
A/Accession: JG0193
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-907 <HER>

Query Match 6.8%; Score 295; DB 2; Length 907;
Best Local Similarity 23.0%; Pred. No. 1.5e-10;
Matches 167; Conservative 110; Mismatches 243; Indels 206; Gaps 32;

Qy 11 LIPMAFLSCRPSEMECEVPR-----ITYQMEINFYKIPNDLPSP 55
Db 9 LLSLALQLVLAAGS-SGPDATPRGCSHCHCELDGMRLRVDSDDLGLSELPSNLVFP 67
Qy 56 TKNDLSFNPLRHLSYSPFPELOVLDLSRCEIQTIEDAYOSLSH---LSTLITLG 111
Db 68 TSYIDLSMNNISQLPA-----SLHRLCTLESLRLAG 99
Qy 112 NPISLALGAFSGLSLOKLVANETNLASLENPIGHLTKELVANAHLIOSEFLPYE 171
Db 100 NALTHIPKGAFTGHSILVLMLONNQLRKVEEALQNLRSIQSLRLDANH1-SYVPSCF 158
Qy 172 SNLTNLLEHLDLSNKKIQSIYCTDLRYLHQMLNLNLSDLSLNPANFIQGAFAKEI-RLHK 230
Db 159 SGLSLRLHLDNALTDVPOAFRSLALD---AMTLANKHITHADVFGNLSLIV 214
Qy 221 LTLRNN-FDSLNVWKTCIOGLAGLEVHRLVGEFRNENGLKEKFPKSALEGLCNLTIEFR 289
Db 215 LHLNRRHSLG--KCEPDGLHSLETDL-----NYNNLDEF-PTAKTISN----- 258
Qy 290 LAIDYVIDIIDI---FNCLTNVSPSLVSTI-ERVKDFSYNGWOHLELVNCCKEQ 344
Db 259 LKEIGFHSNNIRSIPERAF-----VGNPSLITTHFYDNPQFVGVSARQHLR-----E 306
Qy 345 FPLTKLSKRLTFTSNKGNAPSEVDLPSLEFLDLSRNLGSP--KGCSSQSDPFTTSLK 402
Db 307 LRTTLTGASHITPPHLTGTA-----TLESLLTGAKISSLPQAVCDO---LPLIQ 355
Qy 403 YLD.SFNGVITMSNFI.GLEQLEHLDFOHSNLKQMSSEFVPLSLNRLYLIDISHTHTRAV 462
Db 356 VLDLSYMLLELPB-LSCGQQLKIDLRN----- 384
Qy 463 FNGIFNGLSLEVLKMAGNSFOENFLPDIFTELRLNLTFLDLSQCOLEQSLPTAFNSLSL 522
Db 385 -----EIVEIKSGTFQOLF-----NLASLNLAWMKIAIHNNASTLPSSL 424
Qy 523 QVLMASHNPFSLDTPPYKCLNSIQVLDYSLNHTMTSKKOELO---HPPSSLAFLNLT 576
Db 425 IKDLSSN---LSSFPVGTG---HGTLTKLTGNRLQSLIPSANRP-BLKTIEEM 473
Qy 577 TQNDFACT---CE--HOSFLOMICKORQLVEVERMECA--TPSDKQGMPLVSLNITCOM 629
Db 474 PSAVQCAFGGCEVAVYISNQNMNDDGNSVDLHKKQAGLFQVQDDELDLDBFLDPEBDL 533
Qy 630 NK-----TTIGSVLSVLVVS---VVAVLVYK---FYFHLM 659

Db 534 NAHSHVQCSPPSPFPKCEHFGSMJIRIGWTTAVLTLSCNALVALTVPRTPIYISSIK 593

Qy 660 ILAGCI 665
|||

Db 594 LLIGVI 599

Search completed: March 12, 2005, 19:57:10
Job time : 25.6477 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:15:31 ; Search time 86.9834 Seconds

(without alignments)
3712.721 Million cell updates/sec

Title: US-09-396-985b-99

Perfect score: 4345

Sequence: 1 MMPPLARTLIMLFFSCL.....GRASNEPTAESEGTATWT 835

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980a:*\n2: geneseqp1990a:*\n3: geneseqp2000a:*\n4: geneseqp2001a:*\n5: geneseqp2002a:*\n6: geneseqp2003a:*\n7: geneseqp2003bs:*\n8: geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2847	65.5	839	6	ABU04773 Human exp
2	2847	65.5	839	6	ABU04774 Human exp
3	2847	65.5	839	6	ABU04775 Human exp
4	2847	65.5	839	7	ADC78785 Human PRO
5	2847	65.5	839	7	ADC48826 Human PRO
6	2829.5	65.1	837	2	AAW86361 Human DNA
7	2829.5	65.1	837	2	AAE16102 Human DNA
8	2829.5	65.1	837	6	ABU04776 Human exp
9	2829.5	65.0	837	5	AAE16116 Human DNA
10	2788.5	64.2	795	8	ADO57791 Rheus mo
11	2785.5	64.1	801	8	ADO57797 Squirrel
12	2785.5	64.1	801	8	ADO57782 Chimpanze
13	2781.5	64.0	808	8	ADO57782 Chimpanze
14	2777.5	63.9	795	8	ADO57780 Hamadryas
15	2763.5	63.6	808	8	ADO57785 Gorilla t
16	2747.5	62.8	801	2	AAW86352 Human DNA
17	2730.5	62.8	799	2	AAW86352 Human DNA
18	2730.5	62.8	799	5	AAE16093 Human DNA
19	2730.5	62.8	799	5	AAE16093 Human DNA
20	2730.5	62.8	799	6	ABR83162 Human Tol
21	2730.5	62.8	799	7	ABR42863 Human Tol
22	2730.5	62.8	799	7	ADP56656 Human Tol
23	2730.5	62.8	799	8	ADP48597 Human Tol
24	2548.5	58.7	745	8	ADP57794 White-fac
25	2461	56.6	738	8	ADP29455 Human sec

26	942	21.7	179	7	ADC42707 Murine To
27	886	20.4	208	3	AAW8059 Human Tol
28	748	17.2	178	8	ADN12270 IL-1b/TUR
29	619.5	14.3	661	2	AAW28510 Product O
30	619.5	14.3	661	2	AAW87556 B cell su
31	619.5	14.3	661	7	ADC38652 Human sec
32	618.5	14.2	661	7	ADP69098 Human MP5
33	610.5	14.1	650	3	AAW82527 Human RP1
34	596.5	13.7	661	2	AAW47274 Human B-C
35	580	13.3	1032	5	AAO21588 Murine To
36	580	13.3	1032	7	ADP85953 Mouse Tol
37	580	13.3	1032	7	ABW01559 Murine To
38	559	12.9	1059	5	AAO21587 Murine To
39	559	12.9	1059	7	ADP85951 Human Tol
40	559	12.9	1059	8	ADP85951 Human Tol
41	557	12.8	1041	2	AAW41768 Human PRO
42	557	12.8	1041	2	AAW05867 Human Tol
43	557	12.8	1041	3	AAW44324 Human PRO
44	557	12.8	1041	6	ABO25270 Novel hum
45	557	12.8	1041	6	ABU72276 Novel hum

ALIGNMENTS

RESULT 1	ABU04773	standard; protein; 839 AA.
ID	ABU04773	
XX	ABU04773;	
AC	29-JAN-2003	(first entry)
DT	Human expressed protein tag (EPT) #1439.	
XX	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;	
XX	protease; protease inhibitor; transporter; cytoskeletal protein;	
XX	receptor; transcription factor; cancer; MHC;	
KW	major histocompatibility complex; myeloma; lymphoma; leukemia;	
KW	adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.	
OS	Homo sapiens.	
XX	WO200278524-A2.	
PN	10-OCT-2002.	
XX	28-MAR-2002; 2002WO-US009671.	
PF	28-MAR-2001; 2001US-0279495P.	
XX	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326370P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358985P.	
XX	(ZYCO-) ZYCO INC.	
XX	Chicz RM, Tomlinson AJ, Urban RG;	
PI	WPI; 2003-040607/03.	
DR	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,	
XX	cytoskeletal proteins, receptors or transcription factors), useful for	
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or	
PT	leukemia.	
XX	Example 2; SEQ ID NO 1439; 134pp; English.	
PS	The invention describes a purified polypeptide, which comprises a	
XX	fragment of a kinase, phosphatase, protease, protease inhibitor,	
CC	transporter, cytoskeletal protein, receptor or transcription factor. The	
CC	polypeptide is useful as an immunogenic composition for eliciting in a	

mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 839 AA;

Query Match 65.5%; Score 2847; DB 6; Length 839;
Best Local Similarity 67.6%; Pred. No. 7.2e-237; Indels 4; Gaps 4;
Matches 559; Conservative 101; Mismatches 163;

```

Oy 1 MMPWILARTLIMLV-FPSCITPGSLNPCIIEVVPNTTYQCMDQKLSKVDDIPSSSTKNID 59
Db 1 MMSASRLAGTILIPMAFLSCVSPESMEPCVEVENVITYQCMELNFKYKIPDMLPSTKXLD 60
Oy 60 LSPNPLKILKYSFESNSELQWLDLSRCEIETIEKAMHGLHLSNLTGNIPIOSFSPG 119
Db 61 LSFNPLRHLSYSFSPFELQVLDLSRCEIOTIEGAYQSLSHSTLLTGPIQSALMG 120
Oy 120 SPSGLTLENIVAVETKSLASLESPIGOLITLKKLVANFNHFSCKLPAYFSNLTNLVAV 179
Db 121 AFSGLSSLOKVAVETNLASLENFPIGHKTKELANVANHLIOSKLEBYFSNLTNLVAV 180
Oy 180 DLSYNYIOTIVNDIQFRENPOVNLSDMSINPIDFIQDAFQGIKIHETLRGNFSS 239
Db 181 DLSNKKIGSIYCTDLRVHQMPLNLSLDLSINPMNFIOPGAFKEIRLHKLTLRNNPDL 240
Oy 240 NIMKTCLONLAGVHRLILGSPKDEBNLEFEPISMEGLCVITIDEPLATYTNDPSNDI 299
Db 241 NIMKTCTIOGLAGLEVHRLVIGEFNENLEKPKSLBELCNLTIEEFLAALDYLDLI 300
Oy 300 VAFHCLANVAMSLAGVSIKYLEDPKHKFQKQSLIIRCOHKOPEPTDLPLKSLITLM 358
Db 301 IULFNCLTNVSSSLVSVTIERKPSYVFGQHLVAVCKGQPFLLKSLKLTPTS 360
Oy 359 NKGSIKFKVALPSLSYLDLSRNVALSFSCCYSYDLGTNSLRHLDSFNGALIMSANG 418
Db 361 NKGNAFSEVDLPSEFLDLNRNGLSFKGCCSDGTTSLKYLDSFNGVITMSSNPLG 420
Oy 419 LBELOHLDPOHSTLKVTERPSAFLSEKLIYLDISTYNTKIDPDGIFLGTLSTNLTKMG 478
Db 421 LBELOHLDPOHSTLKVTERPSAFLSEKLIYLDISTYNTKIDPDGIFLGTLSTNLTKMG 480
Oy 479 NSKNDTLNVFANTNTNLPFLDLSKCOLBOISWGPDTLHRLQDLNMSHNNLLFLDSHY 538
Db 481 NSQENFLPDITFELANLFTLDSQOLBELSTANSLSSLOLVAMSHNNPFLDTPPY 540
Oy 539 NQYSLSTLDCSPNRIETS-KGILQHPKSLAFENLTNNSVACICEHOKFLVWVKQKPF 597
Db 541 KCLNSLOVDLYSLNHNMTSKKQLQHPSSLAFLNTQNFACCTCHOSFLQWIKOROL 600
Oy 598 LVNVEQWTCATPYEANTSLVLDNRNSCTCYKTIISVSYSVIVGVNAFLIHYFPHLI 657
Db 601 LVEVERHECATPDKQMPVLSL-NITCQNNKTIIGVSIVSVLVSVAALVVKFPHLM 659
Oy 658 LINGCKYKSGESITYDAFVIYSSONEDMVNENLVKNLESEVVPFHLCLHYRDTIPGVAL 717
Db 660 LLAGCITKIGZENITYDAFVIYSSODEDMVANELVKLEBEVPPQCLAHRTDIPGVAL 719
Oy 718 ANIIQEGFHKSRKIVVSSHPIQSRWCIFEYELAQTQFPLSSRGGIIFLVEKESKL 777
Db 720 ANIIHEBFHRSRKIVVVSQHFIOSRWCIFEYELAQTQFPLSSRGGIIFLVEKESKL 779
Oy 778 RQVEVLYRLSRNTYLEWEDNPLGRHIFWRRLKALLDGRASNEQT 824

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Db 780 RQVEVLYRLSRNTYLEWEDSVLGRHIFWRRLKALLDGRASNEQT 826

RESULT 2
ABU04774
ID ABU04774 standard; protein; 839 AA.

XX ABU04774;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1440.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO5 INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.

XX Example 2; SEQ ID NO 1440; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

XX Sequence 839 AA;

Query Match 65.5%; Score 2847; DB 6; Length 839;
Best Local Similarity 67.6%; Pred. No. 7.2e-237; Indels 4; Gaps 4;
Matches 559; Conservative 101; Mismatches 163;

Oy 1 MMPWILARTLIMLV-FPSCITPGSLNPCIIEVVPNTTYQCMDQKLSKVDDIPSSSTKNID 59

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Db      1  MMSASRLAGTILIPMAAFISCAPBESWEPCEVAVPNITQCMELNFKYKIPDNLPESTKND 60
Qy      60  LSFNPLKILKYSFNSFSELQWLDLSRCEIETIEDKAMHGHLSNLITGNPIOSFSPG 119
Db      61  LSFNPLRHLSGYSFSPPELQVLDLSRCEIETIEDGAYOSLSHSLITLITGNPIOSLALG 120
Qy      120  SFGSLTSENLVAVETKSLASLESFPIGQILITLKKLVANANFHSCKLPAYFSNLTNLVHV 179
Db      121  AFSGLSSLOKLVAVETNLASLENPPIGHLKTLKELVANANLQSPKLEPEFSNLTNLEHL 180
Qy      180  DLSVNYIQTITVNDLOFLRENPOVNLSDMSLNPIIDFIOQAFOGKIKHELTLRGNFSS 239
Db      181  DLSNKKIOSIYCTDLRLVHOMPLNLSDLSLNPNNFTOPGAFKEIRLHKLTLRNNPDSL 240
Qy      240  NIMKTCLONLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCVTIDEFRLTYTNDPSDDI 299
Db      241  NNMKTCIOGAGLEVHRLVIGEFNENLEKDKALSGLCNLTIEFRILAVLDYIYDDI 300
Qy      300  VK-FHCLANVSAMSLAGVSIKYLEDPVPHFKWQSLIIRCOLKOPPTLDLPFLKSLTLM 358
Db      301  IDLFNCLTNVSSFSFVSVTIERVKDFSYNFGWQHELVNCKRGCPPTLKLKSLKTLFTS 360
Qy      359  NKGSIKPKVALPSLSYLDLSRNALSPSGCCSYDGLNSLRHLDSFGALIMSANFMG 418
Db      361  NKGNAFSEVDLPSEFLDLSRNGLSFKGCCSQSDFGTSLKYDLSFNGVITMSNBLG 420
Qy      419  LEELOHLDFOHSTLKRVTESFAFLSEKLYLDISYTNKIDFDGIFGLTSNLTLMKAG 478
Db      421  LEQLEHLDFOHSTNKKOMSEFVFLSLRNLIVLISHTRVAFNGIFNGLSLEVLKXAG 480
Qy      479  NSFQDNTSNVPAANTNLITFDLSKCCQLEQISWGVFTLHRLQILNMSHNNLFLDSSH 538
Db      481  NSFQENLPDIFTELRLNLTFDLSQCCQLEQLSPFAFNSLSLQVLMNSHNNFSDTPPY 540
Qy      539  NQVLSLGLDSCFNRIFETS-KGILQHPKSLAFPLTNNSVACCEHOKFLOMKEQOF 597
Db      541  KCLMSLOVLDYLSLHIMTSSKQEOLOHFPSSLAFLNLTYNDPACTCEHOSFLQMKDQOL 600
Qy      598  LVNVEOMTCATPVENNTSLVLDFNNSSTCYMYKTIISVSVAVIYVSTVAFILYHFLHI 657
Db      601  LVEVERRECATPSPKQGMVLSL-NITQOMKTIIGVSVLSLVVSVAVIYKRYFLHM 659
Qy      658  LIAGCKYISRGESYIDAFVIYSSQNEDEWVNLVKNLEEGVPRFLCLHYDPFIPGAIA 717
Db      660  LIAGCIXKXRGENIYDAFVIYSSQDEDEWVNLVKNLEEGVPPQLCLHYDPFIPGAIA 719
Qy      718  ANIOEGFHSRKXIVVVRHFIOSRNCIEFEYETAOQWOFISSRSGLIFLYLEKVEKSL 777
Db      720  ANIIEGHFHSRKXIVVVSQHFIOSRWCIFFEYETAOQWOFISSRAGIIFVLOKVEKTL 779
Qy      778  ROQVELYRLSLRNTYLEWEDNPLGRHIFWRRLKNALLDGKASNPQOT 824
Db      780  ROQVELYRLSLRNTYLEWEDSVLGRHIFWRRLKALLDGKSWNPBGT 826

```

RESULT 3
ABU04775
ID ABU04775 standard; protein; 839 AA.

XX ABU04775;
XX
XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1441.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX Homo sapiens.

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XX      XX      WO200278524-A2.
XN      PD      10-OCT-2002.
XX      XX      28-MAR-2002; 2002WO-US009671.
XX      XX      28-MAR-2001; 2001US-0279495P.
PR      PR      21-MAY-2001; 2001US-0292544P.
PR      PR      08-AUG-2001; 2001US-0310801P.
PR      PR      01-OCT-2001; 2001US-0326370P.
PR      PR      04-DEC-2001; 2001US-0336780P.
PR      PR      20-FEB-2002; 2002US-0358985P.
XX      XX      (ZYCO-) ZYCO INC.
PA      PA      Chicx RM, Tomlinson AJ, Urban RG;
XX      XX      WPI; 2003-040607/03.
XX      XX      New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT      PT      cytoskeletal proteins, receptors or transcription factors), useful for
PT      PT      treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX      XX      leukemia.
XX      XX      Example 2; SEQ ID NO 1441; 134bp; English.
XX      XX      The invention describes a purified polypeptide, which comprises a
CC      CC      fragment of a kinase, phosphatase, protease, or protease inhibitor.
CC      CC      transporter, cytoskeletal protein, receptor or transcription factor. The
CC      CC      polypeptide is useful as an immunogenic composition for eliciting in a
CC      CC      mammal an immunogenic response directed against any of the purified
CC      CC      polypeptide. The purified polypeptide, or the antibody that binds to this
CC      CC      polypeptide, is useful for treating cancer. The polypeptide is also
CC      CC      useful for identifying compounds that binds to a naturally processed
CC      CC      class I or class II MHC-binding polypeptide. The polypeptides and
CC      CC      polynucleotides are particularly useful for treating or preventing
CC      CC      myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC      CC      lymphoma or leukemia. These are also useful for screening agents for
CC      CC      treating the above mentioned diseases. This sequence represents an
CC      CC      expressed protein tag (EPT) isolated from human tissue for translational
CC      CC      profiling. Note: This sequence does not appear in the printed
CC      CC      specification but was obtained in electronic format directly from WIPO at
CC      CC      ftp.wipo.int/pub/published_pct_sequences
XX      XX      Sequence 839 AA:
SQ
Qy      Qy      Query Match      65.5%; Score 2847; DB 6; Length 839;
Qy      Qy      Best Local Similarity 67.6%; Pred. No. 7.2e-237;
Db      Db      Matches 559; Conservative 101; Mismatches 163; Indels 4; Gaps 4;
Qy      Qy      1  MPPFWILARTLIML--FFSCLTSGSLNPCIENVVNTTYQCMQDQLSKVPDDIPSTKND 59
Db      Db      1  MMSASRLAGTILIPMAALSCVRPESWEPCEVAVPNITQCMELNFKYKIPDNLPESTKND 60
Qy      Qy      60  LSFNPLKILKYSFNSFSELQWLDLSRCEIETIEDKAMHGHLSNLITGNPIOSFSPG 119
Db      Db      61  LSFNPLRHLSGYSFSPPELQVLDLSRCEIETIEDGAYOSLSHSLITLITGNPIOSLALG 120
Qy      Qy      120  SFGSLTSENLVAVETKSLASLESFPIGQILITLKKLVANANFHSCKLPAYFSNLTNLVHV 179
Db      Db      121  AFSGLSSLOKLVAVETNLASLENPPIGHLKTLKELVANANLQSPKLEPEFSNLTNLEHL 180
Qy      Qy      180  DLSVNYIQTITVNDLOFLRENPOVNLSDMSLNPIIDFIOQAFOGKIKHELTLRGNFSS 239
Db      Db      181  DLSNKKIOSIYCTDLRLVHOMPLNLSDLSLNPNNFTOPGAFKEIRLHKLTLRNNPDSL 240
Qy      Qy      240  NIMKTCLONLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCVTIDEFRLTYTNDPSDDI 299
Db      Db      241  NNMKTCIOGAGLEVHRLVIGEFNENLEKDKALSGLCNLTIEFRILAVLDYIYDDI 300
Qy      Qy      300  VK-FHCLANVSAMSLAGVSIKYLEDPVPHFKWQSLIIRCOLKOPPTLDLPFLKSLTLM 358

```

Db 301 IDLFLNCLTNVSSFLSVITIERVKDFSYNFGWQHELVNCKFGQPEPTLKLSKRLTFTS 360
Qy 359 NKGSIFFPKYALPSLSYLDLSRNAALSFSGCCSYSDLGTSNLRHLDLSPNGAIIIMSANFMG 418
Cc 361 NKGNAFSEVDLPSELFLDLISRNGLSPKGCOSQSDGFTSLKTYLDLSPNGVITMSNPLG 420
Xx 419 LEBLOHLDPOHSTLKRATPSAFLSEKLYLDISYNTKIDPDGIFLGTSINTLKMG 478
Qy 421 LEBLOHLDPOHSTLKRATPSAFLSEKLYLDISYNTKIDPDGIFLGTSINTLKMG 480
Db 479 NSFKDNTLSNVFANTTNLTFLDLISKQLEQISWGVFDTLRHLDLNNSHNNLPLDSSH 538
Qy 481 NSFGENFLPDIFTELRLNLTFLDLISQCOLEQISPAFNSLSLDVLANSHNNFSLDTPPY 540
Db 539 NQVSLSTLDCSFNRIETS-KGILQHPKSLAFNLTNNSVACICEHOKFLOMWKEOKOF 597
Qy 541 KCLNSLOVLDVSLNHIWTSKQELQHPSSLAFLNLTQNDPACTCEHOSFLQWIKDOROL 600
Db 598 LVNVEQMTCAFPVENMTSLVLDPNNSCTCYMYKTIISVSVSIVVSTVAFLIYHFFHLI 657
Qy 601 LVEVERMECATPSPDKQMPVLSL-NITCOMNKTIIGVSVLSVLVSVVAVLVYKFFPHLM 659
Db 658 LIAGCKKYSRGEISYDAFVIYSSQNEWDVNRNLYKNLEEGVPRPHLCLHYRDPFGVAIA 717
Qy 660 LIAGCIKRGENTYDAFVIYSSQDEWDVNRNLYKNLEEGVPRPOLCLHYRDPFGVAIA 719
Db 718 ANIIQEGHFKSRKVIYVVSRRHFIQSRWCIFEYELIAQTMQPLSSRGGIIFIVLEKYEKSL 777
Qy 720 ANIIHEGFHKSRRKVIYVVSQHPFIQSRWCIFEYELIAQTMQPLSSRGGIIFIVLEKYEKSL 779
Qy 778 RQOVELYRLLSRNTYLEMEDNPLGRHIFWRRLKNALLDGKSNPEQT 824
Db 780 RQOVELYRLLSRNTYLEMEDSVLGRHIFWRRLKALLDGKSNPEQT 826

RESULT 4
ADC78785
ID ADC78785 standard; protein; 839 AA.
XX
AC ADC78785;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human PRO protein #7.
XX
KX human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX
OS Homo sapiens.
XX
PN MO2003034984-A2.
XX
PD 01-MAY-2003.
XX
PF 15-OCT-2002; 2002MO-US033070.
XX
PR 19-OCT-2001; 2001US-0340083P.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL;
XX
DR WPI, 2003-481990/45.
XX
N-PSDB; ADC78784.
XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
PT disorder e.g., ulcerative colitis or Crohn's disease.
XX
PS Claim 12; SEQ ID NO 14; 327bp; English.
XX
CC The invention comprises the amino acid and coding sequences of human PRO
CC proteins. The DNA and protein sequences of the invention are useful for
CC

CC the diagnosis and treatment of cancer and inflammatory bowel disease
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
CC sequence represents a human PRO protein of the invention.
Xx
SQ Sequence 839 AA;
Query Match 65.5%; Score 2847; DB 7; Length 839;
Best Local Similarity 67.6%; Pred. No. 7, 2e-237;
Matches 559; Conservative 101; Mismatches 163; Indels 4; Gaps 4;
Qy 1 MMPFWLARTLIMAL-FSGLTPGSLNPCIYEVNPTTYQCMQKLSKYPDDIPSSRTKND 59
Db 1 MMSASLACGLIPAMAFSLCVBPESWPCVEVVPNTTYQCMELNFKYKIDNLPSTKAMD 60
Qy 60 LSFNPLKILKYSFSSNFSFLQWLDLSRCEIETEDKAMGLNHLNLTITGNPIQSPBQ 119
Db 61 LSFNPLRHLGSYSFSPFLQVLDLSRCEIQTIEDQAYOSLSLSTLITLGNPIQSLAG 120
Qy 120 SPSGLTSLENLVAVETKSLASFSFPIGOLITLKKLVANANFJHSCKLPAYFSNLTNLVHY 179
Db 121 AFSGLSLQKLVAVETNLASLENFPIGHLKTLKELVANAHLIQSPKLPYFSNLTNLVHL 180
Qy 180 DLSYNYIQITTVNDLOFLRENPOVNLSDMSLNPIPIQDAQGIKTHETLRGNPNS 239
Db 181 DLSNKLQSIYCTDLRLVHQMPPLNLSLDLSLPMNFIOGAKKEIRLKLTLRNNFSL 240
Qy 240 NIMKTCIQNLAGLHVRHLIIEGFERENLEIFPSSIMEGCDVTIDEFRLLTYNDSDDI 299
Db 241 NMKTCIQLAGLEVHVLVGEFRNENLEKFDKSALEGICNLTIEFRRLAYDYLDI 300
Qy 300 VK-FHCLANYSAMSIAVSILKYLEDVYKHFQMSLIIRCOLQOPTLDPFLKSLTLM 358
Db 301 IDLFLNCLTNVSSFLSVITIERVKDFSYNFGWQHELVNCKFGQPEPTLKLSKRLTFTS 360
Qy 359 NKGSIFFPKYALPSLSYLDLSRNAALSFSGCCSYSDLGTSNLRHLDLSPNGAIIIMSANFMG 418
Db 361 NKGNAFSEVDLPSELFLDLISRNGLSPKGCOSQSDGFTSLKTYLDLSPNGVITMSNPLG 420
Qy 419 LEBLOHLDPOHSTLKRATPSAFLSEKLYLDISYNTKIDPDGIFLGTSINTLKMG 478
Db 421 LEBLOHLDPOHSTLKRATPSAFLSEKLYLDISYNTKIDPDGIFLGTSINTLKMG 480
Qy 479 NSFKDNTLSNVFANTTNLTFLDLISKQLEQISWGVFDTLRHLDLNNSHNNLPLDSSH 538
Db 481 NSFGENFLPDIFTELRLNLTFLDLISQCOLEQISPAFNSLSLDVLANSHNNFSLDTPPY 540
Qy 539 NQVSLSTLDCSFNRIETS-KGILQHPKSLAFNLTNNSVACICEHOKFLOMWKEOKOF 597
Db 541 KCLNSLOVLDVSLNHIWTSKQELQHPSSLAFLNLTQNDPACTCEHOSFLQWIKDOROL 600
Qy 598 LVNVEQMTCAFPVENMTSLVLDPNNSCTCYMYKTIISVSVSIVVSTVAFLIYHFFHLI 657
Db 601 LVEVERMECATPSPDKQMPVLSL-NITCOMNKTIIGVSVLSVLVSVVAVLVYKFFPHLM 659
Qy 658 LIAGCKKYSRGEISYDAFVIYSSQNEWDVNRNLYKNLEEGVPRPHLCLHYRDPFGVAIA 717
Db 660 LIAGCIKRGENTYDAFVIYSSQDEWDVNRNLYKNLEEGVPRPOLCLHYRDPFGVAIA 719
Qy 718 ANIIQEGHFKSRKVIYVVSRRHFIQSRWCIFEYELIAQTMQPLSSRGGIIFIVLEKYEKSL 777
Db 720 ANIIHEGFHKSRRKVIYVVSQHPFIQSRWCIFEYELIAQTMQPLSSRGGIIFIVLEKYEKSL 779
Qy 778 RQOVELYRLLSRNTYLEMEDNPLGRHIFWRRLKNALLDGKSNPEQT 824
Db 780 RQOVELYRLLSRNTYLEMEDSVLGRHIFWRRLKALLDGKSNPEQT 826

RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
XX
AC ADD48826;
XX

DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
DE Human Protein AAF05316, SEQ ID NO 14536.
XX
XX Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SN1; Chung.
OS Homo sapiens.
XX Unidentified.
XX MO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX (GEMO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'Urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; AAF05316.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SN1)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (described in Table 3
XX of the specification) which is differentially expressed during pain.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 839 AA;
SQ
Query Match 65.5%; Score 2847; DB 7; Length 839;
Best Local Similarity 67.6%; Pred. NO. 7.2e-237;
Matches 559; Conservative 101; Mismatches 163; Indels 4; Gaps 4;
QY 1 MPPMLARTLIMLV-FPSCLTPGSLNPCIENVNITVQCMQKLSKVPDDIPSTKIID 59
DB 1 MMSASRLAGTLIPAMAFSLSCRPSPSWECVEVNNITVQCMELNFKYKIPDLPTSTKIID 60

QY 60 LSFNPKILKYSFSGNFSELOMDLSRCEIETIEDKAMHGLHLSNLITGNPIQSFSG 119
DB 61 LSFNPLRLHGSYSFSPFELQVLDLSRCEIQTIEDGAVQSLSHSTLITGNPIQSLMG 120
QY 120 SFGSLTSLNVAVETKLASLESPPIGQITLTKLVANHNTHCKLPAVYSNLTVLVH 179
DB 121 AFSGLSSLOKVAVAETNLASLENFPIGLTKLKELVANHNTHCKLPAVYSNLTVLH 180
QY 180 DLSVYIQTITVNDQFRENPOVNLSDMSINPDIQDOAFQGIKLHELTIRGNFNS 239
DB 181 DLSNKKIOSICTDLRLVHOMPLNLSDLSINPNFIQPGAFKIRLHKILTRNNFSL 240
QY 240 NIMKTCIQNLAGLHVHRLILGEFDERNLJIFBESIMEGLCDVITDERLTYTNDPFSDI 299
DB 241 NIMKTCIQNLAGLHVHRLILGEFDERNLJIFBESIMEGLCDVITDERLTYTNDPFSDI 300
QY 300 VK-FHCLANVAMSISAGISITKLEVDVPHFQMSLSITRCQLKQPTLDLPELSLITM 358
DB 301 IDLFNCLTNVSSFSLVSTIERKDFSYNFMQHLVNCCKFGQPTLKLKSLRLPETS 360
QY 359 NKGSIFFKVALPSISYDLISRNALSPGCSYSDLGTSNLRHDLSPNGAIIINGANPMG 418
DB 361 NKGNAFSEVLPSELEFLDLSRNGLSFGCCSQSDFGTTSKYLDSLFGNVTMSSNPLG 420
QY 419 LEELOHLDFOHSTLKRVTFESGAPLSLEKLYLDISYTNKIDPDGIFGLTSLNTLKNAG 478
DB 421 LEOLEHLDFOHSTLNKQMSFVFLSLRLIYLDISHTRVAFNGIFNGLSLEVLKNAG 480
QY 479 NSFKDNTLSNVFANTNLTLPDLDSKQLEQISMGVPTDHLQLANSHNNLPLDSSH 538
DB 481 NSFQENFLPDLFTSLRLNLTFLDLSQCLEQISPPAFNSLSLQVLNMSHNNFSLDTPY 540
QY 539 NQLVSLSTLDCSPRIETS-KGILOFPKSLAFNLITNSVACICEHOKFQWVWEOKOF 597
DB 541 KCLNSLOVLDVSLNHNTHSKQELQHPSSALFNTQNDPACTCEHOSFLQMDKQOL 600
QY 598 LVNVEQWTCATPEVEMNTSLVLDNFNSSTCYMYKTIISVSVSVIYSTVAFLLIYHFFHLI 657
DB 601 LVEVERMECAPPSDKQGMPLVSL-NITQNMKTIIGVSVLSVLVAVLVYKFFILM 659
QY 658 LIACKKYSRGSSTYDAFVYISSQNMWYNELVKNLEEGYPRHLCLHTRDPIPGVAIA 717
DB 660 LLAOCITYGRENITDAFVYISSQDEDMVRELKMLEEGVPPQOLCLHTRDPIPGVAIA 719
QY 718 ANIOEGHRSRKATVIVVSRHFIQSRMCIFEYEAQTOMPLSSRSGIIFVLEKVERSL 777
DB 720 ANIHGEFHRSRKATVIVVSRHFIQSRMCIFEYEAQTOMPLSSRSGIIFVLEKVERSL 779
QY 778 RQVELYRLLSRNTYLEMEDNPLGRHIFWRRLKNALDGRKANPEQT 824
DB 780 RQVELYRLLSRNTYLEMEDSVLGRHIFWRRLKALLDGRKANPEGT 826
RESULT 6
ID AAW86361 standard; protein; 837 AA.
XX
XX AAW86361;
AC
XX 15-MAR-1999 (first entry)
DT
XX
XX Human DNAX toll-1ike receptor DTLR4.
DE
XX
XX DNAX toll-1ike receptor; DTLR; Drosophila toll receptor; Il-1 receptor;
XX interleukin 1 receptor; phosphate metabolism; innate immunity response;
XX modulate inflammatory function; morphological effect;
XX immunological disorder.
OS Homo sapiens.
XX
XX W09850547-A2.
XX
XX 12-NOV-1998.
PD

XX 07-MAY-1998; 98WO-US008979.
 XX 07-MAY-1997; 97US-0044293P.
 PR 22-JAN-1998; 98US-0072212P.
 PR 05-MAR-1998; 98US-0076947P.
 XX (SCHE) SCHERING CORP.
 PA Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
 PI MPI: 1999-059670/05.
 DR N-PSDB; AAV80675.
 PT Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
 XX metabolism, modulate inflammatory function or innate immunity responses.
 PS Claim 3; Page 147-149; 171pp; English.
 XX The present invention specifically describes human DNAX toll-like
 CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
 CC in the present invention. Also described are: (1) a fusion protein
 CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
 CC an antibody or antibody fragment which specifically binds to a DTLR
 CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
 CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a
 CC host cell comprising the vector of (4). The host cell of (5) can be used
 CC to produce the DTLR proteins. The DTLR proteins can be used to alter
 CC phosphate metabolism, to modulate inflammatory function, innate immunity
 CC responses or morphological effects. The DTLR proteins can be used in the
 CC treatment of conditions exhibiting abnormal expression of the receptors
 CC of their ligands. These abnormalities are typically manifested by
 CC immunological disorders
 XX Sequence 837 AA;
 SQ
 Query Match 65.1%; Score 2829 5; DB 2; Length 837;
 Best Local Similarity 67.7%; Pred. No. 2.4e-235;
 Matches 556; Conservative 101; Mismatches 159; Indels 5; Gaps 5;
 QY 7 LARTLIMAL-FSPCITPGSLNFCIEVFNITQCMDQKSKSPDDIPSTKINIDLSFNPFL 65
 DB 6 LAGTILPMAFLSCRPBSEBECVE-VNITTYQCEHAINYYKIPDLNPFSTKIDLSFNPFL 64
 QY 66 KILKYSFSGNFSLOLMDLSRCEIETIEDKXAHGLHLSNLLITGNPIQSFSPGSGFGIT 125
 DB 65 RHIGSYFSPFPELQVLDRSCEIQTEBDGAYQSSHSTLLITGNPIQSLALGAFSGIS 124
 QY 126 SIENIVAVETKIASSEFPISGILITLKLIVAHNFHSGCLPAYFSNLTNLVHVDLSVYX 185
 DB 125 SIQKLVAVETNLASLENFPIGHLKILKEIVAHNLQSFKLPEYFSNLTNLHLDLSNK 184
 QY 186 IOTITVNDIQFLRENQVNLSDMSINPIIDFIDQAFQGIKLBELTLRGFNSSNIMKTC 245
 DB 185 IGSIVCTDRAVHLQWPLNLSDLSLNPNNFIQPGAFKEIRLHKILRNNPFSGLNVMKTC 244
 QY 246 LQNLAGLHVHRLILGFFKDERNLIEPESIMBGLCVTTIDERRITLTNDPSDDIVK-FHC 304
 DB 245 IQGLAGLEVHRLVILGFEFRNENLEKFDKALBGLCNLTIEEPRLAYLDYLDIDLFNC 304
 QY 305 LANVSMILAGVSIKYLEVDPKHFKWOSLSIIRCOLKOPPTDLPLKSLITLTMKGSIS 364
 DB 305 LTNVSSFSIVSVTIEVKDPSPYNGWQHELAVNCKGQGFPLTKLKLKRLITFSNKGNA 364
 QY 365 FKVALPSLSYLDLSRNALSFSGCYSVDLGTNSLHLDLSPNGALIMSANFNGLELOH 424
 DB 365 FSVVDLPSEFLDLSNGLSFKGCCQSDGCTSLKXIDLSFNGVITWSNFIQLGLOLH 424
 QY 425 LDFQHSHTLKRVTFSAFLSLKLEKLYLDISYNTNKIDPDGIFGLTSLNTLKAAGNFKDN 484
 DB 425 LDFQHSNLIKQMSBFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSLIEVLKXAGNSFOEN 484
 QY 485 TLSNVAANTNTNLFLDLSKQLEQISMGVDPDLHRLQLLMSNNLLFLDSSHYNDLSL 544

DB 485 FLDPDITELRNLFLLDLSQOQLEQLSPTAFNLSLSQVLNMSHNNFSLDTPFYKCLNSL 544
 QY 545 STLDGSEFNRIETS-KGILQHPKSLAFPNLTNNNSVACICGHQKFLQMVKEOKQFLVNVQ 603
 DB 545 QVLDYSINHIWTSKQELQHPSSLAFNLNTQNDFACTGHSQSLQWIKQROLLEVER 604
 QY 604 MTCATPEVNTSLVLDFNNSTGCMYKTIISVSVSVIVVSTVAFVLYHFFYHILLAGCK 663
 DB 605 MECHTPEBCKQGMVLSL-NITCOMKNTIIGVSLVSVVAVLVVYKFFHMLLAGCI 663
 QY 664 KYSGESIYDAFYIYSSQNEQWVRNELLVKNLEEGVPRFHLCLHYRDFIPVAILAANIQ 723
 DB 664 KYSGENIYDAFYIYSSQDEQWVRNELLVKNLEEGVPRFQCLHYRDFIPVAILAANIHE 723
 QY 724 GFHKSRKVIYVSRHFIQSRWCIPEVEIAQTQWFLSRSGIIFLYLEKVEKSLRQOVEL 783
 DB 724 GFHKSRKVIYVSRHFIQSRWCIPEVEIAQTQWFLSRSGIIFLYLEKVEKSLRQOVEL 783
 QY 784 YRLISRTYLEWEDNPLGRHIFWRRLKNALLDGKASNPQOT 824
 DB 784 YRLISRTYLEWEDSVLGRHIFWRRLKALLDGKSNPEOT 824
 RESULT 7
 ID AAE16102 standard; protein: 837 AA.
 AC AAE16102;
 DT 26-MAR-2002 (first entry)
 DT Human DNAX Toll like receptor (DTLR) 4 #2.
 DE Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
 KW interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
 XX Homo sapiens.
 XX OS WO200190151-A2.
 XX 29-NOV-2001.
 XX 23-MAY-2001; 2001WO-US016766.
 XX 25-MAY-2000; 2000US-0207558P.
 XX (SCHE) SCHERING CORP.
 XX Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
 PI MPI: 2002-083085/11.
 DR N-PSDB; AAD26292.
 PT New DNAX Toll like receptor (DTLR) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 XX Claim 3; Page 41; 297pp; English.
 XX The invention relates to mammalian receptor proteins, e.g., primate,
 CC human DNAX Toll like receptor (DTLR) protein and their corresponding
 CC nucleic acids. The DTLR is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTLR is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTLR is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g. capable of distinguishing between other fragments. The
 CC receptor family members, for the DTLR or its various fragments. The
 CC purified DTLR can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression

CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTR or cells that express it. The present sequence is
 CC human DTR4 protein. The DTR4 gene is located on chromosome 9q32-33.
 CC Note: The present sequence SEQ ID NO 26 is stated to be similar to the
 CC sequence shown in page 240-243 (AAB16116). However these sequences differ
 CC at several locations

XX Sequence 837 AA;

Query Match 65.1%; Score 2829.5; DB 5; Length 837;
 Best Local Similarity 67.7%; Pred. No. 2,4e-235;
 Matches 556; Conservative 101; Mismatches 159; Indels 5; Gaps 5;

```

QY 7 LARTLIMAL-PPSCITPGSLNPCIIEVVPNTTYQCDQKLSKVPDDIPSSSTKNDLSFNPL 65
DB 6 LAGTILIPAMAFILSCVRESMEPCVE-VPNITYQCEMLNPFYKIPDNLPESTKNLDSFNPL 64
QY 66 KILKYSFSPNSELOMDLSRCEIETIEDKAMHGLHLSNLTGNPIQSPGSGSGLT 125
DB 65 RHLSGSYFSPFELQVLDLSRCEIOTIEDGAYOSLSHSTLITGNPIQSLALGAFSGLS 124
QY 126 SLENVAVETKLASIESPFIQOLITLKKLVANHFISCKLPAYPSNLTNLVHVDLSVNY 185
DB 125 SLQKIVAVETNLASLENPFIQHLTKLKELVANHLIQSKLPESYNTNLNLSHLDLSNK 184
QY 186 IQTITVNDLQFLRENPOVNLSDMSLNPIIDFIDQAFQGIKLEHETLRGNFSSNMKTC 245
DB 185 IQSIVCTDLRVLHQMPNLNLSLDSLNPNFIQPGAFKIRLHKILTRNPFSLNVMKTC 244
QY 246 IQNLAGLHVHRLILGEPKDERNLEIFEPBSIMEGLCDVTIDEERLTYTNDSDDIYK-FHC 304
DB 245 IQGLAGLEVHRLVLDGEPNENLEKFKDSKALEGLCNLTIEERLTYLVDYLDIIDLFFNC 304
QY 305 LANSAMSILAGISIKYLEDPVPGHFKQKOSLSIRCOLKOPETDLPEFLSLTLTMNKGSS 364
DB 305 LTNVSFSLVSTIRKVDPSFNFGKQHLNCKFCGPPKILKSLKRLITSNKGVNA 364
QY 365 FKQVALPSLSDLSRNALSPSGCCSYSDLTGNSLRHDLSPNGAIIINSANFMGLELQH 424
DB 365 FSEVDLPSELFLDLSRNGLSFKGCCSQSPGTTSLKYLIDLSNGVITMSSNLTGLGLEH 424
QY 425 LDFOHSTLKRVTEBFAFISLEKLYLDISYNTKIDFDGIFLGTSLNTLMKAGNSPKDN 484
DB 425 LDFOHSTLKRVTEBFAFISLEKLYLDISYNTKIDFDGIFLGTSLNTLMKAGNSPKDN 484
QY 485 TLSNVEFANTNLTPFLDLSKCOLEOISWGVEDTLHRLQLIMSHNNLTLFDSHNYQYSL 544
DB 485 FLPLDFTLRLNLTFLDLSQCOLEOISPTAFNSLSLQVLMNSHNPFLDTPPYCLNSL 544
QY 545 STLDGSENRIS-EGILQHPKSLAFPNLTNNSVACICEHQKFLQWVEQKQFLVNEYQ 603
DB 545 QVLDSYSLNHLMTSKKQELQHPSSLAFPNLTNDPACCEHQSFLQWKDQQLVVER 604
QY 604 MTGATPVEAMNTSLVDENNSTCYMYKTIISVSVAIVVSTAYFLIYHFFHLIIIAACK 663
DB 605 MECAITPSKQKQMPVLSL-NITCOMAKTIIIGVSLVSVAVAVLYKFEFLMLACGI 663
QY 664 KYSRGEISTYDAFVITYSSQNDPMVRELVKNLEEGVPRPHLCIHYDFTPGVAILANITQE 723
DB 664 KYRGENIYDAFVITYSSQNDPMVRELVKNLEEGVPRPHLCIHYDFTPGVAILANITQE 723
QY 724 GFHRSKRVIVVSRHFIQSRWCIFFEYIAQTWQFLSSRSGIIFYLEKESLIRQOVEL 783
DB 724 GFHRSKRVIVVSRHFIQSRWCIFFEYIAQTWQFLSSRSGIIFYLEKESLIRQOVEL 783
QY 784 YRLSRNTYLEWEDNPLGRHIFWRRLKVALIDGRASNPQOT 824
DB 784 YRLSRNTYLEWEDNPLGRHIFWRRLKVALIDGRASNPQOT 824

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RESULT 8
 ABU04776

ID ABU04776 standard; protein; 837 AA.
 AC ABU04776;
 XX 29-JAN-2003 (first entry)
 DT XX
 XX Human expressed protein tag (EPT) #1442.
 DE XX
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 XX Homo sapiens.
 OS MO200278524-A2.
 XX
 XX 10-OCT-2002.
 PD 28-MAR-2002; 2002WO-US009671.
 XX
 XX 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358955P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX Chicz RM, Tomlinson AJ, Urban RG;
 PI WPI: 2003-040607/03.
 DR
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1442; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, or protease inhibitor.
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_poc_sequences

XX Sequence 837 AA;

Query Match 65.1%; Score 2829.5; DB 6; Length 837;
 Best Local Similarity 67.7%; Pred. No. 2,4e-235;
 Matches 556; Conservative 101; Mismatches 159; Indels 5; Gaps 5;

```

QY 7 LARTLIMAL-PPSCITPGSLNPCIIEVVPNTTYQCDQKLSKVPDDIPSSSTKNDLSFNPL 65
DB 6 LAGTILIPAMAFILSCVRESMEPCVE-VPNITYQCEMLNPFYKIPDNLPESTKNLDSFNPL 64
QY 66 KILKYSFSPNSELOMDLSRCEIETIEDKAMHGLHLSNLTGNPIQSPGSGSGLT 125
DB 65 RHLSGSYFSPFELQVLDLSRCEIOTIEDGAYOSLSHSTLITGNPIQSLALGAFSGLS 124

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QY 126 SLENLVAVETKLASLSPFPIGQILITLKKLVANAHNFHSCKLPAYFSNLTNLVHVDSLSTNY 185
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 125 SLQKLVAVETNLASLENFPIGHLKTLKELVNAHNLQSPFLPEFYSNLTLEHLDLSNKK 184
XX
XX
XX
QY 186 IQTTIVNDLOFLRENPOVNLSDMSLNPIDFQDAFOGKIKHELTLRGNFSSNIMKTC 245
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 185 IQSIYCTDLRVLHQMPNLNLSDLSLNPMPNFIOPGAKFELRLHKLTLRRNFDLSLVNWKTC 244
QY 246 LQNLAGLHVRLILGEFKDERNLEIFPSPIMEGLCDVTIDEFRLTYTNDSDDIK-FHC 304
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 245 IQGLAGLEVRLVGEFRBGNLEKFPKSALEGLCNLTIEFRFLAYLDYLDIDIDFNC 304
QY 305 LANVSAMSLAGVSIKYLEDPVPRKFWQSLIIRCOLKOPPTLDPLKSLTLTMKSGIS 364
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 305 LTNVSSFLSVSVTERVKDPSYNGWQHLVNCFKQFPPLKLSKRLTLFTSNKGGNA 364
QY 365 FKXVALPSLSTYDLSSRNALSPSGCCSYSDGTLNLRHLDSFNCAITMSANFMGLELOH 424
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 365 FSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTSLKLYDLSPFNGVITMSSNLFLEOLEH 424
QY 425 LDPQHSITLKRTEBSAPFLSEKLYLDISYNTKIDFPGIFLAGTSLNTLMAGNSFKDN 484
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 425 LDFQHSNKKQWSEBSVFLSNLNYLDLSHTHTVAFNGITNGLSLEVLKMAQNSQEN 484
QY 485 TLSVVPANTTNLTFLDLSKCOLBQISWGVFDTLRLQLLNNSHNNLFLDSSHYNQYSL 544
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 485 FLRPIFELRLTLFLDLSQCLEQSLSPYAFNSLSIQLVANNSHNNFSLDTPPYKCNLSL 544
QY 545 STLDGSRRIETS-KGIIQHPKSLAFNLTNNSVACICEHOKFLOWKQKOPLVNVEQ 603
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 545 QVLVYSLNHNITSKQELQHPSSLAFLNLTQNDPACCEHOSFQOMKQDQLLVEYER 604
QY 604 MTCATPVMNTSLVLDNNSTCYMYKTIISVSVSVIYVAVFLIYHRYFHYLLIACCK 663
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 605 MECATPSPKQGMPLVSL-NITCOMAKTIIGSVLSLVAVSVAVLYVFYFHYLLIACCI 663
QY 664 KYSRGESIYDAFVYISSQNEDEWVNNELVKNLEEGVPRFHLCLHYRDFIPGVAIANIIOE 723
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 664 KYGREGNIYDAFVYISSQDEDEWVNNELVKNLEEGVPPQLCHYRDFIPGVAIANIIOE 723
QY 724 GFHNSRKIVVVSRRPIQSRMCIFFEYELAQTMQFLSSSGIIFYLEVEKESILMQOVEL 783
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 724 GFHNSRKIVVVSRRPIQSRMCIFFEYELAQTMQFLSSSGIIFYLEVEKESILMQOVEL 783
QY 784 YRLLSRNTYLEWEDNPLGRHIFMRRLKXNLLDGKASNPQOT 824
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 784 YRLLSRNTYLEWEDSVLGRHIFMRRLKXNLLDGKASNPQOT 824
RESULT 9
AAE16116
ID AAE16116 standard; protein; 837 AA.
XX
XX
XX
AAE16116;
XX
XX
XX
26-MAR-2002 (first entry)
DE Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.
XX
XX
XX
Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
XX
OS Homo sapiens.
XX
XX
XX
Key Location/Qualifiers
FH Misc-difference 211
FT /label= Unknown
FT /note= "Encoded by AAY"
PN MO200190151-A2.
XX
XX
PD 29-NOV-2001.
```

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XX
XX 23-MAY-2001; 2001MO-US016766.
PF
XX
XX 25-MAY-2000; 2000US-0207558P.
PR
XX
XX (SCHE ) SCHERING CORP.
PA
XX
XX Hardman GT, Rock FL, Bazan JF, Kaestlein RA, Ho SWK, Liu Y;
PI WPI, 2002-083085/11.
XX N-PSDB; AAD26306.
DR
XX
XX New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
XX Claim 3; Page 240-243; 297pp; English.
XX
XX The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR4 protein, alternative version. The DTLR4 gene is located on
CC chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
CC be similar to the sequence shown in page 41 (AAE16102). However these
CC sequences differ at several locations
SQ
XX
XX Sequence 837 AA;
Query Match 65.0%; Score 2822.5; DB 5; Length 837;
Best Local Similarity 67.6%; Pred. No. 9.5e-235;
Matches 555; Conservative 101; Mismatches 160; Indels 5; Gaps 5;
QY 7 LARTLTMAL-FPSCITPESLNPCTIEVVPNTIYQCCMDQLSVPPDIPSTKXIDLSFNP 65
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 6 LAGTLIPAMAFISCVRPESWEPVE-VENITTYQCEHLNFPYKIPDLPLPSTKXIDLSFNP 64
QY 66 KILKSYSPNSFSELOMDLSRCEIETIEDKAMHGHLNLIITGNPIQSPSPGSGFGLT 125
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 65 RHLSGSYSPFPELOVDLSRCEIOTIEDGAYQSLSHSTLITGNPIQSLALGAFSGIS 124
QY 126 SLENLVAVETKLASLSPFPIGQILITLKKLVANAHNFHSCKLPAYFSNLTNLVHVDSLSTNY 185
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 125 SLQKLVAVETNLASLENFPIGHLKTLKELVNAHNLQSPFLPEFYSNLTLEHLDLSNKK 184
QY 186 IQTTIVNDLOFLRENPOVNLSDMSLNPIDFQDAFOGKIKHELTLRGNFSSNIMKTC 245
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 185 IQSIYCTDLRVLHQMPNLNLSDLSLNPMPNFIOPGAKFELRLHKLTLRRNFDLSLVNWKTC 244
QY 246 LQNLAGLHVRLILGEFKDERNLEIFPSPIMEGLCDVTIDEFRLTYTNDSDDIK-FHC 304
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 245 IQGLAGLEVRLVGEFRBGNLEKFPKSALEGLCNLTIEFRFLAYLDYLDIDIDFNC 304
QY 305 LANVSAMSLAGVSIKYLEDPVPRKFWQSLIIRCOLKOPPTLDPLKSLTLTMKSGIS 364
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 305 LTNVSSFLSVSVTERVKDPSYNGWQHLVNCFKQFPPLKLSKRLTLFTSNKGGNA 364
QY 365 FKXVALPSLSTYDLSSRNALSPSGCCSYSDGTLNLRHLDSFNCAITMSANFMGLELOH 424
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 365 FSEVDLPSEFLDLSRNGLSFKGCCSQSDPGTSLKLYDLSPFNGVITMSSNLFLEOLEH 424
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QY 425 LDFOHSTLKRVTESAFSLSEKTLTLDISTYNTKIDPDGIFLGSLTSLNTLTKAAGNSFKDN 484
DB 425 LDFOHSTLKRVTESAFSLSEKTLTLDISTYNTKIDPDGIFLGSLTSLNTLTKAAGNSFKDN 484
QY 485 TILSNFANTMTLTFDLSCQLEJOISWGVFDTLHLLOLNMHNNLLFLDSSHYNQVSL 544
DB 485 TILSNFANTMTLTFDLSCQLEJOISWGVFDTLHLLOLNMHNNLLFLDSSHYNQVSL 544
QY 545 STLDGSEFRIETS-KGIIQHPKSLAFPLNTNNSVACICEHOKFLQWVEQKOPLVNEQ 603
DB 545 STLDGSEFRIETS-KGIIQHPKSLAFPLNTNNSVACICEHOKFLQWVEQKOPLVNEQ 603
QY 604 MTCATPEMNTSLVLDPNNTSTYMTKTIISVSVSIVYVSTAFLIYHFFHLIIAGCK 663
DB 604 MTCATPEMNTSLVLDPNNTSTYMTKTIISVSVSIVYVSTAFLIYHFFHLIIAGCK 663
QY 605 MECALPSPKQGPVLSL-NITCQNMKTIIGVSVLSLVVSVVAVVYKFFHMLAGCI 663
DB 605 MECALPSPKQGPVLSL-NITCQNMKTIIGVSVLSLVVSVVAVVYKFFHMLAGCI 663
QY 664 KYSRGEISTYDAFVITYSSQEDBVRNELVKNLEEGVPRFHLCHYRDFIPGVAIAANTIOE 723
DB 664 KYSRGEISTYDAFVITYSSQEDBVRNELVKNLEEGVPRFHLCHYRDFIPGVAIAANTIOE 723
QY 724 GFHRSRKIVVVSRRHFIOSRMCIFEYETIAQTWQPLSRSGIIFIVLEKESKILRQVEL 783
DB 724 GFHRSRKIVVVSRRHFIOSRMCIFEYETIAQTWQPLSRSGIIFIVLEKESKILRQVEL 783
QY 784 YRLLSRNTYLEMEDNPLGRHIFWRRLKVALLDGKASNPBQT 824
DB 784 YRLLSRNTYLEMEDNPLGRHIFWRRLKVALLDGKASNPBQT 824

RESULT 10

ID ADOS7791 standard; protein; 795 AA.
XX AC ADOS7791;
XX 12-AUG-2004 (first entry)
XX Rhesus monkey toll-like receptor 4 SEQ ID NO:12.
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
XX sepsis; severe sepsis; septic shock; asthma; rhesus monkey.
OS Macaca mulatta.
FH Key Location/Qualifiers
FT Misc-difference 635
FT /label= Lys, Asn
XX W02004042365-A2.
XX 21-MAY-2004.
XX 03-NOV-2003; 2003WO-US036247.
XX 01-NOV-2002; 2002US-0423113P.
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX Messier W;
XX WPI; 2004-400726/37.
XX N-PSDB; ADOS7789, ADOS7790.
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX sequence of the Old World monkey with that of a human.
XX Disclosure; SEQ ID NO 12; 11pp; English.
XX The invention relates to a novel method for identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an old world monkey
XX comprising comparing the TLR4 polynucleotide sequence of the Old World

CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiaesthetic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents rhesus monkey TLR4.

SQ Sequence 795 AA;

Query Match 64.2%; Score 2788.5; DB 8; Length 795;

Beet Local Similarity 68.3%; Pred. No. 7.7e-232;
Matches 543; Conservative 98; Mismatches 151; Indels 3; Gaps 3;

QY 31 VVPNTTTCQMOCKLSKVPDDIPSSSTKNDLSFNPPLIKSYSFSSFSELOMDLSRCRE 90
DB 1 VVPNTTTCQMOCKLSKVPDDIPSSSTKNDLSFNPPLIKSYSFSSFSELOMDLSRCRE 90
QY 91 TIEDKAMHGLHLSNLITGNPIOSFSPGSGSLLENLVAVERKLASLESFPIGOLIT 150
DB 61 TIEDKAMHGLHLSNLITGNPIOSFSPGSGSLLENLVAVERKLASLESFPIGOLIT 150
QY 151 LKCANVAFHSHCKLPAYFSNLNLVAVDLSYNTYQITTVNDLOFLBNPQVNLSDMS 210
DB 121 LKCANVAFHSHCKLPAYFSNLNLVAVDLSYNTYQITTVNDLOFLBNPQVNLSDMS 210
QY 211 LNPIDFIDQDAFOGKJLHETLIRGPNFNSNMKTCLQWLAGHVRLLTGEFKDERNLEI 270
DB 181 LNPIDFIDQDAFOGKJLHETLIRGPNFNSNMKTCLQWLAGHVRLLTGEFKDERNLEI 270
QY 271 FEPSIMEGLCDVTIDEFRLTYTNDPSDDIVK-FHCLANVAMSAGVSIKYLEDPKHF 329
DB 241 FEPSIMEGLCDVTIDEFRLTYTNDPSDDIVK-FHCLANVAMSAGVSIKYLEDPKHF 329
QY 330 WQSLIIRCOUKOPPTLDPFLKSLITLTANKGISFPKVAAPSLSYLDSRNALSFSGCC 389
DB 301 WQSLIIRCOUKOPPTLDPFLKSLITLTANKGISFPKVAAPSLSYLDSRNALSFSGCC 389
QY 390 SYSIDGTSLSHLHLSFNGALITMSANFGLBLOHLDFOHSTLKRVTESAFSLSEKTL 449
DB 361 SYSIDGTSLSHLHLSFNGALITMSANFGLBLOHLDFOHSTLKRVTESAFSLSEKTL 449
QY 450 LDISTYNTKIDPDGIFLGSLTSLNTLTKAAGNSFKDNTLSNVPANTMTLTFDLSCQLEJOI 509
DB 421 LDISTYNTKIDPDGIFLGSLTSLNTLTKAAGNSFKDNTLSNVPANTMTLTFDLSCQLEJOI 509
QY 510 SWGVFDTLHLRIQLNMHNNLLFLDSSHYNQVSLSTLDGSEFRIETS-KG-IIQHPKSL 568
DB 481 SWGVFDTLHLRIQLNMHNNLLFLDSSHYNQVSLSTLDGSEFRIETS-KG-IIQHPKSL 568
QY 569 AFFNLTNNSVACICEHOKFLQWVEQKOPLVNVEQMCATPEMNTSLVLDPNNTSTYMT 628
DB 541 AFFNLTNNSVACICEHOKFLQWVEQKOPLVNVEQMCATPEMNTSLVLDPNNTSTYMT 628
QY 629 KTIISVSVSIVYVSTAFLIYHFFHLIIAGCKKTSRGESIIDAFVITYSSQEDBVRN 688
DB 600 KTIISVSVSIVYVSTAFLIYHFFHLIIAGCKKTSRGESIIDAFVITYSSQEDBVRN 688
QY 689 ELVKNLEEGVPRFHLCHYRDFIPGVAIAANIIOGPFHRSRKIVVVSRRHFIOSRMCIFE 748
DB 660 ELVKNLEEGVPRFHLCHYRDFIPGVAIAANIIOGPFHRSRKIVVVSRRHFIOSRMCIFE 748
QY 749 YEIAQTWQPLSRSGIIFIVLEKESKILRQVELYRLLSRNTYLEMEDNPLGRHIFWR 808
DB 720 YEIAQTWQPLSRSGIIFIVLEKESKILRQVELYRLLSRNTYLEMEDNPLGRHIFWR 808
QY 809 LKVALLDGKASNPBQT 823
DB 780 LKVALLDGKASNPBQT 823

RESULT 11

AD057797
ID AD057797 standard; protein; 801 AA.
XX
AC AD057797;
XX
DT 12-AUG-2004 (first entry)
XX
DE Squirrel monkey toll-like receptor 4 SEQ ID NO:18.
XX
KM toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; squirrel monkey.
XX
OS Saimiri sciureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 14
FT /label= Leu, Phe
XX
FN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PE 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Meslier W;
XX
XX WPI; 2004-400726/37.
DR N-PSDB; AD057795; AD057796.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Disclosure; SEQ ID NO 18; 11pp; English.
XX
XX The invention relates to a novel method for identifying a nucleotide
XX sequence in a TLR4 polynucleotide sequence of an old world monkey
XX comprising comparing the TLR4 polynucleotide sequence of the Old World
XX monkey with corresponding TLR4 polynucleotide sequence of a human. The
XX method of the invention has antibacterial, immunosuppressive, and
XX antiasthmatic activity. The method is useful in identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an Old World monkey where the
XX change may be associated with reduced sensitivity to Gram-negative
XX bacterial infection. The methods, agents and composition are useful in
XX treating sepsis, severe sepsis or septic shock and asthma. The present
XX sequence represents squirrel monkey TLR4.
XX
SQ Sequence 801 AA;
Query Match 64.1%; Score 2785.5; DB 8; Length 801;
Best Local Similarity 68.3%; Pred. No. 1.4e-231;
Matches 544; Conservative 90; Mismatches 159; Indels 3; Gaps 3;
QY 31 VVPNTTYQCMQDKLSKVPDIPSTKYNIDLSFNPILKLSYSFNSFSELOMIDLSRCEIE 90
DB 1 VVPNTTYQCMELNXYKIPDNIPSTKNLDSFNPILRSHSHSPFNPPELOVDLSRCDIQ 60
QY 91 TIEDKAMHGLHLSNLTILGNPIQSFGSGLSLLENLVAVETKGLASLESFPIQOLIT 150
DB 61 TIEDGAYQSLSHSLTILGNPIQLALGAFSGLSLQKLVAVETHLISLENPFICHLXT 120
QY 151 LKLVANVAFHISCKLPAYFSNLTNIVHDLSTNYQITVNDIQGLRBNPOVNLSDMS 210
DB 121 LKDLNVAHNLIOFSLPEYFSNLTNLEHLDLSNNIQLNYCKDLQVLRHQPPLNLSLDLS 180
QY 211 LNPIDPFOQAFQGIKLHETLRLGNFNSNIMKTCLONLAGLHVRLLIGEPFDERNLEI 270
DB 181 LNPINIQGAFKEIRHLHKLTLRNNFDLSNAMKTCIQGLAGLEVHRLVIGEPFNERNIED 240

QY 271 FEPISMEGLCDVTIDEFRLTYTNDPSDDIVK-FHCLANVSAMSLAGVSIKYLEDPGRHFK 329
DB 241 FDKSALBGLCNLTINERLAIYDDFLDDITDLNCLANVSFPLVNVHIRKVEDPFSYNFR 300
QY 330 WQSLIIRCOLKQPTLDPFLKSLTLTNKKSISFEKVALPSLSTYLDLSRNALSEGCC 389
DB 301 WQHLVAVCVFOQFPFKLSLRLFTANKGRHNFSEVPLPSLEFLDLSRNGLSFPGCC 360
QY 390 SYSDPLGNSLRHLDLSNGAIIIMSANFMGLEEHLQHDFOHSTLKRVRVSAFSLSEKLY 449
DB 361 SOSDFGTSLSKYLDSFNDVITGNSNPLGLEQLEHLDFOHNSLKONSEFVFLSRMLIY 420
QY 450 LDISYNTKXIDFDGIFGLTSLNTLKNAGNSFKONTLSNVPANTNLTPDLSKQLEOI 509
DB 421 LDISHTHTRVAFNGITFNGFLPSLKLKMAAGNSFOQNFEJFTDLNMLIFLDLSRQLEQL 480
QY 510 SWGVFDTLARLQILNMSHNNLLFDSSHYNOLYSLSTLDCSFNRIETSKG-ILOHPRKSL 568
DB 481 SPTAFDSLPRRLRLNMSHNNFPALDTPPYKGLYSLOVLDSYLNHIGTSKQELQHPSSL 540
QY 569 AFENLTNNSVACTGEHOKFLQWYKQKQFLVNVQOMTCAPPEVNTSLVLDPNNSTCYMY 628
DB 541 AFLNLTQNDFACTGEHOSFLOMTKQORLLVEYQMECAPLNKKGIPVLSL-NITCOMS 599
QY 629 KTIISVSVSVIYVSTVAFIYHFYFHLILLAGCKTSRGEISYDAFVIYSSQNEDWVRN 688
DB 600 KTIIGVSVLSLVSVVAVLVYKFFHMLLAGCITKGRGENTYDAFVIYSSQNEDWVRN 659
QY 689 ELVKNLEGVPRFHLCLHYRDFIPGVAIAANIIOEGHFKSRKIVVVSRRHIOGRWCIFE 748
DB 660 ELVKNLEGVPRFQCLHYRDFIPGVAIAANIIEGHFKSRKIVVVSRRHIOGRWCIFE 719
QY 749 YEIQOTQWFLSSRGIIITVLEKYEKSLRQOVLELYRLSNTKYLEMEDNPLGRIHIFWR 808
DB 720 YEIQOTQWFLSSRGIIITVLEKYEKSLRQOVLELYRLSNTKYLEMEDNPLGRIHIFWR 779
QY 809 LKNALLDGKASNPQOT 824
DB 780 LKRALLDGRPMNPQGT 795
RESULT 12
AD057803
ID AD057803 standard; protein; 808 AA.
XX
AC AD057803;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX
KM toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS Pan troglodytes.
XX
FN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PE 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Meslier W;
XX
XX WPI; 2004-400726/37.
DR N-PSDB; AD057801; AD057802.
XX

PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 PS Disclosure; SEQ ID NO 24; 11pp; English.
 XX
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents chimpanzee TLR4.
 XX
 SQ Sequence 808 AA;
 Query Match 64.1%; Score 2785.5; DB 8; Length 808;
 Best Local Similarity 68.2%; Pred. No. 1.4e-231;
 Matches 543; Conservative 99; Mismatches 151; Indels 3; Gaps 3;
 QY 31 VPPNTTQCMQDKLSKVPDDIPSSSTKNDLSFNPPLKILKSYFSNSELQWLDLSRCEIE 90
 DB 1 VPPNTTQCMELNFKYKIPDNLPSSTKNDLSFNPPLRHLSGSYFSPFPELQVLDLSRCEIQ 60
 QY 91 TIEDKAMHGLHNLILITGNPIQSFGSGFSLSTLENLVAVETKLASLESFPIGQILT 150
 DB 61 TIEDGAYOSLSHSLTILITGNPIQSIALGAFSGLSLQKLVAVETNLASLENFPIGHILKT 120
 QY 151 LKKLVANFNHISCKLPAYFSNLTNLVHVDLSYNYIQTITVNDILOFLRENQVNLSDMS 210
 DB 121 LKELVAVANHLIQSFKLPPEYFSNLTNLEHDLSSNNKIQSYCTCDLRLHQMPLNLSDLS 180
 QY 211 LNPIDFIQDAQOGIKHELTIRGNPNSSNIMKTCLQNLAGLHVHRLIIGERKDERNLIEI 270
 DB 181 LNPMPFIQPGAFKEIRLHKLTLIRNPNFDSLNVMKTCIOGLAGLEVHRLVIGERFNEENLEK 240
 QY 271 FEPSIMEGLCDVTIDBFRLTYTNDSPDDIVK-FHCLAVNSAMSAGSVSKYLEVDYPRKHK 329
 DB 241 FDKSLBEGLCNLTIEBFLAYIDYLDLIDLPNCCLTNVSSSLVSVTKSVKXDSYNG 300
 QY 330 WQSLIIRCOLKQFPPTLDLPFLKSLTLTNWKGSIKFKVVALPSLYLDSRNALSPSGCC 389
 DB 301 WQHLVLVCKEFGQFPTLKLKSLKRLITFSNKGNAFSEVDLPSEFLDLSRNGLSFKGCC 360
 QY 330 SYSIDGTSRLRLDLSFNCAIIMSANFNGLELOHLDFQHSITLKVTEFSAFLEKLIY 449
 DB 361 SOSDGGTTSLLKYLDSFNGVIMSSNFIQLEQLEHLDFOHSNMLKOMSEPSVFLSLRNLIY 420
 QY 450 LDISYTNNTKIDPDGIFLGITSLNLTLMKMGNSFKDNTLSVNPANTNLPLFLDLSKCOLBOI 509
 DB 421 LDISITHIRVAFNGIFNGLSLSEVLKMGANSQENFPLDPIELRNLTFLDLSQOLEL 480
 QY 510 SMGVEDTLHRLQLLMSHNNLLFLDSHYNOLYSLSLDCSFNRLETS-KGILQHPKSL 568
 DB 481 SPTAFNSLSLQVLMSHNNFSLDTPPYKCLNSLQVLDYSLNHLMTSKQKQLQHPSSL 540
 QY 569 AFENLTNNSVACICGHOKFLQWKEQKQFLVAVNEQMTCAPIVEMNTSLVLDNNSTCMY 628
 DB 541 AFLNLTQNDFACTCHQSFLOWIKDORQULVEVERMECATPDKQGMPLSL-NITCOMN 599
 QY 629 KTIISVSVSYIYVSTVAFLIYHFEYFHLILTAGCKKYSRGSIIYAPVYSSQNDWDRN 688
 DB 600 KTIIGVSTLSVLYVSVVAVLYKFFHMLLAGCKIKYRGSENIYDAFYIYSSQDDWDRN 659
 QY 689 ELVKNLEEGVRFHLCIHYRDFIPGVAIANIIOGFHKSRKVIYVVSRRHPIQSFWCFE 748
 DB 660 ELVKNLEEGVRPFQCLHYRDFIPGVAIANIHHGFHKSRKVIYVVSQHPIQSFWCFE 719
 QY 749 YEIAQTWQPLSGRSQIIFIVLEKVKSLRQVVELYRLLSRNTYLEMEDNPLGRHIFMR 808

DB 720 YEIAQTWQPLSGRAGIIFIVLOKVEKTLRQVVELYRLLSRNTYLEMEDSVLGRHIFMR 779
 QY 809 LKNALLDGKASNPBOT 824
 DB 780 LKRALDGKSNPEGT 795
 RESULT 13
 ADOS7782
 ID ADOS7782 standard; protein; 808 AA.
 XX
 AC ADOS7782;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Chimpanzee toll-like receptor 4 SEQ ID NO:3.
 XX
 KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KW sepsis; severe sepsis; septic shock; asthma; chimpanzee.
 OS Pan troglodytes.
 PN WO2004042365-A2.
 PN 21-MAY-2004.
 PD 03-NOV-2003; 2003WO-US016247.
 PF 01-NOV-2002; 2002US-0423113P.
 PR (EVOL-) EVOLUTIONARY GENOMICS LLC.
 PA Messier W;
 PI WPI; 2004-400726/37.
 DR N-PSDB; ADOS7780, ADOS7781.
 XX
 PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 PS Example 1; SEQ ID NO 3; 11pp; English.
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents chimpanzee TLR4.
 XX
 SQ Sequence 808 AA;
 Query Match 64.0%; Score 2781.5; DB 8; Length 808;
 Best Local Similarity 68.2%; Pred. No. 3.2e-231;
 Matches 543; Conservative 98; Mismatches 152; Indels 3; Gaps 3;
 QY 31 VPPNTTQCMQDKLSKVPDDIPSSSTKNDLSFNPPLKILKSYFSNSELQWLDLSRCEIE 90
 DB 1 VPPNTTQCMELNFKYKIPDNLPSSTKNDLSFNPPLRHLSGSYFSPFPELQVLDLSRCEIQ 60
 QY 91 TIEDKAMHGLHNLILITGNPIQSFGSGFSLSTLENLVAVETKLASLESFPIGQILT 150
 DB 61 TIEDGAYOSLSHSLTILITGNPIQSIALGAFSGLSLQKLVAVETNLASLENFPIGHILKT 120
 QY 151 LKKLVANFNHISCKLPAYFSNLTNLVHVDLSYNYIQTITVNDILOFLRENQVNLSDMS 210

Db 121 LKELNVAHNLIOSEFKLEPEYSNLTNLEHLDSNNKIOSICTDRLVHOMPLNLSLDS 180
Qy 211 LNPIDFIDODAFQGIKIHLELTIRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270
Db 181 LNPINFIQPGAFKRIHLKLTIRNNFDSLNAMKTCIGLAGEVHRLVLGEFRNENLEK 240
Qy 271 PEPIMEGLCVTIDEPRLTYTNDPSDDIVK-FHCLANVAMSAGVSIKYLEVPPKHF 329
Db 241 FDKSALBGLCNLTIEEPRLTYLDYLDIIDLFCNLTNVSFSVSVYIKSVKXDFSYNFG 300
Qy 330 WQSLIIRCOLKOPPTLDLPFLKSLTLTMNGKSIKPKVALPSLSDYDLSNNALSFGCC 389
Db 301 WQHELVNCKKFGQPTLTKSLKRLTFSNKGNAFSEVDLPSEFLDLSNNGLSFGCC 360
Qy 390 SYSDLGTSNLRHLDSFNGALIMSANFNGLELQHLDPQHSITLKRVTESAFSLKLY 449
Db 361 SOSDFGTSLSKYLDSFNGVITMSNFIQLEQLBHLDPQHSITLKRVTESAFSLKLY 420
Qy 450 LDISYNTKIDPDGIFLGLTSLNLTAKAGNSFKDNTLSNVPANTNLTFLDLSKQLEOI 509
Db 421 LDISHTHTRVAFNGIFNGLSLLEVLKMAAGNSFOENFLDIFTELRLNLTFLDLSQQLBOL 480
Qy 510 SMGVDPDLRLQLMNSHNNLLFLDSHYNOLYSTLDCSPNRIETS-KGILQHPKSL 568
Db 481 SPTAFNSLSLQVLNMSHNNPFLSDTTPYKCLNSLQVLDLSLNHMTSKQELQHPSSL 540
Qy 569 AFENLTNNSVACICEHOKFLQWKEOKQFLVNVVEQNTCATPVEAMTSLVDFNNSTCYW 628
Db 541 AFLNLTQNDFACTCEHOSFLQWIKQORQLVEVERMECATPDKQGMPLSLV-NITCQW 599
Qy 629 KTIISVSVSVIVSTVAFLIYHFFPHLLILGCKKYSNGESIYDAFVITYSSQNDVW 688
Db 600 KTIIGSVSVSVIVSVAVLVYKFFHMLLAGCIRYGENIYDAFVITYSSQNDVW 659
Qy 689 ELVKNLEBVPREHCLHYRDPFPGVALANIIIOEGFHKSRYIVVSHFIQSEWCFE 748
Db 660 ELVKNLEBVPREHCLHYRDPFPGVALANIIIOEGFHKSRYIVVSHFIQSEWCFE 719
Qy 749 YEIAQWQFLSSRSGLIFVLEKVEKSLRQOVELYRLSRNTYLEMEDNPLGRHFW 808
Db 720 YEIAQWQFLSSRSGLIFVLEKVEKSLRQOVELYRLSRNTYLEMEDNPLGRHFW 779
Qy 809 LKNALIDGKASNEOT 824
Db 780 LKRALIDGKASNEOT 795
RESULT 14
AD057800 standard; protein; 795 AA.
ID AD057800
AC AD057800;
XX
DT 12-ANG-2004 (first entry)
XX
DE Hamadryas baboon toll-like receptor 4 SEQ ID NO:21.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
immunopressive; antiaesthetic; Gram-negative bacterial infection;
sepsis; severe sepsis; septic shock; asthma; hamadryas baboon.
XX
OS Papio hamadryas.
XX
PN MO2004042365-A2.
XX
PD 21-MAY-2004.
XX
XX 03-NOV-2003; 2003MO-US036247.
XX
XX 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.

PI Mesier W;
XX WPI; 2004-400726/37.
DR N-PSDB; AD057798, AD057799.
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
XX Disclosure; SEQ ID NO 21; 11pp; English.
XX
XX The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of a human. The
CC method which corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunopressive, and
CC antiaesthetic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents hamadryas baboon TLR4.
XX
XX Sequence 795 AA;

Query Match 63.9%; Score 2777.5; DB 8; Length 795;
Best local similarity 68.2%; Pred. No. 6.9e-231;
Matches 542; Conservative 95; Mismatches 155; Indels 3; Gaps 3;

Qy 31 VVPNTYQCMQDKSLVPPDDIPSTKNIKIDSFNPLKILKYSFNSFSELQHLDSRCEIE 90
Db 1 VVPNTYQCMELNFKYKIPDNIPFSTKNIKIDSFNPLRHSYFPLRPELQVLDLSRCEIQ 60
Qy 91 TIEDKAMGLHLSNLTITGNPIOSFSGSPGSLTSENVAVETKSLASFPICGLIT 150
Db 61 TIEDKAYOSLSHLSLTITGNPIOSLAGASGSLQKLVAVETNLSLENFPGHKT 120
Qy 151 LKKNVANPFIHSCGLPAYFENLTNLVHVDLSYNYITITVNDILOFRENQVNLSDMS 210
Db 121 LKELNVAHNLIOSEFKLELTIRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 180
Qy 211 LNPIDFIDODAFQGIKIHLELTIRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270
Db 181 LNPINFIQPGAFKRIHLKLTIRNNFDSLNAMKTCIGLAGEVHRLVLGEFRNENLEK 240
Qy 271 PEPIMEGLCVTIDEPRLTYTNDPSDDIVK-FHCLANVAMSAGVSIKYLEVPPKHF 329
Db 241 FDKSALBGLCNLTIEEPRLTYLDYLDIIDLFCNLTNVSFSVSVYIKSVKXDFSYNFG 300
Qy 330 WQSLIIRCOLKOPPTLDLPFLKSLTLTMNGKSIKPKVALPSLSDYDLSNNALSFGCC 389
Db 301 WQHELVNCKKFGQPTLTKSLKRLTFSNKGNAFSEVDLPSEFLDLSNNGLSFGCC 360
Qy 390 SYSDLGTSNLRHLDSFNGALIMSANFNGLELQHLDPQHSITLKRVTESAFSLKLY 449
Db 361 SOSDFGTSLSKYLDSFNGVITMSNFIQLEQLBHLDPQHSITLKRVTESAFSLKLY 420
Qy 450 LDISYNTKIDPDGIFLGLTSLNLTAKAGNSFKDNTLSNVPANTNLTFLDLSKQLEOI 509
Db 421 LDISHTHTRVAFNGIFNGLSLLEVLKMAAGNSFOENFLDIFTELRLNLTFLDLSQQLBOL 480
Qy 510 SMGVDPDLRLQLMNSHNNLLFLDSHYNOLYSTLDCSPNRIETS-KGILQHPKSL 568
Db 481 SPTAFNSLSLQVLNMSHNNPFLSDTTPYKCLNSLQVLDLSLNHMTSKQELQHPSSL 540
Qy 569 AFENLTNNSVACICEHOKFLQWKEOKQFLVNVVEQNTCATPVEAMTSLVDFNNSTCYW 628
Db 541 AFLNLTQNDFACTCEHOSFLQWIKQORQLVEVERMECATPDKQGMPLSLV-NITCQW 599
Qy 629 KTIISVSVSVIVSTVAFLIYHFFPHLLILGCKKYSNGESIYDAFVITYSSQNDVW 688
Db 600 KTIIGSVSVSVIVSVAVLVYKFFHMLLAGCIRYGENIYDAFVITYSSQNDVW 659


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QY 669 ELVKNLEGGVPRFHLCHHYRDFIPGVAIAANIIOGFFHKSRYIVVNSHPIQSRWCIPE 748
Db 660 ELVKNLEGGVPRFQCLHYRDFIPGVAIAANIHHGFFHKSRYIVVNSHPIQSRWCIPE 719
QY 749 YEIAQTWQFLSSRSRGIIFFIVLEKYEKSLLRQOVELYRLLSRNTYLEMEDNPLGRHIFMR 808
Db 720 YEIAQTWQFLSSRAGIIFIVLQKYEKTLRQOVELYRLLSRNTYLEMEDSVLGGHIFMR 779
QY 809 LKNALLDGKASNPQOT 823
Db 780 LKRALLDGKSWNPPE 794

RESULT 15
AD057785
ID AD057785 standard; protein; 808 AA.
XX
AC AD057785;
XX
DT 12-AUG-2004 (first entry)
XX
DE Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
KM toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; gorilla.
XX
OS Gorilla gorilla.
XX
PN MO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR WPI: 2004-400726/37.
XX
N-PSDB; AD057783; AD057784.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Example 1; SEQ ID NO 6; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiaesthetic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents gorilla TLR4.
XX
SQ Sequence 808 AA;

Query Match 63.6%; Score 2763.5; DB 8; Length 808;
Best Local Similarity 67.8%; Pred. No. 1.2e-229;
Matches 540; Conservative 99; Mismatches 154; Indels 3; Gaps 3;
QY 31 VVNNITVQCMQOKSKVPPDDIPSSSTKXNDLSFNPPLKIKSYFSFNSFELQWDLRSCEIE 90
Db 1 VVNNITVQCMQMLNFKIPIDNLPFSTKXNDLSFNPPLRHLGYSFSPFPPELOVLDLSRCEIQ 60
QY 91 TIEBKAMHGLHLSNLIITGNPIQSFSPGSGLTLENLVAVETKTLASLESFPIGLIT 150

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Db 61 TIEBAYOSLSHSLTLLITGNPIQSLAGAFSGSLSLKTLVAVENTLNLSENFPIGHLKT 120
QY 151 LKKLVANFNHSCCLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLKENPOVNLSDMS 210
Db 121 LKELVANNLNLSQFCLPPEYFSNLTNLVHVDLSYNYIQTITVNDLQFLKENPOVNLSDMS 180
QY 211 LNPIDFIDQAPFOGKJHETLTKGNFNSNMKTCLQNLAGLHVHRLILGEFKDERNLEI 270
Db 181 LNPWFIIQGAAPKEIRLHKLTLRNNFDSLNMWKTICIGLAGLEVRLVILGEFRNGNLEK 240
QY 271 FEPSEMEGLCDVTIDEFRLTITNDPSDIYK-FHCLAVNSAMSLAGVSIKYLEVDPKHF 329
Db 241 FDKSALBGLCNLTIEEFRLAVLDYLDIDLFNCLITVSSSPSLVSVIERKDFSYNFG 300
QY 330 MOSLIIRCOLKOPFTLDPFLKSLTTLTMNGKSJSFKKVALPSLSYLDLSRYALSFSQGC 389
Db 301 WQHLVKNCKGQFPFTLKLKSLRTFTSNKGNAFSEVDLPSEFLDLSRNGLSFKGCC 360
QY 390 SYSIDGINSLSRLHLSFNGALIMSNFMLELQHLDPQHSCLKVTEFSAPLSLEKLY 449
Db 361 SQSDRGTTSLKYLDSLSENGVITMSNFIQLDQLEHLDQHNLMQMSSEFVLSRLNLY 420
QY 450 LDISTYNTKIDPDIPLGLTSLNTLKMAKNSPKDNTLSNFPANTNLTFPLDISKQLEQI 509
Db 421 LDISTHTRVAFNGIFNGLSLEVLKMAKNSFOENFLPDITELNLNLFPLDISQCLEQL 480
QY 510 SMGVPTDLHRLQOLNMSNNNLPLDSSHYNOLYSLTDCSFNRIETS-KGILQHPFSL 568
Db 481 SPTAFNSLSLQVNLMSNNPPLDTPPYKCLNSLRVLDLSLNMHTSKDQLQHPFSL 540
QY 569 AAFNLTNNSVACICEHQKFLQWVKEQKQFLVNVQMTCAEVENMTSLVLPNNSTCYMY 628
Db 541 AFINLTQNDPACTCEHQSFLOMIDQRLIVEVERMECATSDQGMVLSL-NITCGMN 599
QY 629 KTIISVSYSVIVYSTVAFLYHNYFHLILAGCKTSRKGSYDAPVITYSQNEDWYRN 688
Db 600 KTIIGSVSLVLYVSVAVLVYKFFHMLMLAGCIKYGRGENVYDAFITYSQDDBWYRN 659
QY 689 ELVKNLEGGVPRFHLCHHYRDFIPGVAIAANIIOGFFHKSRYIVVNSHPIQSRWCIPE 748
Db 660 ELVKNLEGGVPRFQCLHYRDFIPGVAIAANIHHGFFHKSRYIVVNSHPIQSRWCIPE 719
QY 749 YEIAQTWQFLSSRSRGIIFFIVLEKYEKSLLRQOVELYRLLSRNTYLEMEDNPLGRHIFMR 808
Db 720 YEIAQTWQFLSSRAGIIFIVLQKYEKTLRQOVELYRLLSRNTYLEMEDSVLGGHIFMR 779
QY 809 LKNALLDGKASNPQOT 824
Db 780 LKRALLDGKSWNPPE 795

Search completed: March 12, 2005, 19:55:11
Job time : 90.9834 secs

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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:46 ; Search time 22.9539 Seconds

(without alignment)
2715.523 Million cell updates/sec

Title: US-09-396-985b-99

Perfect score: 4345
Sequence: 1 MMPPLMLRTLMALFSCCL.....GKSNPEQTAEDEETATWT 835

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5
513545 segs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2786.5	64.1	844	4	US-09-949-016-9438
2	619.5	14.3	661	1	US-08-514-014-4
3	619.5	14.3	661	2	US-08-833-823-4
4	494	11.4	784	4	US-09-983-308B-23
5	432.5	10.0	775	4	US-09-949-016-8799
6	317.5	7.3	603	1	US-08-190-802A-50
7	317.5	7.3	603	3	US-08-477-346-50
8	317.5	7.3	603	4	US-08-473-089-50
9	317.5	7.3	603	3	US-08-487-072A-50
10	316.5	7.3	603	3	US-09-063-950-5
11	291.5	6.7	605	1	US-08-190-802A-49
12	291.5	6.7	605	3	US-08-477-346-49
13	291.5	6.7	605	3	US-08-473-089-49
14	291.5	6.7	605	4	US-08-487-072A-49
15	291.5	6.7	605	4	US-09-538-092-1087
16	291.5	6.7	623	4	US-09-949-016-10995
17	287.5	6.6	1119	4	US-09-907-794A-294
18	287.5	6.6	1119	4	US-09-905-125A-294
19	287.5	6.6	1119	4	US-09-902-775A-294
20	287.5	6.6	1119	4	US-09-906-700-294
21	287.5	6.6	1119	4	US-09-903-603A-294
22	287.5	6.6	1119	4	US-09-904-920A-294
23	287.5	6.6	1119	4	US-09-909-064-294
24	287.5	6.6	1119	4	US-09-905-381A-294
25	287.5	6.6	1119	4	US-09-906-618-294
26	286.5	6.6	1112	3	US-09-353-585-2
27	285.5	6.6	1112	3	US-09-353-585-3

28	285.5	6.6	1525	3	US-09-191-647-2	Sequence 2, Appli
29	285.5	6.6	1525	3	US-09-540-245A-2	Sequence 2, Appli
30	285.5	6.6	1525	3	US-09-540-153-2	Sequence 2, Appli
31	282	6.5	1529	4	US-09-312-283C-396	Sequence 396, App
32	273	6.3	1480	3	US-09-191-647-7	Sequence 7, Appli
33	273	6.3	1480	3	US-09-540-245A-7	Sequence 7, Appli
34	273	6.3	1480	3	US-09-540-153-7	Sequence 7, Appli
35	273	6.3	1480	5	PCR-US91-09055-2	Sequence 2, Appli
36	271	6.2	1480	5	US-09-182-024A-5	Sequence 5, Appli
37	269.5	6.2	1059	4	US-09-907-794A-290	Sequence 290, App
38	269.5	6.2	1059	4	US-09-905-125A-290	Sequence 290, App
39	269.5	6.2	1059	4	US-09-902-775A-290	Sequence 290, App
40	269.5	6.2	1059	4	US-09-906-700-290	Sequence 290, App
41	269.5	6.2	1059	4	US-09-903-603A-290	Sequence 290, App
42	269.5	6.2	1059	4	US-09-904-920A-290	Sequence 290, App
43	269.5	6.2	1059	4	US-09-909-064-290	Sequence 290, App
44	269.5	6.2	1059	4	US-09-905-381A-290	Sequence 290, App
45	269.5	6.2	1059	4	US-09-906-618-290	Sequence 290, App

ALIGNMENTS

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RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Query Match      64.1%; Score 2786.5; DB 4; Length 844;
Best Local Similarity 68.3%; Pred. No. 1.8e-238;
Matches 544; Conservative 98; Mismatches 152; Indels 3; Gaps 3;

QY 30 EVNNITTCQCMDOQSKVDDIPSTKNIDISFNPDIKTKYSFNSFELQMDLSRCEI 89
DB 36 EVNPVITTCQCMELNPKYKIPDNLPSSTKNIDISFNPDLRLGYSFSPFELQMDLSRCEI 95
QY 90 ETIEDKAWHGHHLSNLTGNPIQSPGSGTSLSHNVAVETTKLASIESPFIQOLI 149
DB 96 QTIIDGAVQSSHSHTLITGNPIQSLALGAFSGLSISQKIVAVETTKLASIESPFIQOLI 155
QY 150 TLKLANVAHNFHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDIQFLRENPQVNLSDM 209
DB 156 TLKELANVAHNIQGFKLPEYFSNLTNLHDLDSNKLQISIVCTDIRVHQMPLNLSTDL 215
QY 210 SLNIDFPODAFGQIKLHETLTGPNSSNMTCQNLGALVHRLIIGFEFDERLTLE 269
DB 216 SLNPNMFIQPGAFKIRLHKLTLNNPDSLVNMTCTCQGLAGLEVHRLVIGEFNREGYLE 275
QY 270 IFESINIEGLCDVTITDEFRLTYTNDPSDDIYK-FHCLANYSAMSLAGVSIKYLEDPVPGHF 328
DB 276 KFDSSALEGLCNLTIEFRRLAYLDIYDDIIDLNFCLTNSSPFLSVTIERVQDFSYNF 335
QY 329 KWQSLSTIRCOLKOPFTLIDLPFLKSLTLTNKGSISFKVVALPSLSYIDLSSRNALSPSGC 388

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Dp	336	GM0HLELVNCKRGQPPPTLKLSKKLTPTSNKGANPSEVDLPSEFLDLSRNGLSFKKC	395
Qy	389	CSYSDLGNTSLRHLDLSFNGALIMSANFWELELOHLDPEQHSHTLKRVTEFSAFLSDEKL	448
Dp	396	CSQSPFGTSLTKYLDLSPFGVITMESNFIQDLQLEHLDPEQHSHLKMQSEFSVPLSRNLI	455
Qy	449	YLDISYNTKIDPDGFIPLGJLSLNTLKAAGSNFKDNTLSNVFANTTNLTPDLISKQOLQ	508
Dp	456	YLDISHTRVAFNGFIPLNGLSLEVLKAGANSFOENFLDPIFELRNLTPLDLSQOLQLO	515
Qy	509	ISMGVFDTLHRQOLNMSNNLTLPLDSSHYNOLYSTLDCSEFNRIETS-KGILQHFPKS	567
Dp	516	LSPTAFNSLSIQVILNMSHNNFPESLDTPFYKCLNSIQVLDYLSNHTMITSKKQOLQHPBS	575
Qy	568	LAFNLTNNSVACICEHQFLQVXEXQKQFLVNVEMQTCATPEVMMTSLVLDENNSTCYM	627
Dp	576	LAFNLTLQNDFACTCEHQSFQLOMKIDQROLIVEVERMECATPBDQGMPLYLSL-NITCOM	634
Qy	628	YKTIISVSVAJYVSVTAFLYHPFPHLLAGCKKYSRGESITYAFVYSSONEDWR	687
Dp	635	NKTIIGVSLVSLVSVAVLXKFFPHMLLAGCIKYGGENIYDPAFVYSSQDEDMWR	694
Qy	688	NELVKNLEBGVRFHLCIAYRDPFIPGVALAANIIOEGFHKSRKVIIVVSRHFTQSRWCIF	747
Dp	695	NELVKNLEBGVRFPOCLATYRDPFIPGVALAANIIEHGFHKSRKVIIVVSGHFIQSRHCIF	754
Qy	748	EYEIAQTFWQFLSSRSQIIFIYLEKVEKSLRQOVELYRLISRNTTYLEMEDNPGRHIFWR	807
Dp	755	EYEIAQTFWQFLSSRAQIIFIYLOKVEKTLRQOVELYRLISRNTTYLEMEDNSVIGRHIFWR	814
Qy	808	RLKNALNLOGKASNPBCT	824
Dp	815	RLKRALNLOGKASNNPBCT	831

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1      RESULT 2
2      US-08-514-014-4
3      ; Sequence 4, Application US/08514014
4      ; Patent No. 5707829
5      ; GENERAL INFORMATION:
6      APPLICANT: Jacobs, Kenneth
7      APPLICANT: McCoy, John
8      APPLICANT: Kelleher, Kerry
9      APPLICANT: Carlin, McKeough
10     TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
11     TITLE OF INVENTION: ENCODED THEREBY
12     NUMBER OF SEQUENCES: 12
13     CORRESPONDENCE ADDRESS:
14     ADDRESSES: Genetics Institute, Inc. -- Legal Affairs
15     STREET: 87 CambridgePark Drive
16     CITY: Cambridge
17     STATE: Massachusetts
18     COUNTRY: USA
19     ZIP: 02140
20
21     COMPUTER READABLE FORM:
22     MEDIUM TYPE: Floppy disk
23     COMPUTER: IBM PC compatible
24     OPERATING SYSTEM: PC-DOS/MS-DOS
25     SOFTWARE: Patentin Release #1.0, Version #1.25
26     CURRENT APPLICATION DATA:
27     APPLICATION NUMBER: US/08/514, 014
28     FILING DATE:
29     CLASSIFICATION: 514
30     ATTORNEY/AGENT INFORMATION:
31     NAME: Brown, Scott A.
32     REGISTRATION NUMBER: 32,724
33     REFERENCE/DOCKET NUMBER: G16000
34     TELECOMMUNICATION INFORMATION:
35     TELEPHONE: (617) 498-8224
36     TELEFAX: (617) 876-5851
37     INFORMATION FOR SEQ ID NO: 4:
38     SEQUENCE CHARACTERISTICS:

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; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-514-014-4

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Query Match	14.3%	Score 619.5;	DB 1;	Length 661;
Best Local Similarity	28.6%	Pred. No. 4.4e-46;		
Matches 187;	Conservative 126;	Mismatches 296;	Indels 45;	Gaps 18;

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QY 28 CIEVVPNTYCCMOQKSLKSVDDIPSSSTKNIDLEFNNPKLIKXSVSFSELOWQIDLSRC 87
Db 28 CIEKXANTYCNCEMLGISEIPDTLPNTELEBSEFNFPLPIHNKTFSELMNLTFDLJTRC 87
QY 88 EIEETIEDKAMGHLLHLSNLITNPPIOSFSGSGSLTSENLVAVEFKLASLESFPICQ 147
Db 88 QINNIHEDTFQSHHQLSLTLYLTGNPLIFMAETSLNKGPSLKHPLIOTGISENLEPIVHN 147
QY 148 LITLKULVANANFIHSCLEPAVFNPNLNLVAVHDSVNYIQITVYNDLOFLEBENQVNLST, 207
Db 148 LENIEBLSYLSNNHISLKEPPROPF-ARNLKVLADPQNNAHYHISREDMASLQ--AINSL 204
QY 208 DMSLNPIDFIDOAFOQIKIHELTLRGNFNSSNIMKTCLQNLAGLAVHRLIIGEFKDERN 267
Db 205 NFNGNNVXGILGAFDSVTFQSLNFGGPRNLVIFNG-LQNST--TQSLMGTEPDIDD 260
QY 268 LEIEPPISEGLCVDTIDEFRLYTTNDSFD-DIKYFHLANVSAMSLSAGVSIKTYEDVP 326
Db 261 EDI--SSAMKKGICEMSVESLNL-DEHRPDSISSTFFOCTOLOBLDLYAT--HKGKPS 315
QY 327 HPKMQSLIIR-----COLK--OPPTLDLPKLSLITLMNKGISFKKVALPS 372
Db 316 GKK--GLWLLKLVLSVNHFDOLCOISANPFSPLHLXIRGVKVKHLHGVGLEK--LGN 371
QY 373 LSYLDLSRNALSFSGCCSYSDLGNSLRLHLDLSENGAI-IMSANFMGLEBLDHPNST 431
Db 372 LQTDLSHNDIEABDCCSLQOLKNLSHLQTLNLSHNEPGLQSOAFKECPOLELDLIAFTR 431
QY 432 LKRVTEBAFSLSEKLVLDISYNTTKIDPFOGIFGLGSLMNTKMAAGSFONLT--SNV 489
Db 432 LHINAPQSPONLHPLQVNLNLTYCELDTSNOHLGLBVLRLHNLKGNHFOGTTTKTNL 491
QY 490 FANTNLVFLDLSKCOLBQISWGVEDTLRLQLLMSHNNLL--FLDS-SHYNDUSYST 546
Db 492 LQTVSLEVLILISSGGLSIOQAHSHSGKXSHVDLSHNSLDCSIDLSHLKGIY--- 547
QY 547 LDCSFNRIETSKGILLQHPFKSLAFNLTNNVSACICEHOKFLQWYKQKQFLVAVNEQMTG 606
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QY 607 AHPVEMN-----TSLVDFNNSTCWYMKTLISVSVSVSVFVAFVLYHYPFL 656
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RESULT 3
 US-08-833-823-4
 ; Sequence 4, Application US/08833823
 ; Patent No. 5965093
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Jacoby, Kenneth
 ; APPLICANT: McCoy, John
 ; APPLICANT: Kelleher, Kerry
 ; APPLICANT: Catlin, McKeough
 ;
 ; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
 ;
 ; TITLE OF INVENTION: ENCODED THEREBY
 ;
 ; NUMBER OF SEQUENCES: 12
 ;
 ; CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
 ; STREET: 87 Cambridgepark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA

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; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,823
; FILING DATE: 10-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/514,014
; FILING DATE: 11-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G16000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-823-4

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Query Match      14.3% Score 619.5; DB 2; Length 661;
Best Local Similarity 28.6%; Pred. No. 4,4e-46;
Matches 187; Conservative 126; Mismatches 296; Indels 45; Gaps 18;

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QY 28 CIEVPPNITTCOMQDKLSKVPDDIPSSSTKNIDLSFNPRLIKLSYFSNFSBLQWMLDLSRC 87
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DB 88 QINNIHETFOSSHQSLTLVLGNPLIFMAETSLNGPSSLKGLFLIQGISLLEFIPVHN 147
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QY 208 DMSINPDIQDQAFQIKHETLRGNFNSNIMKTCLQNLAGLHVHRLIIGERKDERN 267
DB 205 NFNANNVGIELGAFSTVFOSLNFGTPNLSVIFNG-LQNST--TQSLMLGTEDIDD 260
QY 268 LEIEPESIMEGLCVTIDEPRLTYTNDPSD-DIYKHCNAVMSAGLSVSIKYLEDVVK 326
DB 261 EDI-SSANLKGCLCEMSVESLNL-OEHRSFDSSTTFQCFQLOEIDLTAAT--HLKGLPS 315
QY 327 HFKQSLIIR-----COLK--OEPPLDLPRLKSLTLTMNKGSIKPKVALPS 372
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QY 373 LSYLDLSRNALSFSGCCSYDLGNSLRHLDSFNGAI-IMSANFMGLEELQHLDFQST 431
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QY 432 LKRTESAPLSLEKLYLDISYNTYKIDPFGIFGLTSLNTLKAAGNSFPDNTL--SNV 489
DB 432 LHNAPSPFONLHFLVNLTYCFPLDTSNQHLAGLPLVHLNLKGNHFPDGTITTKNL 491
QY 490 FANTTNLTFDLSCQLEQISWGVFDLHRLQOLNMSHNNL--FLDS-SHYNDLXLSST 546
DB 492 LQTYGSLLEVLLISCGSLSDIQOAFHSLGKMSHYDLSHNSLTCSIDLSHLKGIY--- 547
QY 547 LDCSFNRIETSKGILQHPKSLAFENLTNNSVACICEHQKFLQWVKEQKQFLVAVNEQWTC 606
DB 548 LNLANSINIIISPLRLILSQGSTINLSHNDLCTCSNHFLLTWYKEMLHKLBSSEETJC 607
QY 607 ATPENK-----TSVLDPNNSTCYMYKTIISVSIVSVIYVSTVAFLLIHFYHL 656

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DB 608 ANPSELGVKLDVYKLSGCTAIGIFFLIVFLLALILFPAVKYLLRWKYOH 661
RESULT 4
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
; APPLICANT: Dalié, Barbara
; APPLICANT: Pan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tan, Jimmy C.
; APPLICANT: Zavodny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: JBO601QC
; CURRENT APPLICATION NUMBER: US/09/982,308B
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,163
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-982-308B-23

```

```

Query Match      11.4% Score 494; DB 4; Length 784;
Best Local Similarity 25.9%; Pred. No. 8.2e-35;
Matches 218; Conservative 131; Mismatches 319; Indels 174; Gaps 34;

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QY 44 LSKVPDDIPSSSTKNIDLSFNPRLIKLSYFSNFSBLQWMLDLRCIEFIEDKAMHGLHNL 103
DB 43 LNSIPSGLEAVKSGIDLSNNRITYISN-----SDIQRCV-----NL 78
QY 104 SNLITGNPIOSFSGSGLSLNVAVERKLASLESFPIGQITLTKLVANFTHS 163
DB 79 QALVLTSGINTIIEEDSFSSLSGLEHLDLSYNYLSNLSWFKPLSLTFLNLGNPKYT 138
QY 164 CKLPAYNSNLTLVHVLD-----SYNYIQTITVNDLQFLRNPOVNLSDMSINPDIQD 219
DB 139 LGFTSLFSHLTKQLIRGNMDTFTKIQKDFAGLTFLE-----LEIASDQSYEP 191
QY 220 QAFQGI-----KLHETLRGNFNSNIMKTCLQ-----NLAGLHVHRLIGEPD- 264
DB 192 KSLKSLQNVSHLILAMQHILLLLEIFVDYTSVE-CLELRDTDDTFRFSLSYGETNSL 250
QY 265 -----ERNLEIEPESIME-----GLCDVTIDEPRLTYTNDP--SDIYKHCPLANV 308
DB 251 IKKFTFNVKLTDESLRQVMKLNQISGLELEBDDCTLNGVGRFASDN----- 300
QY 309 SAMSAGVSIKYLEDVYKHFQWQSLIIRQLKQFPL-DLPFLKSLTLTMNKGSIKPK 367
DB 301 -----DRVIDPGVETLTIIRLHIPEFYLDSTYSILTERYKRIYVENS 347
QY 368 V-----ALPESLYLDLSRNA-----LSFSGC-CSYSDLGNSLR--HL-DLSFNGA 409
DB 348 VFVLPCLLSGHKSLLEFIDLSLENLMBEYKLNKSCEDAMBSLOTLILRQNLASLEKGE 407
QY 410 IMSANFMGLEELQHLDFQSTLKRVTESAFSLKLYLDISYNTYKIDPFGIFGLT 469
DB 408 TLLT-----LKNLTINIDISKNSFSHMPETCOM--PEKRYKLNLSST----- 446
QY 470 SLNTLKAAGNSFPDNTLNPANTTNLTFDLSCQLEQISWGVFDLHRLQOLNMSHNN 529
DB 447 -----RHVSYTGCIPT--LEIIVDSNNNLNPLSL--NLPLKELIYISRNK 488

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[illegible]

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RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/094949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PR1
; ORGANISM: Human
US-09-949-016-8799

Query Match          10.0%; Score 432.5; DB 4; Length 775;
Best Local Similarity 25.4%; Pred. No. 2,36-29;
Matches 207; Conservative 116; Mismatches 290; Indels 201; Gaps 33;

44 LSHVDDIPSTXNIDISFNPDLTKLSYFSNSELQWLDISREIETIEDXAHGHLHL 103
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
78 LNSIPSGLTAEVXSLDLSNNRITYSN-----SDLRQCV-----NL 113

104 SNLILTNPNQSPFGSPGSLGTSENVAVETKLASIEPFIQGLITTKLVANHFIS 163
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
114 QALVLTNGNGINTTIEBDSFSLGSEHLDDLSTNYNLSNLSMFKPLSLTFLNLGNPKYT 173
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

164 CKLPAYSNSLTNLVHVL-----SYNYIQTITVNDLQFLRENPQVNLSDMSLNPDIQD 219
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
174 LGEISLFSHLTKQLIKVGNMDTFTYKQKDPAGATFEE-----LEIDASDQSYEP 226
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

220 QAFQGI-----KLHLLTLRGNFSSNIMKTCLO-----NLAGLVHRLILGEFKD- 264
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
227 KSLMSIQVSHLILHMKGHILILEFVYDVTSVE-CLLELPDIDLDLTFRSELSGTETNSL 285
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

265 -----ERNLEIFPESIME-----GLCVYTIDEFLTYTNDP--SDDIYKFCILNV 308
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
286 IKKETFPRVVKITDBSLFQVMTLNLQISGLLELEFPDCTLNGVGNFRASDN----- 335

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QY 309 SAMSLAGVISTYKLEDEYKHFHMOSLTIIRQMKOFPIL-DLPEYKSLTUTNMKNGSIFPK 367
Db 336 -----RVIDPGVEVETLTIIRHHIPFYUFDLSTLYSLTERVAKRITYENK 382
QY 368 V-----ALPSLSYDLISRNA-----LSPSGC-CSYSDLOTNSLR--HU-DLSFNGA 409
Db 383 VLVPECLLSOHLKSLIEYLDLSENLMBEYKLNACSEDMPSLOTLLRQHLHSLSEKTEB 442
QY 410 IIMSANFMGLEBELQHLDPFHSTLRKVTESFAPLSLEKLYLDISYNTKIDEPGIFLGLT 469
Db 443 TLTL-----LKNLTNIDISKNSPHSMETQCM--PEKRYLANLST-----481
QY 470 SLNTLKMGNSPKONTLSNFPANTTNLTFLDLSKCCQLEQISNKGVPDTIHRLOLNMSHNN 529
Db 482 -----RHSYGCIPKT--LEILDVSNMNNLNPSSL-----NLPLKELYLSRNK 523
QY 530 LFLFDSHNTQYLSSTLDGSPNRIET-SKGLDHPKSLAFNLTVNSVACICEHQKEL 588
Db 524 LMTLPDA--SLIPMLLYIKIRNALTYPFSKQDQSP-HTLKTELAGANNITGCE---FL 577
QY 589 QAWKEQKOPLVNV-----EQMTCAPEYMNLSLVDENNSTCYMYKTLISVSVAIVAS 643
Db 578 SFTQBO-QALAVYLDIMPRANYLQDSPSYVRQOQYQDVRLSVECHRALVALSGMCCAL---633
QY 644 TYAFLTYHFYFHLIAG--CKKY-----SRGESIYDAFVY 678
Db 634 -----FLIILLTGVLCRHFPLWYMKMMAMLAQAKKPRKAPSR-NICIDAFVSY 682
QY 679 SSONEDWVRELKYLIEBQVPRFHLCHYRDPICGVAMIANIIOEGFHKSRKVLVVVSRH 738
Db 683 SERDAVAVENIMVQELLENPPFKCLCHKRDPFPEKMTIDNII-DSIEKSHKIVFLSEN 741
QY 739 FIOSRWCTFEYELAQTMQFLSRGSLIFVLEKV 772
Db 742 FVKSSEWCKTELDSPSHRFLPDEMNDAAIILILEPI 775

```

RESULT 6
 US-08-190-802A-50
 Sequence 50, Application US/08190802A
 Patent No. 5519003
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Ron, Dosit
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: P.O. Box 60850
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190,802A
 FILING DATE: 01-FEB-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ. ID NO. 50:
 SEQUENCE CHARACTERISTICS:

LENGTH: 603 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
 INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
 US-08-190-802A-50

Query March 7.3%, Score 317.5; DB 1; Length 603;

Best Local Similarity 24.1%, Pred. No. 2.6e-19;

Matches 159; Conservative 86; Mismatches 223; Indels 193; Gaps 24;

QY 39 CMDOKLSKVPDDISSTKNDLSFNPPLIKLSYFSNFSLEQWDLSCETIEDKAMH 98
 DB 60 CSSKNLTHLPDDIVSTRALMDGNLSSIPSAFQNLSSIDFLNLSQSWLRSLPOLL 119
 QY 99 GLHLSNLILTGPNIQSPSPSGSLTSLNVLAVETKLASLSPPIQOLITLKKLVAN 158
 DB 120 GLQNLVYHLHERNRLRNLAAGLFTHTPRLASLSSNLGRLEBGLFQGLSHLMDNLGW 179
 QY 159 NF-----IHSCUL-----PAYSNLTNVHVDLSYNYQTITVNDLQ 195
 DB 180 NSLVLPDVTYFQGLGNLHVLNAGNKLTYLOPALFCGELRELDLSRNALRSYKAVFV 239
 QY 196 FLRENPOV-NLSLDSINPIDIODAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLH 253
 DB 240 HL---PRLQKLYLDRNL--ITAVAPGAFGLKALRWDLDSIN-RVAGLMETTPGLGLH 293
 QY 254 VHRLLIGEFKDERNLLEIFEPSIMEGLCDVTIDEFRLTYTNDPSDDIVKFCIANVSAMSL 313
 DB 294 VLR-----LAHNAIASL 305
 QY 314 AGVSIKYLEDPKHKFKQSLIIRCOLKQPTLDLPFLKSLTLMNK-----GSISEPKVA 369
 DB 306 R-----PRTFK-----DLHFLBELQIGHNRIRQIGERTFE--G 336
 QY 370 LPSLSYDLDSRNAL-----SFGCCSYS--DLGTNSLRHDLSPNGAIIIMSNPMGLEE 421
 DB 337 LGQLEVLTLNDNQTEVRVAGFSGLFNVAVMNLSGNCRLSP-----ERFQGLDK 387
 QY 422 LQHLDPQSTLKRVTESAPLSLEKLYLDISYNTKIDPGLIFGLTSLNTLMKAGNSF 481
 DB 388 LHSIHLBHSCLGHVRLHT-----FAGLSGLARFL----- 417
 QY 482 KQNTLSNV-----PANTMLTFLDLKSCQLEQISWGVPTTLRLQLLMSHNNLLFLDSSH 537
 DB 418 RDNSSISIEQSLAGLSELLELDLTNRLLTHLPROLFOGLHLELYLLSYNQLTTLSEV 477
 QY 538 YNOLYSISLTDSCFNRIET-SKGILOHPKSLAFPNLTNNSVACIHCQKFLQWYKBO-- 594
 DB 478 LGPQRAFWDISINHLETLAEGLPSSIGR-VRYLSLRNNS-----LQTFSPQPG 526
 QY 595 -KQFLVAVQMTCAQVE-----MNTSLVLDFFNNSTC-----YMYKTIISVSYS 638
 DB 527 LERMLANPMWDCSPLKALRDPALQNGVYVRFVQVTCBGDDCQPVYTYNNITCAGPAN 586
 QY 639 V 639
 DB 587 V 587

RESULT 7

US-08-477-346-50

Sequence 50, Application US/08477346

Patent No. 6262023

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

TITLE OF INVENTION: thereof

NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster
 STREET: 2000 Pennsylvania Avenue, NW
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,346
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/487,072
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 2550-0025.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 603 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
 INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
 US-08-477-346-50

Query March 7.3%, Score 317.5; DB 3; Length 603;

Best Local Similarity 24.1%, Pred. No. 2.6e-19;

Matches 159; Conservative 86; Mismatches 223; Indels 193; Gaps 24;

QY 39 CMDOKLSKVPDDISSTKNDLSFNPPLIKLSYFSNFSLEQWDLSCETIEDKAMH 98
 DB 60 CSSKNLTHLPDDIVSTRALMDGNLSSIPSAFQNLSSIDFLNLSQSWLRSLPOLL 119
 QY 99 GLHLSNLILTGPNIQSPSPSGSLTSLNVLAVETKLASLSPPIQOLITLKKLVAN 158
 DB 120 GLQNLVYHLHERNRLRNLAAGLFTHTPRLASLSSNLGRLEBGLFQGLSHLMDNLGW 179
 QY 159 NF-----IHSCUL-----PAYSNLTNVHVDLSYNYQTITVNDLQ 195
 DB 180 NSLVLPDVTYFQGLGNLHVLNAGNKLTYLOPALFCGELRELDLSRNALRSYKAVFV 239
 QY 196 FLRENPOV-NLSLDSINPIDIODAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLH 253
 DB 240 HL---PRLQKLYLDRNL--ITAVAPGAFGLKALRWDLDSIN-RVAGLMETTPGLGLH 293
 QY 254 VHRLLIGEFKDERNLLEIFEPSIMEGLCDVTIDEFRLTYTNDPSDDIVKFCIANVSAMSL 313
 DB 294 VLR-----LAHNAIASL 305
 QY 314 AGVSIKYLEDPKHKFKQSLIIRCOLKQPTLDLPFLKSLTLMNK-----GSISEPKVA 369
 DB 306 R-----PRTFK-----DLHFLBELQIGHNRIRQIGERTFE--G 336
 QY 370 LPSLSYDLDSRNAL-----SFGCCSYS--DLGTNSLRHDLSPNGAIIIMSNPMGLEE 421
 DB 337 LGQLEVLTLNDNQTEVRVAGFSGLFNVAVMNLSGNCRLSP-----ERFQGLDK 387
 QY 422 LQHLDPQSTLKRVTESAPLSLEKLYLDISYNTKIDPGLIFGLTSLNTLMKAGNSF 481

Db 388 LHSJLHSHSCIGHVRLHT-----FAGLSGLRRLFL----- 417
Qy 482 KDNTLSNV-----PANTNLTFLDLSKQLEISNGVDTLHRLQLMNSHNNLLFLDSH 537
Db 418 RDNSISSIEQSGLAGSELDELDTNRLTLHPROLFGHGLHLYLLSYNQLTTLSAEV 477
Qy 538 YNOLYSTLTDSCFNRIET-SKGILQHPKSLAFNLTNNSVACICEHQKFLQWKEQ-- 594
Db 478 LGPLQRAFWLDISHNHLETLAEGLFSSLGR-VRLSLARNNS-----LQTFSPQPG 526
Qy 595 -KQPLVNEQWTCATPYE-----NMTSLVLDENNSTC-----YMKTTIISVSVS 638
Db 527 LERLMLDANPMWDCSCPLKALRDPAIQNPVPRVQVCEGDQCQPYTYNNITCAGPAN 586
Qy 639 V 639
Db 587 V 587

RESULT 8
US-08-473-089-50
; Sequence 50, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF INVENTION: Thereof
; ADDRESS: Morriison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473.089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
; INDIVIDUAL ISOLATE: Pro. complex-rat, Fig. 33
; US-08-473-089-50

Query Match 7.3%; Score 317.5; DB 3; Length 603;
Best Local Similarity 24.1%; Pred. No. 2.6e-19;
Matches 159; Conservative 86; Mismatches 223; Indels 193; Gaps 24;

Qy 39 CMDQKLSKVPDDIPSTKNIDISFNPDLKLSYFSNFSQELCOWLDISRCEITTDKXMH 98
Db 60 CSSKNLTHLPDDIPVSTRALWLDGNLSSIPSAFQNLSSLDPLNLQSGWLSLEPQALL 119

Qy 99 GLHLSNLTITGNPIQSFPSPGSGLTSLNLTVAETKLASLSPFIQGLITLTKLVVAH 158
Db 120 GLQNLVYIHLERRRLNLAAGLFTHTPSLASLSNLTGLRLEGHFOGLSHLMDINTLGW 179
Qy 159 NF-----IHCKL-----PAYFSNLTUVAVDLSYNYIQITTYNDLQ 195
Db 180 NSIVVLPDVTFOGIGNLHLYLAGNKLTYLQPALFGGLGELRELDLSRNLRSVKNVAV 239
Qy 196 FLRENPOV-NLSDMSNPIDFIQDQAFQIGK-LHETLIRGNFNSSNMKTCQLNLAGLH 253
Db 240 HL---PRLQCLYIDRNL--ITVAPGAFGLMKLRLWLDLSH-RVAGIMEDTTPGLLGLH 293
Qy 254 VRLIIGEFDEBERNLLEIFESBINEGLCDVTIDEFRLLTYTNDFSDDIVKFCILANVSMSL 313
Db 294 VLR-----LAHNAIASL 305
Qy 314 AGVISIKLEDPKPKKQSLSTRCOLKQPTLDPFLKSLTYLTMK-----GSISPKVA 369
Db 306 R-----PRTFK-----DLHFLLEELQGHNRIRQLGERTFE--G 336
Qy 370 LPLSLVLDLSRNL-----SFGCCSYS--DLGTNSLRHLDSFNCAITMSANFMGLRE 421
Db 337 LGQLEVLTLNDNQITTEYRVGAFSGLFNVAVAMNLSGNCRLSP-----EKVFGSLDK 387
Qy 422 LQHLDPQSTLAKETVTERSAFLSEKLYLDISYNTKIDPDGIFLGLTSLNTLKMAGNSF 481
Db 388 LHSJLHSHSCIGHVRLHT-----FAGLSGLRRLFL----- 417
Qy 482 KDNTLSNV-----PANTNLTFLDLSKQLEISNGVDTLHRLQLMNSHNNLLFLDSH 537
Db 418 RDNSISSIEQSGLAGSELDELDTNRLTLHPROLFGHGLHLYLLSYNQLTTLSAEV 477
Qy 538 YNOLYSTLTDSCFNRIET-SKGILQHPKSLAFNLTNNSVACICEHQKFLQWKEQ-- 594
Db 478 LGPLQRAFWLDISHNHLETLAEGLFSSLGR-VRLSLARNNS-----LQTFSPQPG 526
Qy 595 -KQPLVNEQWTCATPYE-----NMTSLVLDENNSTC-----YMKTTIISVSVS 638
Db 527 LERLMLDANPMWDCSCPLKALRDPAIQNPVPRVQVCEGDQCQPYTYNNITCAGPAN 586
Qy 639 V 639
Db 587 V 587

RESULT 9
US-08-487-072A-50
; Sequence 50, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF INVENTION: Thereof
; ADDRESS: Morriison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487.072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor bind
INDIVIDUAL ISOLATE: pro. complex-1a1, Fig. 33
US-08-487-072A-50

Query Match 7.3%; Score 317.5; DB 4; Length 603;
Best Local Similarity 24.1%; Pred. No. 2.6e-19;
Matches 159; Conservative 86; Mismatches 223; Indels 193; Gaps 24

```

QY      39 CNDQKLSKVDDIPDSSTKNADISFNPFLKLKSYSFSNFSLOMDLRSCEIETEDRAMH 98
Db      60 CSSKNLTTHPDDIPVSTRALMTDGNUNLSISPAAQNLSIDPLTQSWLRSLPEPAL 119
QY      99 GJHLNSLLITGPRIOSFSPGSFGITSJENLVAVETKLASIEFPICQLITLKCNVAH 158
Db      120 GLQNLYYLILERNRLNNLAIVGLFTHTPSLASISLSNNLGRLEBGLFOGSHIMDLMLGW 179
QY      159 NF-----IHSCKL-----PAYSNLTNLVHDLVSNTYIGTTIVNDLQ 195
Db      180 NSLVLPDTVPFGSLGYLHELVLAYGNKLTLYLPDALFCGIGELRELDLSNNALRSRANVAV 239
QY      196 FLEENDQV-NLSIDMSLNPDIETODAFQGIK-LHELTLRGNFNSSNMKTCLONTAGLH 253
Db      240 HL---PRLQKLYLDRNL--ITAVAAGAFGMKALRMWLSHN-RVAGLMETTPFGILLGH 293
QY      254 VHRLLIGEKKERBNLEIFEPSSIMEGLCDVTIDEFRLYTYTNDSPSDIVKFHCILANVASMT 313
Db      294 VLR-----LAHNAIASL 305
QY      314 AGVISIKYLEDVDPKHFKMOSLSIIROCLKOPTLIDLPLKSLTLTMNK----GISISPKVA 369
Db      306 R-----DRTFK-----DLHFLEELQIGHNRIROLGERTEP--G 336
QY      370 LPSLSYLDLSRAL-----SFSGCCSYSS-DLGNSLRHLDSLFGNALIMSANGMLEE 421
Db      337 LGQLLEVLTINDNQITBEVAVGAASSGLEFNVAVMNLSCNCRSLRP-----ERYFOGLDK 387
QY      422 LGHLDFQHSTKRVTESFAFLSEKLYLDLISYTNYKIDPDGFIPLGLTSINTLKMAGNSE 481
Db      388 LHSLSLHESHCLGHVRLLHT-----FAGLSGRRLFL----- 417
QY      482 KNTLSNV-----FATYTLULFDLDSKCQDEQISMGVEDTLRLLOLAMSNNMLFFDSSH 537
Db      418 RNNSJSSISEEGSLAGSELBELLEDLITNNLTYLPRQLFGCHLEYLLLSYNQUTLLSAEV 477
QY      538 YNQLVSLSTLSDSPRIET-SKGILQHPKSLAPFNLTNNSVACIGEHQFLQMWEO-- 594
Db      478 LGPIORAFPLDISHHNHLETLABGLFSSIGR-VRYLSLNANS-----LDTFSPPQG 526
QY      595 -KQPLVNEQMTCARPV-----MNTSLVLDENNSTC-----YMKYTIIVSYVS 638
Db      527 LERLMLDANPMDCSPLKALBDPALQNGVVPRVQIVCGSDQCQPYTTYTNITTCAGRAN 586
QY      639 V 639
Db      587 V 587

```

```

US-09-063-950-5
; Sequence 5, Application us/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MRI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-09-063-950-5

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Query Match	7.3%;	Score 316.5;	DB 3;	Length 605;
Best Local Similarity	22.2%;	Pred. No. 3.2e-19;		
Matches 147;	Conservative 89;	Mismatches 238;	Indels 189;	Gaps 17;

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QY      32 VFNITTYQCMQDKLSKVPDDIPBSTYNDLDSFNPLTKLSYSPFSNFSFSELOWLDSRCEIET  91
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      53 VNELSVFCCSSRNILTRPDGIPGCTQALWLDNSNNLSSIPPAFRMLTSLAFLNLQGGQLGS  112
QY      92 IEDKANHGHHSNLLTGNPIQSSPSSFGGLTSLNVAVETKLASLSEFPPIQLITL  151
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      113 LEPQALGLIENLCHLTERNOILRSIAVGFYTPALMLGLSNRLSRLED-  163
QY      152 KKLNVANHFHSCKLPAFYSNLTNLVNHDLSTNYITQITVNDLQFLRENPNVNLSDMSL  211
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      164 -----GLFEGGLNLMDLNGLMSLAV-----  184
QY      212 NPIDFIQDAFOGFI-KLHELTLRGFNSSNIMKTCLONLGLAHVHRLILGPFYDERMLET  270
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      185 -----LPDAAFPGILGGLRELVLAGN-----RLAY  208
QY      271 FEPSIMEGLC-----DVITDEFRLTYTNDSESD--DIYKHCGLANVGSMSLAGVISIKYLED  323
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      209 LQPALFSGLAELRELDLSRNALIRAIKANVFQOLPRLOKYLIDRULIAAVAPGA-----  261
QY      324 VPKHFQMOGLSIIRCOLKQRPFLDLPFLKSLTYLTMNK--GSISPKKVALPSLYLDLRSN  381
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      262 -----FLGILKALRWLDSHNHRAVGLLEDTPPGILGLRYLRISHN  300
QY      382 ALSFGCCSYSD-----LGTNSLRHLDSFNGALIMANSFNKGELEOHLDFOSTLK  433
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      301 ALASLRPRPFEDHLHLELDQGHNRIRQL-----ARSFEGGLQGLVLTLDINQQL  351
QY      434 RYTESAFLTEKLILYDITSTYTKIDPDIFFLGILTSLNTLKRAGNS-----  480
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      352 EV-KVGAFGLITNVAVMNLGNCILRNIPBOVFRGLGKLSHLHSGSLGRIIRPHTFAGLS  410
QY      481 -----PRDNLTSNVFANT-----TNLFLDLSKQLEQISMGVPTDLHLRQLQLMASHNUL  530
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      411 GLRLFLFKONGVGBEBSQMLGAELLELDITSNQLTHLPHOIFQGGKLEYLLLSHNRL  470
QY      531 LFLDSSHYNOULYSLTLDSCFNRIETSKGILQHPKSLAFPNLTNNNSVACICEHQEFLQ-  589
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      471 AELPRADLAGPQQRAFWLDVSHNRLEALPGSLIASLGRLATLNRNNSLRITFTTQPPGLER  530
QY      590 -WVKEQKQFLVNVBQMTCAFPVE-----MNTSLYLDFNNSTC-----YMYKTI  632
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      531 LMLBG-----NPMDCSPLKALRDPALONPSAVBRFAVQICBEGDCQPPVYTYNNIT  582
QY      633 SVS 635
Db      583 CAS 585

```

RESULT 10

RESULT 11
US-08-190-802A-49


```

Query Match 6.7%; Score 291.5; DB 3; Length 605;
Beet Local Similarity 22.0%; Pred. No. 5,3e-17;
Matches 147; Conservative 86; Mismatched 233; Indels 201; Gaps 17.

QY 39 CMDQKLSKVPDDIPSSSTKNIDISFNPDLKLIKSYFSFNSFSELOMLDLSRCEIETEDKAMH 98
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 60 CCSRRLTRLPDGVPGTQALMLDGNLSSVPPAPONLSSLGFINOGQSLSEFQALL 119
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 99 GHHLSNLTITONPIQSPSPSGSGTSTENLVAVETKLASLSEFPIGQITLTKLVANH 158
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 GLENCHLHLEBNQRLSLAGTFAHTPALASIGLSNNRSLRELDGFEFGISLMDLNGM 179
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 159 NFTH-----SCKLPAYSNLTNLVHVDLSNYITQITVNDIQ 195
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 180 NSLAVLPDPAFRGLSGLRELVLAGNRLLALQALPFGSLAELELDELDSRNALRAIKAN--V 237
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 196 FLRENPQVNLSDMSINLPIDFIDQDAFOGIK-LHETLIRGNFNSNIMTKCQLNLAGLHV 254
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 238 FVQGLPRLOKLYIDRL--IAAVAPGAFLGKALRWLDSHN--RVAGLELDDTPGLGLRV 294
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 255 HRLIGEFKDERNLEIFEPSIMEGLCDVTTIDEFRLTYTDFSDDIYKFCILANVAMSIA 314
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 295 LRL-----SHMALA 303
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 315 GVSIKYLEDVPRKHFQMOSITRCQKOPFTLDPFLKSLTYLTNNKGSISFKVALPSLS 374
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 304 SLR-----DLFFLEBEL 319
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 375 YLDLSRNALSPSGCCSYSDLGTNSLRHLDLSPNGAIMSANPMGLSELEIHLDFOHSITLKR 434
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 320 -----QLGHNRIKQL-----ARSPSEGGLQLEVLTLDDNNLOE 352
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 435 VTERSAPLSLEKLYLDISYTNTKLIDPFGIFLGLTSLNTLXMAGNS----- 480
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 353 V-KAGAFGLTNVAAMNLSGNCLRLPRQVPRFGDKLHSIMHEGSCIRIRPHTTGLSG 411
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 481 -----FKRNTLSNVANNT-----TNLTFLDLSKCOLEQISWGVFTLTLRLQLINSHNNLL 531
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 412 LRLFLPKDNGLVGIEEBSLGMGLAELELDLTLSNQLTHLPHRLFOGLGKLEYLLSRNRLA 471
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 532 FLDSHHVQQLSLSTLDCSFNRIENTSKGILQHPRKSLAPFNLTNNSVACIGHOKFTQ-- 589
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 472 ELPPDALGPRLQAFNLDVSHNRLEALPNSLAIPGRLEYLSIRNNSLRTTPQPGRLRL 531
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 590 WKXQKQPLVNEQWTCATPVE-----NMTSLVLDENNSTC-----YMKTIIS 633
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 532 WLFG-----NPMDDCGPLKALRDFAQLNPSANPRVQALCEBDDQCPAYTYNNITC 583
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 634 VSVVSVI 640
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 584 ASPEPV 590
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 13
US-08-473-089-49
; Sequence 49, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/473_089
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: MURASHIGE, KATE H.
? REGISTRATION NUMBER: 29,959
? REFERENCE/DOCKET NUMBER: 2550-0025.22
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 887-1500
? TELEFAX: (202) 887-0763
? INFORMATION FOR SEQ ID NO: 49:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 605 amino acids
? TYPE: amino acid
? TOPOLOGY: unknown
? MOLECULE TYPE: protein
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? INDIVIDUAL ISOLATE:
? INDIVIDUAL ISOLATE: protein complex, Fig. 32
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? US-08-473-089-49
?
?
? Query Match 6.7%; Score 291.5; DB 3; Length 605;
? Best Local Similarity 22.0%; Pred. No. 5.3e-17;
? Matches 147; Conservative 86; Mismatches 233; Indels 201; Gaps 17
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? QY 39 CMDQKLSKVPDDISSTGNIDLSNPLKILKSYSPSFSFSEIOMIDLSRCEIETIEDKAMH 98
?   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
? DB 60 CSSRNLTELPGVPGGQALWLDNNISSVPPAFQNLSSIGFINTLQGGOLSGLEPQALL 119
?
? QY 99 GLHHLNSNLTNGNPLOSPPSGFSGLNLSLVAVETKTLASLESPPIQLTIKKTLNVAH 158
?   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
? DB 120 GLENDCHLHLERNQURLSLASTFAHTPALSLGSSNNRLSLBEGLEFGSLSDNLNGW 179
?
? QY 159 NFII-----SCKLPAYFSNLTNLVAVHDLSTVNYIQTIVYNDLQ 195
?
? DB 180 NSLAVLPDPAARGSLRELYLAGNRLAYIQPALFSGLAELREIDLSNMLRAIKAN--V 237
?
? QY 196 FLRNPVNISLDSNLPIDFIQDAFQGIK-LHELTLRGNFNSNMKTQLQNLGLAHV 254
?   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
? DB 238 FVQPLRLOKLYLDENL--IAAVGAFLGLKALRWLDLSH-RVAGLLEDYFPGLGLRV 294
?
? QY 255 HRLILGFERKERNLEIFEPSIMEGLCDVITDERKLYTTNPSSDIYKFKCLANVSANSLA 314
?   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
? DB 295 LRL-----SHNAIA 303
?
? QY 315 GVSIKYLEVDYKHKFMQSLSIIRCOLKQFPTLDLPKSLTLTMNKGSIQKVALPSLS 374
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? DB 304 SLR-----PRTRY-----DHFLEEL----- 319
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? QY 375 YLDLSRNALSPSGCCSYDLSGTNSLRHLDLISFNCAIIMSANFMGLSEIOLHDPQSTLKR 434
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? DB 320 -----QGHNRIRQL-----AARSFEGLEGLVLTLDHNOQL 352
?
? QY 435 VTRESAFLSLKLLYLDISTYTKKIDPDGIFLGLTSNLTLMAGNS----- 480
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? DB 353 V-KAGATLGLTNVAVMNLSGNCILRNLEQVFRGLGKLSHLSESGCIGRIIRPHFTGLSG 411
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? QY 481 -----FDQNTLSNVFANT-----TNLFTLDSKQLEIDISNGVPTTLARLOLNMSSHNL 531
?   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
? DB 412 LRLFLKONGLVGIEEOSTLGLAELELDLTSNQLTHLRRLFGGLKLEVLTLISNRLLA 471
?
? QY 532 FLDSHYNOLYSYSLTDCSFNRISYKGILOHPKSLAFNLTNNSVACICEHOKFQ-- 589
?   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
? DB 472 ELRPADALGFLQRAFWLIDVSHNRLEALPNSLLAPLGRIRYISLTNNNSLRTRTPQPGELRL 531
?
? QY 590 WKZEKQFLVNVBEOMTCATPVE-----MNTSLVLDENNSTC-----YMYKTIIS 633
?   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
? DB 532 WLBE-----NPMWDGCPYKALRDPALQNPASVPRFVQALCEGDCCCPAPAYVNNITC 583

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Db 180 NSLAIVLPDAFRGLSRLVLAGNRVLAQPALPFGSLAELELDLSRNALPAIKAN--V 237
 QY 196 FIRENPQVNLSDMSINPIDFIQDOAFQGIK-LHEVTLRGNFNSNIMKTCIQNLAGIHV 254
 Db 238 FVQLPRLQKLYIDRNLI--IAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRV 294
 QY 255 HRLIIGEFDEKRNLEIFEPSIMEGLCDVTIDFRLLTYTNDPSDDIVKHFCLANVSAMSLA 314
 Db 295 LRL-----SHNAIA 303
 QY 315 GVSIKYLEVDVPGHFKWQSLIIRCOLKQPTLDLPELKSITLTMKKSISFKKVALPSLS 374
 Db 304 SLR-----PRTFK-----DLHFLEL----- 319
 QY 375 YLDSRNALSFSGCCSYSDLGTSNLRHLDSLFGNGLIMSANFMGLEELQHLDPQHSLEKR 434
 Db 320 -----QLGHNRIQI-----AERSFEGIGOLEVLTLIDHNOLOE 352
 QY 435 VTEFSAFLSEKLYLIDISYNTKIDFDGIFLGITSLNTLTKMAGNS----- 480
 Db 353 V-KAGAPLGLTNVAVVAVNLSGNCLRNIPROVFRGLGKLSLHLEGSCLGRIRPHTFTGLSG 411
 QY 481 -----FKDNTLSNVFANT-----TNLTFLDLSSKCOLQIEMGVEDTLHRLQLLMGSNNLL 531
 Db 412 LRRLFLKONGLVGIEQSLMGIAELLEDDLTISNQLTHLPHRLPQGLKLEYLLLSRNRILA 471
 QY 532 FLDSHYNQLYSLSTLDCSFNRIETSKGILQHFPSLAFFNLTNNSVACICEHOKFIQ-- 589
 Db 472 ELPADALGPLQRAFWLDVSHNRLEALPNSILAPLGRRLYLSLRNNSLRFTTPQPGLERL 531
 QY 590 WVKQKQFLVNEQNTCATPVE-----MNTSLVLDPNNSVC-----YMKTTIIS 633
 Db 532 WLEG-----NPWDCGCPKALRDFALONPFAVPRFVOAICEGDDCQPRPAYTYNNITC 583
 QY 634 VSVVSVI 640
 Db 584 ASPEPVV 590

Search completed: March 12, 2005, 19:59:07
 Job time : 24.9539 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 19:55:29 ; Search time 73.8956 Seconds
(without alignment)

3727.157 Million cell updates/sec

Title: US-09-396-985B-99

Perfect score: 4345
Sequence: 1 MPEPMLARLITLIMLFFSCL.....GKASNPQTAEQEQTATWT 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329644858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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- 16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2829.5	65.1	837	10	US-09-950-041-26 Sequence 26, Appl
2	2730.5	62.8	799	14	US-09-950-041-8 Sequence 8, Appl
3	2730.5	62.8	799	10	US-10-128-166-7 Sequence 7, Appl
4	2730.5	62.8	799	16	US-10-732-563-8 Sequence 8, Appl
5	2730.5	62.8	799	16	US-10-732-796A-8 Sequence 8, Appl
6	619.5	14.3	661	13	US-10-114-893-10 Sequence 10, Appl
7	619.5	14.3	661	13	US-10-038-854-134 Sequence 134, App
8	612.5	14.1	661	15	US-10-038-854-135 Sequence 135, App
9	612.5	14.1	661	15	US-10-037-417-107 Sequence 107, App
10	580	13.3	1032	10	US-09-954-987B-192 Sequence 192, App
11	580	13.3	1032	14	US-10-272-502A-31 Sequence 31, Appl
12	580	13.3	1032	15	US-10-407-952-32 Sequence 32, Appl
13	559	12.9	1059	10	US-09-954-987B-187 Sequence 187, App

14	559	12.9	1059	15	US-10-407-952-30	Sequence 30, Appl
15	559	12.9	1059	17	US-10-753-267-30	Sequence 30, Appl
16	557	12.8	1041	9	US-09-168-978-3	Sequence 3, Appl
17	557	12.8	1041	9	US-09-978-295A-498	Sequence 498, App
18	557	12.8	1041	9	US-09-978-697-498	Sequence 498, App
19	557	12.8	1041	9	US-09-978-122A-498	Sequence 498, App
20	557	12.8	1041	9	US-09-999-832A-498	Sequence 498, App
21	557	12.8	1041	10	US-09-978-189-498	Sequence 498, App
22	557	12.8	1041	10	US-09-978-808A-498	Sequence 498, App
23	557	12.8	1041	10	US-09-978-855A-498	Sequence 498, App
24	557	12.8	1041	10	US-09-978-191A-498	Sequence 498, App
25	557	12.8	1041	10	US-09-978-403A-498	Sequence 498, App
26	557	12.8	1041	10	US-09-978-564A-498	Sequence 498, App
27	557	12.8	1041	10	US-09-999-833A-498	Sequence 498, App
28	557	12.8	1041	10	US-09-981-915A-498	Sequence 498, App
29	557	12.8	1041	10	US-09-978-824A-498	Sequence 498, App
30	557	12.8	1041	10	US-09-918-585A-498	Sequence 498, App
31	557	12.8	1041	10	US-09-999-834A-498	Sequence 498, App
32	557	12.8	1041	10	US-09-978-423A-498	Sequence 498, App
33	557	12.8	1041	10	US-09-978-193A-498	Sequence 498, App
34	557	12.8	1041	10	US-09-999-830A-498	Sequence 498, App
35	557	12.8	1041	10	US-09-978-757A-498	Sequence 498, App
36	557	12.8	1041	10	US-09-978-187B-498	Sequence 498, App
37	557	12.8	1041	10	US-09-978-643A-498	Sequence 498, App
38	557	12.8	1041	10	US-09-978-375A-498	Sequence 498, App
39	557	12.8	1041	10	US-09-978-298A-498	Sequence 498, App
40	557	12.8	1041	10	US-09-978-188A-498	Sequence 498, App
41	557	12.8	1041	10	US-09-978-681A-498	Sequence 498, App
42	557	12.8	1041	10	US-09-978-194A-498	Sequence 498, App
43	557	12.8	1041	10	US-09-999-829A-498	Sequence 498, App
44	557	12.8	1041	10	US-09-978-299A-498	Sequence 498, App
45	557	12.8	1041	10	US-09-978-544A-498	Sequence 498, App

ALIGNMENTS

RESULT 1
US-09-950-041-26
Sequence 26, Application US/09950041
Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
APPLICANT: Ho, Stephen W.K.
TITLE OF INVENTION: RECEPTOR PROTEINS, RELATED REAGENTS AND METHODS
FILE REFERENCE: DX0724XK1
CURRENT APPLICATION NUMBER: US/09/950,041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293
PRIOR FILING DATE: 1997-05-07
PRIOR APPLICATION NUMBER: 60/072,212
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 60/076,947
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 837
TYPE: PRT
ORGANISM: Homo sapiens
US-09-950-041-26
Query Match 65.1%; Score 2829.5; DB 10; Length 837;

QY 758 LSSRSGLIFVLEKREKSLRQOVELYRLLSRNTYLEMEDNPLGRIHFRRLKALLDGK 817
DB 720 LSSRSGLIFVLEKREKSLRQOVELYRLLSRNTYLEMEDNPLGRIHFRRLKALLDGK 779
QY 818 ASNPEQT 824
DB 780 SWNPEGT 786

RESULT 3
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US20030077279A1
; GENERAL INFORMATION:
; APPLICANT: ARDITI, MOSHE
; APPLICANT: RAJAVASHISTH, TRIPATHI
; APPLICANT: SHAH, PREMIDAN K.
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
; TITLE OF INVENTION: TOLL-LIKE RECEPTOR-4
; FILE REFERENCE: 81476-0255398
; CURRENT APPLICATION NUMBER: US/10/128.166
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-166-7

Query Match 62.8%; Score 2730.5; DB 14; Length 799;
Best Local Similarity 67.9%; Pred. No. 4.2e-216;
Matches 534; Conservative 98; Mismatches 152; Indels 3; Gaps 3;

QY 40 MDQKLSVYDDIPSTSTKIDLSFNPILKLSYSPNSFSELOMDLSRCEIETIEDKAWHG 99
DB 1 MELNPFYKIPDNLPTSTKIDLSFNPILKLSYSPNSFSELOMDLSRCEIETIEDKAWHG 60
QY 100 LHLHSLNLTGNPIQSFGSPGSGTSLNVLAVETKLASLESPPIGQLITLKKLVANAHN 159
DB 61 LSHLSTLITGNPIQSFGSGTSLNVLAVETKLASLESPPIGQLITLKKLVANAHN 120
QY 160 FHSCKLPAYFSNLTNVLAVETKLASLESPPIGQLITLKKLVANAHN 219
DB 121 LIQSFKLPEYFSNLTNVLAVETKLASLESPPIGQLITLKKLVANAHN 180
QY 220 QAFQGLIHLHETLGNFNSNIMKTCLQNLAGLHVHLLIGEFKDERNLLEFESIMEGL 279
DB 181 GAFREIRLHKLTLNNDLSLNMKTCLQNLAGLHVHLLIGEFKDERNLLEFESIMEGL 240
QY 280 CDVTIDEFRLTYTNDPSDDIVK-FHCLANVSAMSLAGVISIKYLEDVPHKFMQSLIIRC 338
DB 241 CNLTIEBFRLAYLDYDDIIDLFPNCLTNVSSFSVLVETTERVDFSYNFMQHLBYNC 300
QY 339 QLNQFPLTDLPLKSLTLTNMKGSIKFKYALPBLSTYLDLSRNALSFSGCCSYSDLGTS 398
DB 301 KFGQFPPLTKLKSRLTLFTSNKGNASEVDLPBLSTYLDLSRNALSFSGCCSYSDLGTS 360
QY 399 LRHLDSFNAGIIMSANFMGLELQHDLPQSTLKRTVESAFSLSEKLYLDISYNTK 458
DB 361 LKYLIDSFNGVITMSSNFMGLELQHDLPQSTLKRTVESAFSLSEKLYLDISYNTK 420
QY 459 IDPDGIFLGLTSLNLTLMAGNSFKDNTLSNVFANTNLTFLDLSKQLEOISWGVPTLH 518
DB 421 VANGNIFNGLSLEVLKMGANSFOENLPDLFTLRNLTLFDLSKQLEOISWGVPTLH 480
QY 519 RLQNLANSNNLLFLDSSHYNOYSLTDCSFNRITS-KGILQHPKSLAPENLTNNS 577
DB 481 SLQVLTNNSHNNFSLDTPFYKCLNSLOVLDYSLHINTSKKQLEOHFPSSLAFLNLQND 540
QY 578 VACICEHQKLOWKEQKOPLVANVEQNTCATPVEMNTSLVDFNNSCTCYKTTIISVV 637
DB 540 VACICEHQKLOWKEQKOPLVANVEQNTCATPVEMNTSLVDFNNSCTCYKTTIISVV 637

DB 541 FACTCEHOSFLQWIKDQRLLEVERMECAPPSDKQMPVLSL-NITCOMNKTIGSVL 599
QY 638 SVIVSVTAFLIYHFEYFPHILLIAGCKYRSRGSYIDAFVYSSQMEDWRNLVKNLEEG 697
DB 600 SVLVSVTAFLIYHFEYFPHILLIAGCKYRSRGSYIDAFVYSSQMEDWRNLVKNLEEG 659
QY 698 VPRFHLCHYRDPFIPGVAIAANIIQEGFHKSRKVIIVVSRHFIQSRWCIFEYEAQWQF 757
DB 660 VPPFOLCHYRDPFIPGVAIAANIIQEGFHKSRKVIIVVSRHFIQSRWCIFEYEAQWQF 719
QY 758 LSSRSGLIFVLEKREKSLRQOVELYRLLSRNTYLEMEDNPLGRIHFRRLKALLDGK 817
DB 720 LSSRSGLIFVLEKREKSLRQOVELYRLLSRNTYLEMEDNPLGRIHFRRLKALLDGK 779
QY 818 ASNPEQT 824
DB 780 SWNPEGT 786

RESULT 4
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarnu K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Assays Relating to Toll-like Receptor Activity
; FILE REFERENCE: 58183W0003
; CURRENT APPLICATION NUMBER: US/10/732.563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-563-8

Query Match 62.8%; Score 2730.5; DB 16; Length 799;
Best Local Similarity 67.9%; Pred. No. 4.2e-216;
Matches 534; Conservative 98; Mismatches 152; Indels 3; Gaps 3;

QY 40 MDQKLSVYDDIPSTSTKIDLSFNPILKLSYSPNSFSELOMDLSRCEIETIEDKAWHG 99
DB 1 MELNPFYKIPDNLPTSTKIDLSFNPILKLSYSPNSFSELOMDLSRCEIETIEDKAWHG 60
QY 100 LHLHSLNLTGNPIQSFGSPGSGTSLNVLAVETKLASLESPPIGQLITLKKLVANAHN 159
DB 61 LSHLSTLITGNPIQSFGSGTSLNVLAVETKLASLESPPIGQLITLKKLVANAHN 120
QY 160 FHSCKLPAYFSNLTNVLAVETKLASLESPPIGQLITLKKLVANAHN 219
DB 121 LIQSFKLPEYFSNLTNVLAVETKLASLESPPIGQLITLKKLVANAHN 180
QY 220 QAFQGLIHLHETLGNFNSNIMKTCLQNLAGLHVHLLIGEFKDERNLLEFESIMEGL 279
DB 181 GAFREIRLHKLTLNNDLSLNMKTCLQNLAGLHVHLLIGEFKDERNLLEFESIMEGL 240
QY 280 CDVTIDEFRLTYTNDPSDDIVK-FHCLANVSAMSLAGVISIKYLEDVPHKFMQSLIIRC 338
DB 241 CNLTIEBFRLAYLDYDDIIDLFPNCLTNVSSFSVLVETTERVDFSYNFMQHLBYNC 300
QY 339 QLNQFPLTDLPLKSLTLTNMKGSIKFKYALPBLSTYLDLSRNALSFSGCCSYSDLGTS 398
DB 301 KFGQFPPLTKLKSRLTLFTSNKGNASEVDLPBLSTYLDLSRNALSFSGCCSYSDLGTS 360
QY 399 LRHLDSFNAGIIMSANFMGLELQHDLPQSTLKRTVESAFSLSEKLYLDISYNTK 458
DB 361 LKYLIDSFNGVITMSSNFMGLELQHDLPQSTLKRTVESAFSLSEKLYLDISYNTK 420
QY 459 IDPDGIFLGLTSLNLTLMAGNSFKDNTLSNVFANTNLTFLDLSKQLEOISWGVPTLH 518
DB 421 VANGNIFNGLSLEVLKMGANSFOENLPDLFTLRNLTLFDLSKQLEOISWGVPTLH 480

Db 421 VAFNGIFNGLSLEVLKMGNSFOENFLPDIPTFELRNLTFLDLSQCOLEQSPFAFNSLS 480
Qy 519 RLQLLMNSHNNLLFLDSSSHYNOLYSITLDCSFNRLETS-KGILQHPKSLAFENLTNNS 577
Db 481 SLQVLNMSHNNPFSLDTPFYKCLNSLQVLDYSLNHIMTSSKQELQHPSPSLAFLANLTQND 540
Qy 578 VACICHQKFLQWVKQKQFLVNVQWTCATPYEMNTSLVLDPNNSICVMYKTIISVSV 637
Db 541 FACTCEHQSLQWIKQORQLLVEVERECATPSDKQMPVLSL-NITCQNNKTIIGSVL 599
Qy 638 SVTVSVTAFLIHFYFHYLLIAGCKYSRGESIYDAFVIYSSQEDWVNEVLKMLEEG 697
Db 600 SVTVSVTAFLVLYKFYFHYLLMGLAGCIKYGGENIYDAFVIYSSQEDWVNEVLKMLEEG 659
Qy 698 VPRFHLCLHYRDFIPGVAIAANIIQSGFHKSRKVIYVVSRRHFIOQRWCIFEYETIAQTWOF 757
Db 660 VPPFQCLHYRDFIPGVAIAANIIHGGFHKSRKVIYVVSQHFIOQRWCIFEYETIAQTWOF 719
Qy 758 LSSRSGLIIFLYLEKVEKSLRQOVELYRLSRNTYLEMENDPILGRHIFMRRLKALLDGG 817
Db 720 LSSRAGIIFLYLOKVEKTLRQOVELYRLSRNTYLEMEDSVLGRHIFMRRLKALLDGG 779
Qy 818 ASNPEQT 824
Db 780 SNNPEGT 786

RESULT 5

US-10-732-796A-8
; Sequence 8, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarnu K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732,796A
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-796A-8

Query Match 62.8%; Score 2730.5; DB 16; Length 799;
Best Local Similarity 67.9%; Pred. No. 4,2e-216;
Matches 534; Conservative 98; Mismatches 152; Indels 3; Gaps 3;

Qy 40 MDQKLSKVPDDIPSSSTKNIDISFNPILKLSYFSNFSFELQWLDLSRCEIETIEDKAWHG 99
Db 1 MEINLYKIPDNLPSTKNLDLSFNLRLHLSYSFSPFELQVLDLSRCEIETIEDGAYQS 60
Qy 100 LHLISNLLITGNPIOSFSPGSGSLTSLLENVAVETKLASLESFPIGQILITKIANVAN 159
Db 61 LSHLSTLLITGNPIOSLAGFSGSLQKLVAVETNLASLNFPIGHLKTLKEINVAN 120
Qy 160 FHSOKLAVFENLNLVAVDLSYNYIOTITVNDILOFLENQVNLSDMSINPIDFIOD 219
Db 121 LIQSFLEPBYFNLNLLEHLDLSNKOISICTDLRAVHOMPLNLSLDLSINPMNFIOF 180
Qy 220 QAFQGIKTLHELTLRGNFSSNIMKTCLQNLAGLHVHRLILGFKDERMLEIFEPSIMEGL 279
Db 181 GAFKRIHLKLTLRNPFSLNWKTCIOGLAGLEVHRLVIGFPRNGNLEKFDKSLBGL 240
Qy 280 CVVITDEFRLTYTNDSDIVK-FHCLANVSAMSLAGVISIKYLEDVYKFKKQSLSTIRC 338
Db 241 CNLTIEEFRLAYLDYLDIIDLFNCLTNVSSFSILSVTIERKQFSYXNFGQHLVANC 300
Qy 339 QAKQPPTLDPFLKSLTLTMNGKSLSPKVALPSLSYLLSRNALSFSGCCSYSDLGTS 398

Db 301 KFGQPTLKLKSLKRLFTSNKGNAPSEVDLPJSLFELDSLNRGLSPKCCSQSDFGITS 360
Qy 399 LRHLDSFNGAIIIMSANFMGLEBELHLDPOHSTLKRTEPSAFLSTLEKLYLDISYNTX 458
Db 361 LKYLDSFNGVLTWSSNPLGELHLDPOHSTLKRTEPSAFLSTLEKLYLDISYNTX 420
Qy 459 IDPDGIFLAGITSLNLTLMKAGNSFKDNTLSNVFANTTNLTFLDISKQLEQISMGVEDTLH 518
Db 421 VAFNGIFNGLSLEVLKMGNSFOENFLPDIPTFELRNLTFLDLSQCOLEQSPFAFNSLS 480
Qy 519 RLQLLMNSHNNLLFLDSSSHYNOLYSITLDCSFNRLETS-KGILQHPKSLAFENLTNNS 577
Db 481 SLQVLNMSHNNPFSLDTPFYKCLNSLQVLDYSLNHIMTSSKQELQHPSPSLAFLANLTQND 540
Qy 578 VACICHQKFLQWVKQKQFLVNVQWTCATPYEMNTSLVLDPNNSICVMYKTIISVSV 637
Db 541 FACTCEHQSLQWIKQORQLLVEVERECATPSDKQMPVLSL-NITCQNNKTIIGSVL 599
Qy 638 SVTVSVTAFLIHFYFHYLLIAGCKYSRGESIYDAFVIYSSQEDWVNEVLKMLEEG 697
Db 600 SVTVSVTAFLVLYKFYFHYLLMGLAGCIKYGGENIYDAFVIYSSQEDWVNEVLKMLEEG 659
Qy 698 VPRFHLCLHYRDFIPGVAIAANIIQSGFHKSRKVIYVVSRRHFIOQRWCIFEYETIAQTWOF 757
Db 660 VPPFQCLHYRDFIPGVAIAANIIHGGFHKSRKVIYVVSQHFIOQRWCIFEYETIAQTWOF 719
Qy 758 LSSRSGLIIFLYLEKVEKSLRQOVELYRLSRNTYLEMENDPILGRHIFMRRLKALLDGG 817
Db 720 LSSRAGIIFLYLOKVEKTLRQOVELYRLSRNTYLEMEDSVLGRHIFMRRLKALLDGG 779
Qy 818 ASNPEQT 824
Db 780 SNNPEGT 786

RESULT 6

US-10-114-893-10
; Sequence 10, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John W.
; APPLICANT: Lavalie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Metberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; EARLIER FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-10

Query Match 14.3%; Score 619.5; DB 13; Length 661;
Best Local Similarity 28.6%; Pred. No. 5,2e-42;
Matches 187; Conservative 126; Mismatches 296; Indels 45; Gaps 18;

Qy 28 CIEVVPNTIYQCMQDKSKVPDDIPSSSTKNIDLSNPLKLSYFSNFSFELQWLDLSRCEI 87
Db 28 CIEKANKYNCENGLSBIPTLNTTBELEFSFNPFLTIHNRFSRLMNLTLFLDLTRC 87

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0Y 88 ELETEDKAMHGHHNSNLIITGNPLOSPPGSGGLTSELENVAEETKLASLESPIQG 147
0Y 88 QINMHEDPQSHQSLTYLTGNPLIEMAETSLNGKSLKHLPLIQTGISNNEPFIWHN 147
Db 88 QINMHEDPQSHQSLTYLTGNPLIEMAETSLNGKSLKHLPLIQTGISNNEPFIWHN 147
0Y 148 LITLKLVAHNEFIHSCKLPAFFSNLTNLVHVDLSYNYIQTITVNDLQFIREBPVNLST 207
Db 148 LENLESYLGNHNSISIKFPPKPP-ARNIKVLDFOUNNAIHYISREDBRSLSEQ--AINLSL 204
0Y 208 DMSLNPIDPFOQAFQGIKYLHELTLTGNFNSSNIMKTCLONLAGLHVHRLILCEBFXDERN 267
Db 205 NFNNGNVKQIEIGAFPISTVFOGSLNFGGTNLSTYIFNG-LQNST---TQSLMTLGFEDIDD 260
0Y 268 LEIPEPSIEGCDVITYDEBRLTYTNDPSD-DIVKHCCLANVASMAGSLAGSYKLEBVPK 326
Db 261 EDI-SSAMIKGLCEMSVESLNL-QEHRFSDISSTTQCTQOELDLTAT--HLKGLPSS 315
0Y 327 HFKWQSLSIIR-----CQDK--QFPLLDLPFLKSLTLTNMKGSIPEFKVALPS 372
Db 316 GMK--GLNLKTLKLYSVNHFDQLCOJSAANFBLTHLYIRGNVKKHLHGVGCLEK--LGN 371
0Y 373 LSYLDLNRKALSPSGCCSYSDIGTNSLRHLIDUSFNCAI-IMSANFNGLEBLQHLDPQHS 431
Db 372 LOTLDLSHNDIEASOCCSLOLKNLSHLOTLNLSHNEPLIGIQOAFKCECPQELDLDAFTR 431
0Y 432 LKRVTEFSAFLSEKLYLDISYTNKIDPFQDGLTSLNTLXMGANGSKXQNTL--SNV 489
Db 432 LHIINAPQSPFOULHFLQVNLNTYFCPLDTSNQHILAGLPVLRHNLKGNHFOQDGTIKTIL 491
0Y 490 FANTNLTLFLDLSCOLEQISWGPEDTLHRLQILNNSHNMLL--FLDS--SHYQULSLST 546
Db 492 LOTVGSLEVLILSSGGLSIDQAFHSLGKMSHYVDSLHNSLTDSDISLSHLKGIY---- 547
0Y 547 LDGSFNRIETSKGILQHPEKSLAFENLITNNSVACICEHOKFLQWKEOKOFLVNEQMT 606
Db 548 IMLANSINIISPRLLPIISOOSTINLSHNPIDCTCSNIHFLTWYKXENLHKLEGSBETTC 607
0Y 607 ATPVEMN-----TSLVLDNFNSCTNMYKTIISVSVSVIYVSTYAFILYHFFHL 656
Db 608 ANPBLRGVKLSDVAKSLSCGITAIGIFFLLVFLLLALLIFPAVKYLLRMKTYOH 661

```

US-RESULT 7
US-10-038-854-134
Sequence 134, Application US/10038854
Publication No. US20040023781A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Vennel, Corine
APPLICANT: Eisen, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Maiyanbar, Uriel M
APPLICANT: Shketers, Richard A
APPLICANT: Tchernev, Velizar
APPLICANT: Spaderma, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
APPLICANT: Paturajan, Meera
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gangolli, Esna A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Lucia
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Bugacs, Catherine E
APPLICANT: Edinger, Shlomit R
APPLICANT: Ellenman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle

```

? APPLICANT: MacDougall, John R
? TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
? FILE REFERENCE: 21402-230
? CURRENT APPLICATION NUMBER: US/10/038,854
? PRIOR FILING DATE: 2003-01-22
? PRIOR APPLICATION NUMBER: 60/256,928
? PRIOR FILING DATE: 2000-12-29
? PRIOR APPLICATION NUMBER: 60/255,415
? PRIOR FILING DATE: 2001-01-02
? PRIOR APPLICATION NUMBER: 60/259,785
? PRIOR FILING DATE: 2001-01-04
? PRIOR APPLICATION NUMBER: 60/269,814
? PRIOR FILING DATE: 2001-02-20
? PRIOR APPLICATION NUMBER: 60/279,832
? PRIOR FILING DATE: 2001-03-29
? PRIOR APPLICATION NUMBER: 60/279,833
? PRIOR FILING DATE: 2001-03-29
? PRIOR APPLICATION NUMBER: 60/279,863
? PRIOR FILING DATE: 2001-03-29
? PRIOR APPLICATION NUMBER: 60/283,869
? PRIOR FILING DATE: 2001-04-13
? PRIOR APPLICATION NUMBER: 60/284,447
? PRIOR FILING DATE: 2001-04-18
? PRIOR APPLICATION NUMBER: 60/286,683
? PRIOR FILING DATE: 2001-04-25
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 411
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 134
? LENGTH: 661
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-038-854-134

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QY	28	CIEVVNVIYQCMDDKLSKVPDDI	SSSTKXNDLSFNP	KLTKLSXSPFNSELOWDL	SRC	87	
QY	28	CIEVVNVIYQCMDDKLSKVPDDI	SSSTKXNDLSFNP	KLTKLSXSPFNSELOWDL	SRC	87	
Db	28	CIEKXANKYCNENGLSEIBIDPL	PNTELEBSEFNFPLTHNPTFS	RLANLFLDLTRC		87	
QY	88	EETTEDKAMGHLLHLSMLITGN	PTQSFSGSPGSLTSENVA	VEKTLASLESPTQ		147	
Db	88	QINWIHEDTFOGSHDLSVLT	LVGNPLFMAETSLNGKSL	KHFLIQTJSSNEFIPVN		147	
QY	148	LITTKLVANAHFHSCKLPAV	ESNLTVNLVHDSVNYQIT	YVNDLOFLRENPVNL		207	
Db	148	LENLESLYGSNHSSIKFPKDF	ARLKLALDQNNAHYIS	ESDKRSLEQ--AINLSL		204	
QY	208	DMSLNPIDIFODAFQIKI	HELTKGNFNSNMKTCLQ	NLAGLHNRILJEFKDERN		267	
Db	205	NFGNNVAKIETLGAFDS	TVFQSLNPGGTPLNSVI	FNG-LQNST--TQSLMGTPEDD		260	
QY	268	LEIFERSIMEGCDVTDIE	FLTYTNDSSD-DIYKFC	LANVASMSLAGSIKLE	BYPK	326	
Db	261	EID-SSAMIKGJCEMS	ESLNL-QEHRSIDIS	TTFCFTQLELDLTAN--HLKGLPS		315	
QY	327	HEKMOSSLIR-----	-QOLK--OFTPLD	PEPLKSLVTNNKGS	ISFEKVALPS	372	
Db	316	GMK--GLNLKLKLV	SVNHPDQLQISAN	PPSLTHYINGNV	YKHLGVCLEK--LGN	371	
QY	373	LSYDLSRRAALSFGCCG	SYDLSGNSLRHLDSL	NGAI-IMSANF	GLELOHLDPROHST	411	
Db	372	LQTLDSHNDLEAS	CCSLODKNSHLQTNLS	INEBELQLOSOA	FKBCPLELIDLDAFTR	411	
QY	432	LKRVEFSAFLEBL	LYLDSYNTKIDFPGI	FLGJLS	INTLKMAGNSPKDUTL--SNV	489	
Db	432	LHINAPQSPQULH	LYVLNTYCEFLD	TSNOHLAGPVL	RHLNLMKGNHPODITIKTNL	491	
QY	490	PANTNLFLDL	SKQLEQISGW	PDTLHRLQL	LNNSHNLL--FLDS-SHNQ	YLSLT	546
Db	492	LQTVSSLEVL	LISGCLSLSDQA	FHSIGKXSHVDS	SHNSLTCDSDIS	SHLGLY----	547

Qy 547 LDGSPNRIETSKGILQHPFKSLAFPNLTNNSVACICEHQKFLQWKEQKQFLVAVNEQMT 606
Db 548 LNLASINISIPRLPLTPOOSSTINLSHNPIDCTCSNHPILTWYKENTLKEGSEETTC 607
Qy 607 ATPPEMN-----TSVLDPNNSCTCYMYKTIISVSVSIVVSTVAFLIHYFPHL 656
Db 608 ANPSPRGVAKLSDVGLSCGITAIGIFLIVFLLLAIIILFFAVKYLKMKYQHI 661

RESULT 8

US-10-038-854-135
Sequence 135, Application US/1003854
Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Vernet, Corine
APPLICANT: Eiben, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Malyankar, Uriel M
APPLICANT: Shinkets, Richard A
APPLICANT: Tchernev, Velizar
APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
APPLICANT: Patuturajan, Meera
APPLICANT: Gusev, Vladimiy Y
APPLICANT: Gangoli, Baha A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Burgess, Catherine E
APPLICANT: Edinger, Shlomit R
APPLICANT: Elberman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 135
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus

US-10-038-854-135

Query Match 14.1%; Score 612.5; DB 15; Length 661;
Best Local Similarity 27.0%; Pred. No. 2e-41;
Matches 182; Conservative 129; Mismatches 313; Indels 49; Gaps 16;

Qy 12 IMALFF-SC-LTPSINPCIEVVPNITYOCMDOKLSKVPDDIPBSTKNIDLSFNPLKILK 69
Db 10 LVNLFPLASCRATISSDDCKICEKVENKTYNCENIGLNEI PGLPSTECLEFSEFVLPFIQ 69
Qy 70 SYSPFSFSEIOMDLSCICEIETTEDKAWHGLHLSNLIITGNPIQSPSPSGSLTSEN 129
Db 70 NTTFPSRLINLTFPLDTRCOIYWIHEDTFOGHRIDTLVLPILFMAETLSPKALKH 129
Qy 130 LVAVETKLASLESPIQOLITLKKLVANHFHSCKLPAYFSNLTNLVHVDLSYNYIQT 189
Db 130 LFFIQGTGISIDFPLNOKTLESUYGSNHSISIKLPKPEPT- EKLKVIDPQNALHYL 188
Qy 190 TVNDLQFLRENPOVNLSDMSLNPIDFIODAFQGIKHELTTRGNFNSSNIMTKCQNL 249
Db 189 SKEDMSLIQ--ATNLSINLNGNDIAGIBPAFSAVFOSL---NFGQTQNLVIFKGL 242
Qy 250 AGHVRHLIIGEFDERNLTFEPSIMEGLCDVTIDFRLTYTNDPSDDIVKHECLANVS 309
Db 243 KNSTIOSIMTGTFFDMDDEDI-SPAVEGLCEMSVESINQKHYFFNISSNTFFCFSGLO 301
Qy 310 AMSLAGVSIKYLEVDPKHF-----KMSISITRCQ--KQFPTLDLPFLKS 353
Db 302 ELDLTAT--HSELPGLVGLSLTKLQVLANKFENL---CQISANFSPSLTHLSIKH 354
Qy 354 LTLTNKSGISPKKVALPSLSYLDLSRNALSFSCCSYSIDGTNSLRHLDSFNGAITS 413
Db 355 NTKLELGTCLEN--LENLELDLSHDIDRTSDCCNLQLNLNLSGLSNLSYNEPLSLK 412
Qy 414 AN-FMGLDELHLPQSHSTLKVTFEFSAPLSLEKLYLIDISVTYTKIDFDGIFLGTSIN 472
Db 413 TEAFKECPOLBLDLAFLRLKVKDAQSPQWHLKLVNLSSHLSLSDISSSELPGLPLQL 472
Qy 473 TLKMAQNSFKONTL--SNVFANTTNLTFLDSCQLEBOISGVEFTLRLQLLNMSHNL 530
Db 473 HNLQGNHFPKGNIOKTNLSLQTLGRLILVLSFCDLSSIDGHAFTSLKMMHVDLSHRL 532
Qy 531 LFLD---SSHYNOYLSLTDSCFNRIFTSKGILOHPFKSLAFPNLTNNSVACICEHQF 587
Db 533 TSSIEALSHLKGI-----LNLASNHISIIPLSLPLTPOORTINLRQNPIDCTCSNIYF 588
Qy 588 LQWKEQKQFLVAVNEQMTATPEMN-----TSVLDPNNSCTCYMYKTIISVSVSIVVS 643
Db 589 LEWYKENNQKLEDTEDLCENPPLLRGVRLSDVTLTSCMAVGLFLLIVFLVFAILLF 648
Qy 644 TVAFLIHYFPHL 656
Db 649 AVKTYLRMKYQHI 661

RESULT 9
US-10-037-417-107
Sequence 107, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsebrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patuturajan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Vernet, Corine A.M.
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R

```
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyanxar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Murallidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eissen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 107
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus
US-10-037-417-107

Query Match      14.1%; Score 612.5; DB 15; Length 661;
Best Local Similarity 27.0%; Pred. No. 2e-41;
Matches 182; Conservative 129; Mismatches 313; Indels 49; Gaps 16;

QY 12 IMALFF-SC-LTPGSLNCEIVNPTQCMDOQLSKVPDDIPSTKNIIDLSFNPGLIK 69
DB 10 LVALFLASCRATPSSDQCKIEKVVKYVCNENLGNELPGLPNTSECLSPFVNLPTIQ 69
QY 70 SYSFSELOMLOLDSRCEIETIEDKAWGLHLSNLITGNPISFSGSGLTSEN 129
DB 70 NTSRSRLNLTFLDTRCOIWIHEDTQSOHRDLTVLTANFLFMAETLSGPKALKH 129
QY 130 LVAVETKLASIESPPIGQLITLKKLVANANFHSCKLPAYSNLTNLVHVDLSVNYIOTI 189
DB 130 LFFIQTGSSIDFIPLHNQKTLSELYGSHISSIKLPKGPPT-EKLKVLDFQNNAIHYL 188
QY 190 TVNDLOPARENPOVNLSDMSLNPIDFQDAFOGCIKHELTGKNFNSNIMTKLONL 249
DB 189 SKEDMSSIQQ--ATNLSTNLGNNDIAGIEPAFSAFVSQSL---NFGTONLVITFQGL 242
QY 250 AGLHVHRLILGEFDERNLBIFFPSIMEGLCDVTIIDEFRLTYTNDPSDVIKPHCLANVS 309
DB 243 KNSGTQSLMGTTFEDMDEDI-SPAVFEGLCSEMSVESINLQKHFFNINSSTTFHCFSLQ 301
QY 310 AMSLAGVSIKLDEVPKHF-----KWSISITRCQL--KQPTLDLPFLKS 353
DB 302 ELDLTAT---HISELPSGLVGLSTLKKLVLSANKFENL---CQISANFPSLTGHLSTKG 354
QY 354 LTLTMNGSISFKKVALPSLSTYLDLSRNALSFSCCCSVDSDGTSIRHLDSFPGALIMS 413
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DB 355 NTKRLLELTGCLLEN--LENLERLDISHDDIETSDCCNIQLRNLSHQSLNLSYNEPLSLK 412
QY 414 AN-FMGLLELOHLDFOHSTLKVETFSAPLSLEKLLYLDISYNTKIDPDGIFLGTSLN 472
DB 413 TEAFKECQGLBLLDIAFLRLKVKQKQSPQNNHLLKLVNLSLDDISEQLEFDELPAQ 472
QY 473 TLKAGNSFKONTL--SNVPANTNLVTLDSKCOLEOISWGVPTLHRLQILNNSHNL 530
DB 473 HLNLOGNHFPKGNIOKTNLSLOTLGRLEILVLSFCDLSSIDQHAFTSLKMMNHHVDSLHRL 532
QY 531 LEFD---SSHNQYLSLSTLDCSPFRITSKGILOHFKSLAFPLTNNSVACICEHQKF 587
DB 533 TSSSTIBALSHLKGY---LNLASNHISITILPSLPLISQORTNLRONPILDCSNIYF 588
QY 588 LQWVEKQKQFLVNVQWCTATPVENM---TSIVLDPNNSCTCYMTKTIISVSVSVIYVS 643
DB 589 LEWYKENNQKLEDTEDTLCENPRLRGRLSDVTLSCSMAVGIFFLVFLVFAILLIF 648
QY 644 TVAFLIYHFYFHL 656
DB 649 AVKYFLRWKYQHI 661

RESULT 10
US-09-954-987B-192
Sequence 192, Application US/09954987B
Publication No. US20030104523A1
GENERAL INFORMATION:
APPLICANT: Stefan Bauer
APPLICANT: Grayson B. Lipford
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
FILE REFERENCE: C1041/7016 (AMS)
CURRENT APPLICATION NUMBER: US/09/954,987B
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/233,035
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/263,657
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: US 60/291,726
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 60/300,210
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 230
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 192
LENGTH: 1032
TYPE: PRT
ORGANISM: Mus musculus
US-09-954-987B-192

Query Match      13.3%; Score 580; DB 10; Length 1032;
Best Local Similarity 23.8%; Pred. No. 1.8e-38;
Matches 253; Conservative 160; Mismatches 350; Indels 298; Gaps 43;

QY 2 MPF--WLLARTLIW-----ALFSCLPNGSLNCEIVPN--ITVQCMDOQLSKVPDDIP 52
DB 4 MPQSMILTCFCLSSGTSALFHKANYSRST-PDEIRHNSLVTAECNHRQLEHVPTTG 62
QY 53 SSTNIDLSFNPPLKILKSYSFSELOMLOLDSRCEI-----TIEDKAWGLIHH 102
DB 63 KYVTNIDLSDNAITHIRKESFOKQNTKIDLNNAKQOQHNNKNGMNIIEGALLSLRN 122
QY 103 LSNLITLGNPIQSS--PQSGSLTSENLVAVET-----LASLESFPIG----- 146
DB 123 LTVLLBDNQLXYTPAGLPESLKELSLQNNITPOVTYKNTTFGJRNLERLYGNMCFKCN 182
QY 147 -----QITTEKLVANHN--FIHSCKLP----- 168
DB 183 QTFVEVDGARKNLIHLKVLSTSFNNLFYVPPKLPSSIRKULPLSNAKIMNTIOEDFKLEN 242
QY 169 -----YF 170
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Db 243 LTLTDLGNCRCYNAPPTCPCKENSIHHPAFOSLTQLYLNISSRTIPSTWF 302
Qy 171 SNLTNLVHVDSYNY-IQITIVNDLOFLRENOVNLSDMSLNPIDFIDQAFQIGLHE 229
Db 303 ENLSNLKELHLEFNYLVOELASG--AFITKLPISQI-LDLSFN--FOYKEYLOFINI-- 354
Qy 230 LTLRGFNSSNIMKTCLONLGLHVHRLILGEFDERLLEIFESIMEGLCDVYIDFERL 289
Db 355 -----SSNFSK--LRSLLKHLRGVYFRELKKH----FEH--LQSLPNLATINLGI 398
Qy 290 TYTNDPSDDIVKPHCLANVAMSLSAGVSIKYLEDPVKHFKWQS-----LS----- 334
Db 399 NPIEKI--DPRAFQNFSLDVIYLSGNRIASVLDGTYSWRNRLRKLSTDDDEFDPHV 456
Qy 335 -----IIRCOLKQF--PTLDLP-----LKSITLTMNKSISFKKV- 368
Db 457 NFHYSTKPLIKPQCTAYGKALDLSLNNIFIIKSGQFEGFODIACNLSPNANTOVFNCTE 516
Qy 369 --ALPSLSYLDLSRNALSFSGCCSYSDLGTSNLRHLDSLFGAIIIMSAN-----FMGL 419
Db 517 FSSMHIKYLDTNNRLDFDDNNAFSDI--HDLVLDLSHNAHYPSIAGVTHRLGFIQNL 574
Qy 420 BELQHLDFQHSITLKVTE-----FSAFLSLEKILY 449
Db 575 INLRVLNLSHNGIYTLTRESSELSISLKELVFSGNRLDHLNANDKWTSIFKSLQNLIR 634
Qy 450 LDISYTNKIDPDGIFLGL--TSIANTLKMAGNS--FKDNTLSNVFANTNLTFLDLSKQOL 506
Db 635 LDISYTNNOQIIPNGAFNLPSLOELISGNLRFNNLTLYQF--PHILHLDLSRNL 691
Qy 507 BOISWGVEDTLRLQOLLNMSHNNLLFLDSHYNOLYSITLDCSPNRIB--TSKGILOHP 565
Db 632 YFLPNCISKFAHSLTLLSHNHFSHLPSGFLSEARNLVHDLSPNTIKMINKSLQTKM 751
Qy 566 K-SLAFNLTNNSVACICEHQFLQWVKEQKF---LVNVOQMCATPEVANTSLVDF 620
Db 752 KNLLSILBHGNYFDCTCISDFRSWLDENLNTIIPKLVN--ICSNGDGKXSIMSL 808
Qy 621 NNSCTMYKTIISVSVSVIVSVTV--AFLIYH-----FYFHL--IIACCKYSRGE 669
Db 809 DLTTCVSDTTAAVLFLFTLTSMWMLALVHLLFWDWVFIYHMCASALKGYRTSSTQ 868
Qy 670 SIYDAFVIYSSQN--EDWVNELVKNEEGVPR--PHLGLHROPFPGALIANITIOEF 725
Db 869 TEYDAVISYDTXASVTDWVINELRYHLESSEDKSVLCLBERDMPGPIIDNLMQ--SI 927
Qy 726 HKSRIKIVVSRHFIQSRWCIFEYELAOQTMQFLS-----SRSGIIFIVLEKYE 773
Db 928 NOSKKTIFVLTKKY-----AKSNFKTATFYALQRLMDENMVIIFILLEPYL 975
Qy 774 KSLRQOVELYRLLSRNYLEWEDNPLGRHIFWRLLKNLL 814
Db 976 Q--YSQYLRQRICKSSILQWENPNKAEMLFWQSKKNVYL 1014

RESULT 11
US-10-272-502A-31
Sequence 31, Application US/10272502A
Publication No. US20030139364A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Schetter, Christian
APPLICANT: Bratzler, Robert L.
APPLICANT: Vollmer, Jorg
APPLICANT: Bauer, Stefan
APPLICANT: Burk, Marion
TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
FILE REFERENCE: CO1039, 70065, US
CURRENT APPLICATION NUMBER: US/10/272, 502A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/329, 208

; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1032
; TYPE: PR
; ORGANISM: Mus musculus
US-10-272-502A-31

Query Match 13.3%; Score 580; DB 14; Length 1032;
Best Local Similarity 23.8%; Pred. No. 1.8e-38;
Matches 253; Conservative 160; Mismatches 350; Indels 298; Gaps 43;

Qy 2 MPP--MTLARTIM-----ALPFSCLTPGSLNPCIIEVPR--ITYQCMDKLSKVPDIP 52
Db 4 MPQSMILTEPCLLSSQTSNAIFHKANYSRY-PCDEIRHNSVLVLAECNHRQLHEVPQIG 62
Qy 53 SSTKNIDLSFNPILKLSYSPNSFSELQWIDLSRCEIE-----TIEDQMHGLH 102
Db 63 KYVTNIDLSNAPITHTKESFQKLQNLTKIDLHNAKQHPNENKGNMTTEGALLSLRN 122
Qy 103 LSNILTLGNPIQFS--PSFGSLTLENLVAVETK-----LASLSPFG----- 146
Db 123 LTVLLBDNOLYTPAGLPBSLKELSLQNNIFQVYKNTTGLRNLRLYIGMNCYKCN 182
Qy 147 -----QLITLKLVAH--FIHCKLPA----- 168
Db 183 QTFVEDEGAPFNLHLKVLISFNNLFYVPPKPSLRKLFLSNAKIMNITQEDDFKLEN 242
Qy 169 -----YF 170

Db 243 LTLTDLGNCRCYNAPPTCPCKENSIHHPAFOSLTQLYLNISSRTIPSTWF 302
Qy 171 SNLTNLVHVDSYNY-IQITIVNDLOFLRENOVNLSDMSLNPIDFIDQAFQIGLHE 229
Db 303 ENLSNLKELHLEFNYLVOELASG--AFITKLPISQI-LDLSFN--FOYKEYLOFINI-- 354
Qy 230 LTLRGFNSSNIMKTCLONLGLHVHRLILGEFDERLLEIFESIMEGLCDVYIDFERL 289
Db 355 -----SSNFSK--LRSLLKHLRGVYFRELKKH----FEH--LQSLPNLATINLGI 398
Qy 290 TYTNDPSDDIVKPHCLANVAMSLSAGVSIKYLEDPVKHFKWQS-----LS----- 334
Db 399 NPIEKI--DPRAFQNFSLDVIYLSGNRIASVLDGTYSWRNRLRKLSTDDDEFDPHV 456
Qy 335 -----IIRCOLKQF--PTLDLP-----LKSITLTMNKSISFKKV- 368
Db 457 NFHYSTKPLIKPQCTAYGKALDLSLNNIFIIKSGQFEGFODIACNLSPNANTOVFNCTE 516
Qy 369 --ALPSLSYLDLSRNALSFSGCCSYSDLGTSNLRHLDSLFGAIIIMSAN-----FMGL 419
Db 517 FSSMHIKYLDTNNRLDFDDNNAFSDI--HDLVLDLSHNAHYPSIAGVTHRLGFIQNL 574
Qy 420 BELQHLDFQHSITLKVTE-----FSAFLSLEKILY 449
Db 575 INLRVLNLSHNGIYTLTRESSELSISLKELVFSGNRLDHLNANDKWTSIFKSLQNLIR 634
Qy 450 LDISYTNKIDPDGIFLGL--TSIANTLKMAGNS--FKDNTLSNVFANTNLTFLDLSKQOL 506
Db 635 LDISYTNNOQIIPNGAFNLPSLOELISGNLRFNNLTLYQF--PHILHLDLSRNL 691
Qy 507 BOISWGVEDTLRLQOLLNMSHNNLLFLDSHYNOLYSITLDCSPNRIB--TSKGILOHP 565
Db 632 YFLPNCISKFAHSLTLLSHNHFSHLPSGFLSEARNLVHDLSPNTIKMINKSLQTKM 751
Qy 621 NNSCTMYKTIISVSVSVIVSVTV--AFLIYH-----FYFHL--IIACCKYSRGE 669
Db 809 DLTTCVSDTTAAVLFLFTLTSMWMLALVHLLFWDWVFIYHMCASALKGYRTSSTQ 868

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Qy 670 SIYDAFYVYSSON---EDWVNEVLVKNLEEGVPR-FHCLHYRDPICVAIAANIIOGCF 725
Db 869 TFYDAVYSDTKDASVTDVWVINELRHLEESSEDSKSVLLCLBERDWDPGPIIDNLMQ-SI 927
Qy 726 HKSRRKVIWVSRHFIQSRWCIFEYEIAQWQFLS-----SRSGIIFIVLEKYE 773
Db 928 NQSKKTIFFVLTKKY-----AKSNMFKTAFYIALQRLMDENNDVIIIFILEPVL 975
Qy 774 KSLRQOVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALL 814
Db 976 Q-YSOYLRRLQRICKSSIIQWPNPNPKAENLFWQSLKNVVL 1014

RESULT 12
US-10-407-952-32
; Sequence 32, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligonucleotides
; FILE REFERENCE: C01041.70037.US
; CURRENT APPLICATION NUMBER: US/10/407,952
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-407-952-32

Query March 13.3%; Score 580; DB 15; Length 1032;
Best Local Similarity 23.8%; Pred. No. 1.8e-38;
Matches 253; Conservative 160; Mismatches 350; Indels 298; Gaps 43;

Qy 2 MPP--WLIARTLIM---ALFSCLTPTGSLNPCIENVEN--ITYQCMDOKLSKVPDIP 52
Db 4 MPQSWILTCFCLSSGSAIFHKANYRSY-PCDEIRHNSLVABCHRHQHEVPDTIG 62
Qy 53 SSTNNIDLSFNPILKILSYSPNSFSELOMDLSRCEIE-----TIEDKAMHGLIH 102
Db 63 KYVTNIDLSDNAITHITESFOKLQNLTKIDLNNAQOHENKNGNITREGALLSRN 122
Qy 103 LSNILILGNPIQSPS---PGSFGSLTSLNLANVETK---LASLESFPIG----- 146
Db 123 LTVLLLEDNDOLYTPAGLPESLKEISLQNNIPQVTKNNTFGLNLERLYLGNNCYFKCN 182
Qy 147 -----QLITLKLNVAAHN--FHSCKLPA----- 168
Db 183 QTFKVEDGARKNLIHLKVLISFPNNLFVPPKLSLRKLFSLNAKIMNTIQEDPKGIEN 242
Qy 169 -----SSNFSK--LRSLKLIHLRGVFRLEKKK-----FEH--LQSLPNLATIWLGI 170
Db 243 LTLILDSGNCPRCYNAPPTCPCKENSIHHPALFQSLTQLYLVNLSSTSLRTIPSTWF 302
Qy 171 SNLTNLVHVLNXY-IQITVNDLOFLRENPOVNLSDMSLNIDTIOQDAFGICLHE 229
Db 303 ENLSNLEKELHLEFYVLOEIASG--AFYTKLPISLQI-LDISFN---FOYKEYLOFINI-- 354
Qy 230 LTLRGFNSSNMKTCLQNLAGLHVHRLILGEFDEENLEIFEPSIMEGLCDVTIDEPRL 289
Db 355 -----SSNFSK--LRSLKLIHLRGVFRLEKKK-----FEH--LQSLPNLATIWLGI 398
Qy 290 TYNDSDDIVKFKCLANVSAMSLAGVSITYLEDVPHFKMQS-----LS----- 334
Db 399 NFLEKI--DKAFQNFESKLDVIYISGNRIASVLDGTDYSWRNRLRKPLSTDDDEPDPHV 456
Qy 335 -----IRCOLKQF-PTLULPF-----LKSULTTNMKGSISFKV- 368

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Db 457 NFYHSTKPLIKQCTAYGKALDLSLNINIFIICKSQFEGFODIACINLSFNANTQVFNTE 516
Qy 369 --ALPSTLYDLSSRAALSPSGCCSYSDIGTNSLRHLDSFNCAIIMSAN-----FMLE 419
Db 517 FSSMHIKYLTLNRLRPLDDNNARPSDL--HDEVLDSLHNAHYSIAGVTRHLQFONL 574
Qy 420 BELQHLDFQHSITLAKVTE-----FSAPLSLEKLY 449
Db 575 INLRVNLNSHNGIYITLFESELSKISLKEIVFSGNRDLHMANDKWTSIKSLQNLIR 634
Qy 450 LDISTNTKIDPDGIFGL-TSLNTLKAGNS--FKDNTLSNVFANTTNLTFLDLSKQOL 506
Db 635 LDLSTNNLQOIPNGAFINLPSLOGLISGNKLRFPNNTLLQYF---PHLHLLDSRNL 691
Qy 507 EQISGVEDTLHRLQOLAMSHNNLLFLDSSHYNOIXSLSTDSCNRRLE-TSKGLIQHP 565
Db 692 YFLPNCCKPASHLETLLSHNHPSHLPSGLSEKRNIVHLDLSFNTIKMINKSLSLQTKM 751
Qy 566 K-SLAFFNLTNNSVACICEHOKFLQWYKQKF-----LVNVEQWTCATPEMNTSLVLD 620
Db 752 KTNLSIELHNGYFDCDIDSPSWMDENINITPKLVNV---ICSNPGQKSKSISL 808
Qy 621 NNSCTYMKTIISVSVSVIVSTV--AFYH-----FYHL--ILAGCKYRSGE 669
Db 809 DLITCVSDPTAAVLFELFTLTSWVMLAALVHHLFYMDVWFYHMCSAKLKGYRTSTSQ 868
Qy 670 SIYDAFYVYSSON---EDWVNEVLVKNLEEGVPR-FHCLHYRDPICVAIAANIIOGCF 725
Db 869 TFYDAVYSDTKDASVTDVWVINELRHLEESSEDSKSVLLCLBERDWDPGPIIDNLMQ-SI 927
Qy 726 HKSRRKVIWVSRHFIQSRWCIFEYEIAQWQFLS-----SRSGIIFIVLEKYE 773
Db 928 NQSKKTIFFVLTKKY-----AKSNMFKTAFYIALQRLMDENNDVIIIFILEPVL 975
Qy 774 KSLRQOVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALL 814
Db 976 Q-YSOYLRRLQRICKSSIIQWPNPNPKAENLFWQSLKNVVL 1014

RESULT 13
US-09-954-987B-187
; Sequence 187, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
; APPLICANT: Stefan Bauer
; APPLICANT: Grayson B. Lipford
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
; FILE REFERENCE: C1041/7016 (AMS)
; CURRENT APPLICATION NUMBER: US/09/954,987B
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/233,035
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/263,657
; PRIOR FILING DATE: 2001-01-23
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/300,210
; PRIOR FILING DATE: 2001-06-22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-987B-187

Query March 12.9%; Score 559; DB 10; Length 1059;
Best Local Similarity 22.3%; Pred. No. 1e-36;
Matches 235; Conservative 161; Mismatches 341; Indels 318; Gaps 37;

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27 PCIEVVPN--ITYOCMDOKLSKVDDIPSSSTKNIDLSFNPDLTKLSYFSNFSLOMDL 84
53 PCBEKXKNDVIAECNSRRLOEVPOQVGYVTELDSDNFTITHYNSFOGLONTITKINL 112
85 S-----RCEIETIEDKAMGHLSNLILITGNPIQSPGSPSGU--TSLEN 129
113 NHNPVQHQNGNPQIOGNSGNLITDGAFLNKNLELLEDNQ-----PQIPSGPESLITE 168
130 LVAVETKLASLESPPIGOLITLTKLVANAHN--FIHSCKL-----PAYSNLTNLVHVDLSY 183
169 LSLIÖNNIYNTTKGISRLINLKNLYAMNCYFKNVCEKTIEDGVETITNLELSLSF 228
184 NYIÖTIVNDIQFLRENPQVNLSDMSLNPIDFIQDQAFQ--IKLHETLGN-----FN- 237
229 NSLSHVSKLPSSLRK-----LFLSNTQIKYISEEDFKGLINTLLDLSGNCRCFMA 281
238 -----SSNIMTKCLONLA----- 250
282 PFPVCPCDGASINIDRAFQNLQOLRYLNLSTSLRKINAMFKNMHLKVLDEFNYL 341
251 -----GLVHRLILGEFK 263
342 VGBIASGAFITMLPRLEILDSPNYIKGYPQHINISNFSKPLSLRALHLRGVYFOELR 401
264 DE-----RNLFIPEPSIMEGLCDVTIDEFRILTY 291
402 EDDPQPLMQLPNLSTINGINFIKQIDFKLFQNFSENLBI--YLSERNISPLVYKTRQSY 459
292 TN-----DPSDD-----IYKFHCLANVSAMSLAGVSIKYLEDVPK 326
460 ANSSSFQHIRKRSTDEDFPHSNFYHTRPLRPQCAAYGKALDLSNLSIFFIG--PN 517
327 HFKMOSLSIIRCOLKQFPTLDLPFLKSLTLTNKKSISFKKY--ALPSSLTLDLSRNL 383
518 QFE-----NLPIACLNLSANSNAQVLSGTEFSAIIPHVKYLDTNNRL 560
384 SFGCCSYSDLGTSNLSRLHDLSPNGAIIMSAN-----FMGLBELQHLDFQHSITLKVT 436
561 DFDNASALTEL--SDLEVLDSLNSHYFPIAGVTHLEFIQNFYMLKVLNLSHNNIYTLT 618
437 EBSAFLSLEKLYLDISYNTKID-----PDGIFGLTSLNTLTKMAGSFKDNTLS 487
619 D---KYNLESKSIVELVFSGNRLDILMDDNRYISIFGKGLKULTRLDLSLRK--HLPN 674
488 NVEFAN--TTNLTFLDLSKCOLQEOISWGVFPTLRLQLLNNSHNNLLFLDSSHYNQYLSLT 546
675 EAFNLPLASLTETHINDMLKFPNMTLQOFPRLBELDRGNKLLFLTDSLSDFTSSLRT 734
547 LDGSPNRI-----ETSGIILQHPFKS-----LAFNULTNNSVAC 580
735 LLLSHRISHLPSGFLSEVSSLKHLDLSSNLLKTINKSALERTYTKLSMELHGNPPEC 794
581 IEHQKFLQWVWEQKFLVNV-----QMTCAFPVEMNTSLVLDFFNNSTCYMYKTIISVS 635
795 TCDIGDFRWMQEH---LNVKIPRLVDYICASPGORGSIVLSLETTICVSIVTAVILF 850
636 VVSIVIVSTY--AFILYHFEFH-----LTLIAGCKKYSRGEIYDAFVITYSQN-- 682
851 FFLFFITTMALAAHLHLEFYMDVWFLYVNCCLAKIGYSLSLTSQFYDAYIYSDTKDS 910
683 -EDWVNEVLKNEEGVPR-FHLCIHYDFTPGVAIPANITIQGFHKSRAVIVVSRHFT 740
911 VTDWVINEALRYHLEESRDKVALLCLERDWDPCGAIIDNIMO--SINOSKKTIVLTKKY- 968
741 QSNWCIPEYIAQTMQPLS-----SRSGIIFYLEKYSKLSAQOVELYILS 788
969 -----ASWMEKTAIFYLALQLOLMDENMDVILFILLEPVLQH--SQYLRKORIC 1015
789 RNTYLEWEDNPLGRHIFWRILKNALL--DGKASN 820
1016 KSSILOMPDNPKAEGLPWQTLRVVLTENDSRYN 1050

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RESULT 14
US-10-407-952-30
; Sequence 30, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: Immunostimulatory G, U-Containing Oligonucleotides
; FILE REFERENCE: C01041.70037 US
; CURRENT APPLICATION NUMBER: US/10/407, 952
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-407-952-30

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Query Match      12.9%; Score 559; DB 15; Length 1059;
Best Local Similarity 22.3%; Pred. No. 1e-36;
Matches 235; Conservative 161; Mismatches 341; Indels 318; Gaps 37;

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27 PCIEVVPN--ITYOCMDOKLSKVDDIPSSSTKNIDLSFNPDLTKLSYFSNFSLOMDL 84
53 PCBEKXKNDVIAECNSRRLOEVPOQVGYVTELDSDNFTITHYNSFOGLONTITKINL 112
85 S-----RCEIETIEDKAMGHLSNLILITGNPIQSPGSPSGU--TSLEN 129
113 NHNPVQHQNGNPQIOGNSGNLITDGAFLNKNLELLEDNQ-----PQIPSGPESLITE 168
130 LVAVETKLASLESPPIGOLITLTKLVANAHN--FIHSCKL-----PAYSNLTNLVHVDLSY 183
169 LSLIÖNNIYNTTKGISRLINLKNLYAMNCYFKNVCEKTIEDGVETITNLELSLSF 228
184 NYIÖTIVNDIQFLRENPQVNLSDMSLNPIDFIQDQAFQ--IKLHETLGN-----FN- 237
229 NSLSHVSKLPSSLRK-----LFLSNTQIKYISEEDFKGLINTLLDLSGNCRCFMA 281
238 -----SSNIMTKCLONLA----- 250
282 PFPVCPCDGASINIDRAFQNLQOLRYLNLSTSLRKINAMFKNMHLKVLDEFNYL 341
251 -----GLVHRLILGEFK 263
342 VGBIASGAFITMLPRLEILDSPNYIKGYPQHINISNFSKPLSLRALHLRGVYFOELR 401
264 DE-----RNLFIPEPSIMEGLCDVTIDEFRILTY 291
402 EDDPQPLMQLPNLSTINGINFIKQIDFKLFQNFSENLBI--YLSERNISPLVYKTRQSY 459
292 TN-----DPSDD-----IYKFHCLANVSAMSLAGVSIKYLEDVPK 326
460 ANSSSFQHIRKRSTDEDFPHSNFYHTRPLRPQCAAYGKALDLSNLSIFFIG--PN 517
327 HFKMOSLSIIRCOLKQFPTLDLPFLKSLTLTNKKSISFKKY--ALPSSLTLDLSRNL 383
518 QFE-----NLPIACLNLSANSNAQVLSGTEFSAIIPHVKYLDTNNRL 560
384 SFGCCSYSDLGTSNLSRLHDLSPNGAIIMSAN-----FMGLBELQHLDFQHSITLKVT 436
561 DFDNASALTEL--SDLEVLDSLNSHYFPIAGVTHLEFIQNFYMLKVLNLSHNNIYTLT 618
437 EBSAFLSLEKLYLDISYNTKID-----PDGIFGLTSLNTLTKMAGSFKDNTLS 487
619 D---KYNLESKSIVELVFSGNRLDILMDDNRYISIFGKGLKULTRLDLSLRK--HLPN 674
488 NVEFAN--TTNLTFLDLSKCOLQEOISWGVFPTLRLQLLNNSHNNLLFLDSSHYNQYLSLT 546

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Db 675 EAFNLPASTLTELHNDNMLKFPNMTLLOQFRLLELDLRGNKLLFLTDSLSDFTSSLRT 734
Qy 547 LDCSFNRI-----ETSKGLQHPKRS-----LAFNLTNNSVAC 580
Db 735 LLSHNRISHLPDSGFLEVSLSKHLDLSSNLTINKSALERTKTTKLSMELHGNPEC 794
Qy 581 ICEHQKFLQWVKEQKQFLVNV-----QMTCAPEBANTSLVDLPNNSTCYMYKTIISVS 635
Db 795 TCDIGDRRWMDER-----LNVKIPRLVDVICASPDGRKGSIVSLELTTCVSDVTAIYL 850
Qy 636 VVSIVIVSTV--AFLIYHFYH-----LIIACCKYSRGSIYDAFIYSSON-- 682
Db 851 FFFFTITTMVMAALAHLPYWDWFIYVNCIAKIKGRSLSTSGTFDAIYSTDKDAS 910
Qy 683 -EDWVRNELVKNLEGVPR-FHLCIHYRDFIPGVAIAANIIQEGFHKSRKVIIVVSRHFI 740
Db 911 VDWVINEILRKHLESBRDKNVLCLBERDMDGLAIDNLMQ-SINOSKCVFVLTKKY- 968
Qy 741 OSRMCIFVEYIAQTQOPLS-----SRSGIPIVLEKVEKSLRQOVELYRLIS 788
Db 969 -----AKSNWFKTAFYALQRLMDENMDYIIFLLEPVLQH--SQYLRLRORIC 1015
Qy 789 RNTYLEMEDNPLGRHIFWRRLKNALL---DGKASN 820
Db 1016 KSSILQWDPNPKABGLFMQTLRNVTLTENDSKRYN 1050

RESULT 15
US-10-753-267-30
; Sequence 30, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stegiano, Nancy E.
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Domoghue, Mary A.
; APPLICANT: Rodrique-Way, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 1729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2669654, 33566, 53656, 44143, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8893, 955,
; TITLE OF INVENTION: 32345, 965, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419
; FILE REFERENCE: MP103-003P1RNONMIM
; CURRENT APPLICATION NUMBER: US/10/753,267
; PRIOR APPLICATION NUMBER: 2004-01-08
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-753-267-30
Query Match 12.9%; Score 559; DB 17; Length 1059;
Best Local Similarity 22.3%; Pred. No. 1e-36;
Matches 235; Conservative 161; Mismatches 341; Indels 318; Gaps 37;
27 PCIEVPRV--ITYQCMQDKSKVPPDDIPSTKNDLSNPLKILKYSFNSFELQMDL 84
Db 53 PCDEKQNDVIAECNSRRLQEVQTVGKYVTELDSDNFTHITNESFOGLQNTKINL 112
Qy 85 S-----RCIEITIEDAMGHLHLSLILTGPNIQSFSGSPGL--TILEN 129
Db 113 NNNPNVQHONGNPGIQSNGNLITDGAFLNKLRLLEDNQL---PQIPSGLEBSLTE 168
Qy 130 LVAVETKLASIESPPIGQITLTKLNVANH--FISCKL---PAYFNLTVLVHVDLSY 183
Db 169 LSLIQNNIYNTKSGISRLINKULYLANCYENKVCCKTNIDGVETLNLIELSLSF 228
Qy 184 NYIQTIVNDIQFLRENDQVNLSDMSLNPJDFIODAQOG-IKLHELTLRGN---FN- 237
Db 229 NSLSHVSXPKLPSLRK-----LFLSNTQIKYSEBDFKGLINTLLDLSGNCRCFNA 281
Qy 238 -----SNIMTKCLQNLA----- 250
Db 282 PFCVPCDGGASINIDRAPQNLQRLYNLSSTSLRKINAMFKNMELKVLDELFNVL 341
Qy 251 -----GLHYRLTIGEPK 263
Db 342 VGEIASGAFMLRLRLTLDLSPYIKSGYPOHINISNFKSPSLRALHLRGVPOELR 401
Qy 264 DE-----RNLEIFEPSIMEGLCDVTTDEFRLTY 291
Db 402 EDDQPLQMLNLTNLNGINFIKQIDPKLFQNSNLEII--YISENNISPLVKDTRQSG 459
Qy 292 TN-----DPSDD-----IKFHLAVASAMSLAGVSIKYLEDPK 326
Db 460 ANSSSFQHIRKRSSTPEFPNSNFYFTBPLKPOCAAGKALDLSINISFPG--PN 517
Qy 327 HFKQSLIIRCOQKQFETDLPFLKSLTLTMNKGISIFKCV--ALPISLYLDSRVAL 383
Db 518 QFE-----NLPDIACLANSANSNAOVLSTGESBAYIHVATLIDLTNNRL 560
Qy 384 SFGCCSYSDIGTNSLRHLDSFNGALIMSAN-----FMGLEBLQHLDFQSTLKEVT 436
Db 561 DFDNASALTEL--SDLEVLDSLVSNSHYPRIGVTHHLEFIQNFNLKVLNLSHNNIYTLT 618
Qy 437 EFSAFSLSEKLLYDIDISTYTKID-----FDGIFLGTSNLTLMAGNSFQDNTLS 487
Db 619 D--KYNLESKSLVELVFSGNRLDILMNDDNRYSISIFKGLKNTLRDLSSNRKL-HIPN 674
Qy 488 NVFAN--FTNLFTLDSKCOLEQISMGVEDTLHRLQOLNMSNNNLFLDSSHYNOULYSIST 546
Db 675 EAFNLPASTLTELHNDNMLKFPNMTLLOQFRLLELDLRGNKLLFLTDSLSDFTSSLRT 734
Qy 547 LDCSFNRI-----ETSKGLQHPKRS-----LAFNLTNNSVAC 580
Db 735 LLSHNRISHLPDSGFLEVSLSKHLDLSSNLTINKSALERTKTTKLSMELHGNPEC 794
Qy 581 ICEHQKFLQWVKEQKQFLVNV-----QMTCAPEBANTSLVDLPNNSTCYMYKTIISVS 635
Db 795 TCDIGDRRWMDER-----LNVKIPRLVDVICASPDGRKGSIVSLELTTCVSDVTAIYL 850
Qy 636 VVSIVIVSTV--AFLIYHFYH-----LIIACCKYSRGSIYDAFIYSSON-- 682
Db 851 FFFFTITTMVMAALAHLPYWDWFIYVNCIAKIKGRSLSTSGTFDAIYSTDKDAS 910
Qy 683 -EDWVRNELVKNLEGVPR-FHLCIHYRDFIPGVAIAANIIQEGFHKSRKVIIVVSRHFI 740

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Db      911 VTQVINELRVHLEESRDKNVLLCLERDWDPGIAIIDNLMQ-SINOSKTVFVLTICKY- 968
QY      741 QSRWCIFEYEIAQOTWOFLS-----SRSGIIFIVLEKYEKSLRQOVELYRLLS 788
Db      969 -----AKSMNFRTAFYALQRLMDENMDVIIIFILEPVLQH--SQYLRRLQORIC 1015
QY      789 RNTYLEMEDNPLGRHIFWRRLKNAALL--DGKASN 820
Db      1016 KSSILQMPDNPKABGLFWQTLRNVTLTENDSRNN 1050

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Search completed: March 12, 2005, 20:28:08
 Job time : 79.8956 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:01 ; Search time 21.5445 Seconds

(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985b-99

Perfect score: 4345

Sequence: 1 MPPPLARTLIMLPFSCLE.....GKSNPEQTAEETATWT 835

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	612.5	14.1	661	2	156258
2	457.5	10.5	786	2	T08664
3	406	9.3	1097	2	A29943
4	344	7.9	1389	2	T13852
5	342	7.9	1385	2	T13887
6	319.5	7.4	603	2	UC6128
7	317.5	7.3	603	2	JC1282
8	316.5	7.3	605	2	JC1239
9	315.5	7.3	1066	2	T15864
10	303.5	7.0	1134	1	A29944
11	291.5	6.7	605	2	A41915
12	287.5	6.6	1531	2	T42218
13	283.5	6.5	1112	2	T10504
14	273	6.3	1469	2	B36665
15	273	6.3	1480	2	A36665
16	270	6.2	2026	1	OYBY
17	269	6.2	1143	2	T10636
18	266.5	6.1	1692	2	S42799
19	262.5	6.0	1091	2	A58532
20	260.5	6.0	1523	2	T13953
21	257.5	5.9	1134	2	T04587
22	256	5.9	1120	2	B66479
23	255.5	5.9	994	2	H96510
24	255	5.9	907	2	UG0193
25	254.5	5.9	990	2	T00800
26	253.5	5.8	983	2	G84524
27	249.5	5.7	1027	2	B85089
28	249.5	5.7	1051	2	T13174
29	247.5	5.7	603	2	T24315

30	247	5.7	907	2	J60176	orphan G protein-c
31	244	5.6	1007	2	C84668	probable receptor
32	243	5.6	1016	2	T30553	disease resistance
33	242	5.6	853	2	T17461	disease resistance
34	241.5	5.6	1109	2	T18536	receptor-like prote
35	241	5.5	741	2	T05250	probable disease r
36	240.5	5.5	1232	2	T05322	hypothetical prote
37	238	5.5	1019	2	T22117	hypothetical prote
38	235	5.4	1019	2	C96519	probable disease r
39	234	5.4	855	2	T17460	disease resistance
40	234	5.4	1068	2	H96769	hypothetical prote
41	230.5	5.3	910	2	G84648	probable disease r
42	230.5	5.3	1692	2	A33988	adenylate cyclase
43	230	5.3	1778	2	AF1116	intercalin protein
44	226	5.2	1192	2	T48499	receptor-like prot
45	222.5	5.1	951	2	A96770	hypothetical prote

ALIGNMENTS

RESULT 1

156258
RP105 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 156258
R/Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995

A/Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a me
A/Reference number: 156258; MUID:95204928; PMID:7897216

A/Accession: 156258

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-661 <RES>

A/Cross-references: UNIPROT:062192; GB:D37797; NID:9761711; PIDN:BA07043.1; PID:9761712

Query Match 14.1%; Score 612.5; DB 2; Length 661;
Best Local Similarity 27.0%; Pred. No. 3.3e-30;
Matches 182; Conservative 129; Mismatches 313; Indels 49; Gaps 16;

QY	12	IMALFF-SC-LTPGSLNFCIEVNTYQCKMDQKSKVPDDIPSTKNIDLSFNDPLIKL 69
DB	10	LVALFLASCRAVTSDDCKIEKVKYKNCNLGMLNIPGLPNSTECLEFSFNVLPRTQ 69
QY	70	SYSPSNFSELQMDLSRCEIETIEDKAMGHLSNLILTGNPLOSFPSPGSSGLTSLEN 129
DB	70	NTFSRLNLTFLDLTRCQIWIHEDTFOQHRDLTVLTANPLIFMAETALSGPKALKH 129
QY	130	LVAETKLASIESPPIGQLITLKKLVANFPIHSCKLPAYFSNLTNLVHVDLSVYIQTI 189
DB	130	LFPIQTGSSIDFPIRNQKTLBSLYGSNISSIKLPKGPPT-EKLVLDPFQNNAIHYL 188
QY	190	TVNDIQFRENPOVNLSDMSLNPIDTQDAFOGKIHELTLGNFNSSNIMKTCLONL 249
DB	189	SKEMSSLOQ--ATNLSTNLNGNDIAGIEPAPSAVPSQSL--NFGQNLVLVIFKGL 242
QY	250	AGLVHRLTIGEFDERNLIFEPSIMGCLDVTITDERLTYTNDPSDIYKFKHLAVS 309
DB	243	KNSTIQSLMTGTFEDMDDEI-SPAVFGLCEMVSVESTNLQKHYFNNSTVFHFGSLQ 301
QY	310	AMSLAGVISIKYLEDVPRKH-----KMSISITCOL--KQPTLDPFKS 353
DB	302	ELDLITAT--HLSPLSGVLGSLTKKLVLSANKFNNL---QISASNFSLTHLSLKG 354
QY	354	LITLTMKGSISFKKVALPSLYDLNRNALSPFGCCSYSDIGTNSLRHLDISFGAIIWS 413
DB	355	NTRKLELTGTCLEN--LENIRELDSHDIDTSDCCNLQRLNLSHLSINLSYNEPLSLK 412
QY	414	AN-FMGLBELQHLDFQSTLTKRVTEPSAPLSLEKLVLDISYNTTKIDFQDIFIGTISN 472
DB	413	TEAFKCPQLELLDLAFLTRKLVKDAQSPQNLHLKVLNLSHLSLDISSQQLFGLPALQ 472

Qy	473	TLKAGNSFKDNTL--SNVFANTNTLFLDLKSCQLEISGWGVDTLARLLQLLMSHNTL	530
Qy	473	HLINQGNHFPKGNLQKNTNSLDTGLRLLELVISFCDSLSDGHAFTSLKMMHVDLSNRL	532
Db	531	LFELD--SSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFNLTNNSVACICEHOF	587
Qy	533	TSSSIALSHLKGIY----LNLASNHISIIIPSLPLPILSQORTNLKONPLDCCSNIFY	588
Qy	588	LQWKEQKQPLVNVQNTCATPVEMN-----TSVLDFENSSCYWKKTISVSYSVIVS	643
Db	589	LEWKENNQKLEDEDTLCENPFILRGVRLSDVTLSCSMAVGIPLVILVFAILLIF	648
Qy	644	TVAFLIYHFYFHL	656
Db	649	AVKRYFLRWKYQHI	661

RESULT 2

T08664

Toll protein-like receptor DKFZp547I0610.1 - human

C:Species: Homo sapiens (man)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

R:Accession: T08664

R:Pousterka, A.; Klein, M.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16466

A:Accession: T08664

A:Molecule type: mRNA

A:Residues: 1-786 <PDB>

A:Cross-references: UNIPROT:O15399; EMBL:AL050262

A:Experimental source: fetal brain; clone DKFZp547I0610

C:Genetics:

A:Note: DKFZp547I0610.1

Db 665 -----HKM-----OLMEHLENTILRLPS----- 685
 Qy 447 LLYIDISTYTKIDPDGIFLGLTSLNTLMKAGNSFKDWTLSNVFANTTNLTFPLDLSKCOL 506
 Db 686 -----ANTP-----GYESVTSILHAGNNL-----TSIDVDQLPTNLTHLD----- 720
 Qy 507 EGISGCVPTLHRLDOLLMSHNNLLFLDSSHNQYLSLTDSCNRRLETSKGILOHPK 566
 Db 721 --ISW--NHLQMLN--ATVGLFNRTMKRSV----- 746
 Qy 567 SLAFENLTNNSVACICEHOKFLQWVKEQKFLVNEQMTCAPEVEMNTSLVDFFNNSCY 626
 Db 747 -----KLSGNPMKCDCTAKPILLFTQDNPERRGDNEMMCVN-AMPTRMWELSTNDICP 800
 Qy 627 MYKTI-ISVSVV--SVIVSTVAFPLIYH-----YFH-LILIAQCKYSGESIYD 673
 Db 801 AEKGFIALAVIALTGLAGTALYYKFOEIKIMYAHNLMLPTEBEDLDCKKFD 860
 Qy 674 AFVIYSSQNEQWVRELKYLEGVPRFHLCLHYRDFIPGVALAANIIOEGFHSKRYIV 733
 Db 861 AFISYSHKDOGFIEDYLVPOLEHGPQKQFOLCVHERDMLVGHIIPENIMR-SVADSRRYTI 919
 Qy 734 VSRHFIQSRWCIFEYEAQTMQPLSSRSGLIFIV-----LEKEXSLMQQVETLYML 787
 Db 920 VLSQNFISSEWAKLEFRAHRSALNEGSRRIIVITSDIGVEKLD-----ELKAYL 972
 Qy 788 SRNTYLEWEDNPLGRHIFWRRLKNAL 813
 Db 973 KMNTYLLKW-----GDPWFMDKLRPAL 993

RESULT 4

gene wheeler protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 R:Accession: T13852
 R:Elidon, E.; Kooyer, S.; D'Veelyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Belten, H.
 Development 120, 885-899, 1994
 A>Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simlile
 A:Reference number: 217796; MUID:95324375; PMID:7600965
 A:Accession: T13852
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1389 <EID>
 A:Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:g415682; PID:g1019104; PIDN:AAA7920
 C:Genetics:
 A:Gene: wheeler
 A:Cross-references: FlyBase:FBgn0004364

Query Match 7.9%; Score 344; DB 2; Length 1389;
 Best Local Similarity 20.6%; Pred. No. 3,6e-13;
 Matches 229; Conservative 146; Mismatches 316; Indels 418; Gaps 46;

Qy 41 DQKLSKVPDDIPSTKAIIDSFNPLKLIKYSFSNF-----SEIQ 80
 Db 154 DNNIRQLPBGWCMSPSLQILNTQNNIRSAEFLGSEKLCAGSALSNANGAVGSGSEIQ 213
 Qy 81 WLDLRCEIETIEKAMHG--LHLSNLILGNPISQSPSGGLTSLNLTAVETKLA 138
 Db 214 TLDDSFNELSLPD-AMGASRLRLQTLSTLOHNNISTLAAPALAGLSLRLVNTSYNHLV 272
 Qy 139 SLBS-----PIGQILTLTKLINV-----AHNFISCKLPA 168
 Db 273 SLSEAFANKEKLEHLQGNLDYELPKGLHRLLEQLLVLDLSGNQLTSHHVDST----- 328
 Qy 169 YFSNLTULVHYDLSYNTIQT---TVNDLOFLRNPOVNISLDSNLPIDFIDQDAFGI 225
 Db 329 -FAELIRLIVLNTSNNALTRIGSKTFKELYFLQ-----ILDRNNSIGIIEGAFPL 380
 Qy 226 -KLHELTLRGVFNNSNMKTCLQNLAGLHVRLILGFKDRNLLEIPSPIMEGLCVYTI 284
 Db 381 YNHLTL-----NLAENRLHTL-----DNR-----IFNELYVLT 408

RESULT 5

Qy 285 DEFRLTYNDSDDIVKFEHCLANYSAMSLAGVSIKYLEVDVPHFKQSLIIRC----- 338
 Db 409 ---KTLANNLV-SIVESQAFRNCSDLKEBSSNQLEVEBAV---QDLSMKITDLDGN 462
 Qy 339 QLKQPT-----LDLPKSLTYLTPNK-GSI---SPFK 367
 Db 463 QISEKNNTPFNRLQTLNGLRLIDNRIGNITVGMFODLLRLSVLNAKRIQSIGIEGADPK 522
 Qy 368 -----VALPSLYLDSRAALSFGSCCSYSDGTSNRLDLSF 406
 Db 523 NTEIETALDKQFLTDINGITATYTLASLMLNISENHLV---FDYAFIPSN-LKWLDTHG 578
 Qy 407 NGAIIMSANFGLBE--LOHLDPQSTLAKTERSAFSLSEKLYLIDIS-----YTNF- 457
 Db 579 N-YIEALGNKYKQGEIRVTTLDASHNRIIEGMSVNSIE-LIFINNIIIGQOANTF 636
 Qy 458 -----KIDPDGIFLGLTSNLTLMK-----GNSFKDNTLSNVFANTTNL 496
 Db 637 VDKTRLARVDLYANVLAKISINALRVAVSAKEVPBEFYLGANPECCDSMEWLQRIINL 696
 Qy 497 T-----FLDL-----SKQLE 507
 Db 697 TTRQHPVVDIGNIBCLMPHSRSLAPRLASLASDFVCKYKSHCPPTCHCCCEYQCECE 756
 Qy 508 QISWGEPTLH----- 518
 Db 757 VICGNCSCFHDATWATNIVDGRODLAALPNRIPOVSDLYLDGNMPELEVGLTGR 816
 Qy 519 RLQILNMSHNNLLFLDSSHNQYLSLTDSCFNRIETSKG-----IL 561
 Db 817 NLRALYNASNLMTLQNGSLAQVLNLRVLENNKLTLEGTBEPRLGLRELTYLHNNML 876
 Qy 562 QH-----FPSLAFPNLTNNSVACICEH-QKFLQWV 591
 Db 877 THINATPEPLVSEVLRDLNRRILSSPLHQYRHSLOGLTIGRANWSCRCQOLRELAQV 936
 Qy 592 KEQKQFLVNEQMTCAPEVEM-----NTSLVDFFNNS 624
 Db 937 SDNMMVVRDNDIYCLDAGIRELELGNLANGDCDLDASNSNTSSQDLAAGICP 996
 Qy 625 CYMTKTIISVSQVIV---STVAFIYHFFHLILAGCK-KYSGESIYDAFVIY 678
 Db 997 CWPALVILFLVLLIVFVRESVRLMFLHAYGVV---CPRFEDACKLYDALITLH 1051
 Qy 679 SSQNEQWVRELKYLEGVPRFHLCLHYRDFIPGVALAANIIO-BGFHSKRYIVVS 736
 Db 1052 SEKDYEFVCNNTIALEHGRPPFLCTQQRDLP-----QASHLQLVGEGARASRKITIVLT 1107
 Qy 737 RHFISRWCFEYEAQTMQPLSSRSGLI--FVLEK-----VEKSLRQOVELY 784
 Db 1108 RNLATETMNNIEFPNA---FHESRLDLAQKLVIIETSVSAEADVAELSPYLSKPSVN 1163
 Qy 785 RLISRNLYLEWEDNPLGRHIFWRRLKNAL 813
 Db 1164 RLTLTCDRY-----FWKELRYAI 1180

RESULT 6

Qy 113887 c1r protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 R:Chiang, C.; Beachy, P. A.
 Mech. Dev. 47, 225-239, 1994
 A>Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib
 A:Reference number: 217805; MUID:95151581; PMID:7848870
 A:Accession: T13887
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1388 <CHI>
 A:Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AAB33383

C:Genetics:
A:Cross-references: FlyBase:FBgn004364
A:Note: tlr

Query Match 7.9%; Score 342; DB 2; Length 1385;
Best Local Similarity 20.3%; Pred. No. 4.8e-13;
Matches 223; Conservative 151; Mismatches 325; Indels 402; Gaps 43;

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QY 41 DQKSKVPDDIPSTKNIDLSFNPDLKLSYSPSNF-----SEIQ 80
DB 154 DNNIRQIPBEGWCMSELDLNLQNRIRSAEFLGSEKLCAGSALSNANGAVSGSEIQ 213
QY 81 WLDLSRCEIETIEDKAWHG--LHHLNMLITGNPIQSPGSGSGLTSLNVAVENTKA 138
DB 214 TLDVSEFELSLPD-AWGASRLRLQTLISLOHNNISITLAPNALAGLSLRYLNISYHVL 272
QY 139 SLSEFPIGQILTLKKLVANVNFHSCLP-----AYFS 171
DB 273 SLSEFAPGNKKELEHLQGNLDY--ELPYGLHLRLBQLVLDLSGNQLDHDHVNSTFA 330
QY 172 NLTVLVHVDLSYNYIQTIT--TVNDLQFLRENPQVNLSDMSLNPIDFIQDAFOGI-KL 227
DB 331 GLIRLIYANLSNMLTRIGSKTFEELVFLQ-----ILDWRNNSIGHIEGALPLPYNL 383
QY 228 HELTLRGNFSSNIMKTCLQNLAGLHVRLLGEFKDERNLIEPEPSIMEGLCDVTIDEF 287
DB 384 HTL-----NLAEENRLHTL-----DNR-----IFNGLVYLT----- 408
QY 288 RLTYTNDPSDDIVFHCILANVSAMSLAGVSIKYLEDVFKFKMOSLIIRRC-----QLK 341
DB 409 KLTLLNNMLV--SIVSQAFRNCSDLEKEDLSNQLTEVE--AAQDSLMLTKLIDGENQIS 465
QY 342 QEPF-----LDLPFLKSLTLYTNMK-GSI--SPKK-- 367
DB 466 EFKNTPFNALQTLGLRLIDNRIGNITVGMFOGDLRLSVMLAKRIGISRGADKNTS 525
QY 368 -----VALPSLYLDSRNALSPSCCYSIDGTSLSLHLDSPFGA 409
DB 526 IEAIRLDKKFLTDINGIPATLASLMLNLSNHLVW---FDYAFIPSN-LKWLIDHGN-Y 580
QY 410 IIMSANFNGLEB---LQHLDPQHSFLKQVTEPSAFLSEKLLIYLDIS-----YTNL 457
DB 581 IEALGNVYKLOEIRIVTTLDASHNRITETIGAMSVNSIE-LIFINNIIIGQIANTFVDK 639
QY 458 ---KIDPDGIFLGTSINTLTKA-----GNSFKDNTLSNVFANTNL7- 497
DB 640 TRLAVDLYANVLSKISALALVAVSAKVPBEFYLGSPFECDCSMEMLRINNLTFR 699
QY 498 ---FLDL-----SKQLEQIS 510
DB 700 QHPHVVDLGNIECLMPHSRSLRPLASLASDPVCKESHCPPTCHCCEYQCECEVIC 759
QY 511 WGVFDTLH-----RIQ 521
DB 760 PNCSCFHDATYATNIVDCGRDOLALPNRIPODVSDLYLDGNMPELEVGHITGRNLR 819
QY 522 LNMASHNNLLFLDSHYNQLYSSTLDCSPNRLETSGK-----LLOH- 563
DB 820 ALYINASNMTLQNGSLAQDLVNLRLVLENNKLTALTEGTEFRSLGLRELILHNNMLTHI 879
QY 564 -----FPKSLAFNLTNNSVACICEH-QKELQWVXQ 594
DB 880 SNATFEPLVSLVLRDLNNRSLSLPHLOYRHSLOGLTLLGNMWSGCCOQLRELDAQVSDN 939
QY 595 KQPLVNVBQMTC---APPEV-----NTSLVLDPNNSSTCYM-----YKTIISV 634
DB 940 AMVVRRAHDIIYCLDAGIKRELELIGLNLANGCPDSDLDASASITSSQDLAIGYRLPLA 999
QY 635 SVASVIVSTVAFLIYHF-----YFHLILIAQCKYSGRSIYDAFVIYSSQNDWV 666
DB 1000 AYVAVLFLDVVLLIVFVFRSRYVMMLFAHYGVAVCEPREDAGKLDVAIILHSEKDEYFV 1059
QY 687 RNELVKNLEEGVPRFHLCLHYRDFIPGVAIANIIQ--EGFHKSRRKVIIVVSHRFIOSRW 744

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DB 1060 CENIAAELEHGRPPFLICIQORDLP-----QASHLDLVGAGASARKIILVLRMLLATSW 1115
QY 745 CIFREYIAQTQWPLSRSGII--FVYLEK-----VEKSLRQOVELYVLLSRNTY 792
DB 1116 NRLEPANA-----FHESLRGIAQCVITEETSVSAEADVAELSPYIKSPSRNRLTCDRY 1171
QY 793 LEWEDPLRGHIFWRRLKNAL 813
DB 1172 -----FWELKRYAI 1180

```

RESULT 6

JC6128
Insulin-like growth factor binding complex acid labile chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: JC6128
R:Bolsclat, Y.R.; Seto, D.; Heieh, S.; Hurest, K.R.; Ooi, G.T.
A:Title: Organization and chromosomal localization of the gene encoding the mouse acid labile
A:Reference number: JC6128; MUID:96413591; PMID:8816745
A:Accession: JC6128
A:Molecule type: DNA
A:Residues: 1-603 <BOI>
A:Cross-references: UNIPROT:P70389; GB:U66900; NID:g1621612; PIDN:AA017270.1; PID:g162161
C:Comment: This protein is a serum protein and it is of the ternary complex in the physio
C:Genetics:
A:Gene: als
A:Map position: 17

Query Match 7.4%; Score 319.5; DB 2; Length 603;
Best Local Similarity 24.2%; Pred. No. 3.7e-12;
Matches 159; Conservative 85; Mismatches 228; Indels 185; Gaps 23;

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QY 39 CMDQKSKVPDDIPSTKNIDLSFNPDLKLSYSPSNFSEQLWLDLSRCEIETIEDKAWH 98
DB 60 CSSNNLQLPFGIGIVSTRALWLDGNNLSSIPSAFQWLSIDFNLQSGWLRSLSEPOLL 119
QY 99 GLHLSNMLITGNPIQSPGSGSGLTSLNVAVENTKASLSEFPIGQILTLKKLVANH 158
DB 120 GLQNLVHLHRLNRLSLASLAFPHRTPSLASLGNLGLLEGLPFGLSHLDNINLGV 179
QY 159 NF-----IHSCKL-----PAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195
DB 180 NSLVVLPPTVQGLGNLHVLVLAGNKLTYLQPALCGELRELDLSRNALRSVAN--V 237
QY 196 FLRENPQVNLSDMSLNPIDFIQDAFOGIR-LHELTIRGNPNSSNIMKTCLQNLAGLHV 254
DB 238 FHLPRLOKLYLDRNL--ITAVAPRAFLGMALRWLDLSHN-RVAGLLEDTPFGLLGLHV 294
QY 255 HRLIGEKDERNLIEPEPSIMEGLCDVTIDEFRITVNDPSDDIVFHCILANVSAMSLA 314
DB 295 LR-----LAHNAITSLR 306
QY 315 GVSIXYLEDVPRGFKMOSLIIRCOLKQPTLDPFLKSLTLYTNMK---GSISEKVAL 370
DB 307 -----PRTFK-----DLHFLIEDLQGNHRIQIGKTFE--GL 337
QY 371 PELSYLDSRNAL-----SPSGCCSYG--DIGTNSLRHLDSPFGAIIIMSANFNGLEB 422
DB 338 GQLEVLTLANDQIHVYKVAFFGLFNVAVMNLGNCRLSP-----EHVQQLGRL 388
QY 423 QHLDPQHSFLKQVTEPSAFLSEKLLIYDISYTNKIDPDGIFLGITSINTLKMAGNSPK 482
DB 389 HSLHLEHSCIGRIRLHT-----FAGISGRRLPL-----R 418
QY 483 DNTLISNV-----PANTTNLFLDLSKQLEQISGWVFDTLHRLQLNLMASHNNLLFLDSHY 538
DB 419 DNSISIEBQSLAGSELLELDITANQLTHLRQLFGQIGQLEYLILSNQNLTMLSBDVL 478
QY 539 NQLYSLTLDGCFNRLET-SKGILOHFPKSLAFNLTNNSVACICEHQFLQWVXQKQPE 597

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Db 479 GELQRAFWMLDSHNLLETPEAGLFSSLSGR-LRYILNLRNNSL-----QTFVQPGIERLW 531
QY 598 LVNVEQWTCATPVE-----MNTSLVLDENNSTC-----YMYKTIISVSVS 639
Db 532 L-DANPMDCSCPLKALRDPALQNPVPRFVQVCEGDDCCQPVYTYNNITCAGPANV 587

RESULT 7
JCI282
Insulin-like growth factor-binding protein acid labile chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JCI282
R:Dat, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A:Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A:Reference number: JCI282; MUID:93038676; PMID:1384485
A:Accession: JCI282
A:Molecule type: mRNA
A:Residues: 1-603 <DAL>
A:Cross-references: UNIPROT:P35859; GB:S46785; NID:9258002; PIDN:AAB23770.2; PID:G570593
A:Experimental source: liver
A:Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F:267-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 7.3%; Score 317.5; DB 2; Length 603;
Best Local Similarity 24.1%; Pred. No. 4,9e-12;
Matches 159; Conservative 86; Mismatches 223; Indels 193; Gaps 24;

QY 39 CMDQKLSVDPDIPBSTKNIDLSNPILKLSYSPNSFSELOMIDLSCEITIEDKAMH 98
Db 60 CSSKMLTLPDIPVSTRALMDGNLSSISPAFQNLSDPLNLQSGWLSLEPQALL 119
QY 99 GLHLSNLILGNPIQSPSPSGSLTLENLVANETGLASLESPFIQILTKLTAH 158
Db 120 GLQNLVYHLERNLRNLAIVGLFTPTSLASLSSNLGRLEBGLFQGLSHMDLNGW 179
QY 159 NF-----IHSCKL-----PAYSNLTNLVHVDLSYNYIQTITVNDLQ 195
Db 180 NSLVVLPTVTFQGLGNHBEVLAKNKLTYLPALFCGLRELDLSNNALRSVANYFV 239
QY 196 FLRENPQV-NLSLMSLNPIDFIQDAFGIK-LHELTLRGNFNSNMKTCLQNLAGH 253
Db 240 HL-----PRLOKYLDRNL--ITAVAFGAFGLMKALRWLDSHN-RVAGLMEDTFFPLGLH 293
QY 254 VHRLLGFRKDBRNLEITEPSIMEGLCVTTIDEPRLTYTNDPSDDIVKFCILANVSANSL 313
Db 294 VLR-----LAHNAIASL 305
QY 314 AGVSIKLYEDVPKHKMQSLIIRCOLKQPTLDLPPLKSLTLTMNK-----GSISFKVA 369
Db 306 R-----PRIFK-----DLHFEELQGLGNRRKQGERTFE--G 336
QY 370 LPSLSYLDLSNNAL-----SPSGCCSYS--DLGNSLRHLDSFNCAIIMSANFMGLEE 421
Db 337 LGQLEVLTLNDNQITFVAGFSGLFNVAVMNLISGNCRLSP-----ERVFGQDX 387
QY 422 LGHLDPQSTLKYRTFSAFLSLEKLYLDISYNTKIDPDGIFLGLSLTNTLMAAGNSF 481
Db 388 LHSLSLHESLGHVRLHT-----FAGLSGLRRLFL----- 417
QY 482 KDNLTLSNV-----FANTVTLFLDISKQLEOISWGVFTLRLQLLNNSHNNLFLDSSH 537
Db 418 RDNSSISSIEBQSLAGLSLELDLTLNRNLTHLPRLQGLGHELVLLISYQDLTSLSEV 477
QY 538 YNQLYSLSLDCSNRRIET-SKGLIQHPKSLAFENLTNNNSVACICEHQKFLQWYKEQ-- 594
Db 478 LGPQRAFWMLDSHNLLETPEAGLFSSLSGR-VRYLSLRNNS-----LQFSPQPG 526
QY 595 -KQFLVNEQWTCATPVE-----MNTSLVLDENNSTC-----YMYKTIISVSVS 638

Db 527 LERMLDANPMDCSCPLKALRDPALQNPVPRFVQVCEGDDCCQPVYTYNNITCAGPAN 586
QY 639 V 639
Db 587 V 587

RESULT 8
JCS239
Insulin-like growth factor acid-labile chain - baboon
C:Species: Papio sp. (baboon)
C>Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: JCS239
R:Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
A:Reference number: JCS239; MUID:97040714; PMID:8886027
A:Contents: liver
A:Accession: JCS239
A:Molecule type: mRNA
A:Residues: 1-605 <DBL>
C:Comment: This factor is structurally related to proinsulin and have insuline-like meta

Query Match 7.3%; Score 316.5; DB 2; Length 605;
Best Local Similarity 22.2%; Pred. No. 5.7e-12;
Matches 147; Conservative 89; Mismatches 238; Indels 189; Gaps 17;

QY 32 VENTIQCMDKLSVDPDIPBSTKNIDLSNPILKLSYSPNSFSELOMIDLSCEIT 91
Db 53 VNEISVFSCKNLRPLPGIGTQALMDLSSNLSIPPAFRNLISLAFNLQGGQGS 112
QY 92 IEDKAMGHLHLSNLILGNPIQSPSPSGSLTLENLVANETGLASLESPFIQILTL 151
Db 113 LEQALLGLNLTCHLHERNLRLSLAVGTFAVTPALALLGSNNRSLRED----- 163
QY 152 KKLAVANFTHSCKLPAYFSNLTVHVDLSYNYIQTITVNDLQFLRENPQVNSLMSL 211
Db 164 -----GLFEGIGNLMDLNLGMSLAV----- 184
QY 212 NPIDFIQDAFGI-KHELTLRGNFNSNMKTCLQNLAGLHVRLLGFRKDBRNLEI 270
Db 185 -----LPDAFRGLAGLEVLVAGN-----RLAY 208
QY 271 FEPSEIMEGLC-----DVTIDEPRLTYTNDPSD--DIVKFCILANVSANSLAGSILEYD 323
Db 209 LQPLAFSLALRELDLSRNALRAIKANVFAQLRLOGLYDRNLIAVAGA----- 261
QY 324 VPKHFKMQSLIIRCOLKQPTLDLPPLKSLTLTMNK--GSISFKVALPSLSYLDLSRN 381
Db 262 -----FLGLKALRWLDSHNRVAGLLEDTFPGILGLRVRLSHN 300
QY 382 ALSFGCCSYSD-----LGTNSLRHLDSFNCAIIMSANFMGLEEQLHPDQSTLK 433
Db 301 ALASLRPTTFEDLHPLBELQGLGNRRKQ-----AERSFGLQGLEVLTLDHNOLO 351
QY 434 RTEFSAFSLSEKLYLDISYNTKIDPDGIFLGLSLTNTLMAAGNS----- 480
Db 352 EV-RVGAFLGLTAVVAVNLSGNCRLNPEQVFRGLGKLSHLBGSCLGRIRPHTFAGLS 410
QY 481 -----FKDNTLSNVFANT-----TNLTFLDISKQLEOISWGVFTLRLQLLNNSHNNL 530
Db 411 GLRRLFLKDNGLVIGIEBQSLWGLALELDLTLSTNLQTLPHQLFQGLKLEVLLSHNRL 470
QY 531 LFLDSHYNOLYSLSTLDCSNRIETSKGLIQHPKSLAFENLTNNNSVACICEHQKFLQ-- 589
Db 471 AELPADALGRLQRAFWMLDSHNRLEALPGSLASLGRRYANLTNNNSLRTTTPQPGIER 530
QY 590 -WYKQKQFLVNEQWTCATPVE-----MNTSLVLDENNSTC-----YMYKTI 632
Db 531 LMEG-----NPMDCSCPLKALRDPALQNPVPRFVQVCEGDDCCQPVYTYNNIT 582
QY 633 SVS 635

Db 583 CAS 585

RESULT 9

T15864 hypothetical protein C56E6.6 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T15864

R:Pulson, L. submitted to the EMBL Data Library, November 1995

A:Description: The sequence of *C. elegans* coemid C56E6.

A:Reference number: S69019

A:Accession: T15864

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1066 <FULL>

A:Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIDN:AAA810

C:Genetics:

A:Gene: C56E6.6

A:introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 9

Query Match 7.3%; Score 315.5; DB 2; Length 1066;
Best Local Similarity 21.2%; Pred. No. 1.4e-11;
Matches 180; Conservative 128; Mismatches 217; Indels 323; Gaps 37;

56 KNIDSEFPLKIKSYSPFSFSELOMDLSRCEI-----ETIE----- 93

Db 171 RELDSTYQIQVDSSEFETVGHMSLDSTYRIAYLFRGMUKNPAKTLKTLKLAEMNH 230

94 --DKAMGHLHLSNLIITGNP-----IQSFSGSFGSLTS 126

Db 221 ATPPALRLRLNLTNLNGKNKLRIDGVLKGTDTLVELFANNYLRHPIHGVLSGKQ 290

127 LENVAVETKSLAE-----SFPICQITLTKLVANHFHSCKLPAVFSLTMLVAVD 180

291 LEHLDISNKKIMSLKPKTSLITTEETSTVRLNLAGNRINMMDYLIFFEMPLITYD 350

181 LSYNYIQTIT-----VNDLQ--FLREN-----POV-----NLSDMSLNPIDFIODQ 220

351 VSFNKRIRFISPRVFEKTKNLESLFLONNOAHFPLFRDKLRHMLDN--NQIQKIDNF 408

221 AFQGI-KIHELTLRGN-----FNSNIMTKLCIONLAGLHVRHLIGEKDERNLEI 270

409 SLADI-PKIQHLSIAGNQDLITENMGSSSSSLKSLNLAHKKIHSSRSFSDLDNQ- 467

271 FEBSIMEGLCDVTIDFRLTYTNDPDDIVKHFCLANVAGSLAGV-SIKYEDVPKHK 329

468 -----QRLSHNN-----IRTTISMTFSNLRIKRYL-DLSHN-- 498

330 WOSLSIIRCOLKQFPTLD-----PFLKSLTLTMNK-----G 361

499 -RIIKLIPSAIYLPALDVLHDHNNLNEIDRAPSPFSLQSLKLSHNAFRFSCPEFG 557

362 SISFKVALPSLTYLDSRNALSSFG--CCSYS--DLGTNS-----LRH 401

558 SIS-----QVHQDLSSNQINBIDFICFARGIRKLSLASNSVEKINRKLQDADATLS 610

402 LDISFNGAI-IMSANFMGLELOHDPQHSSTLK-----RVTFESAPLS--L 444

611 IDISHNGIIDVDADAFCECRKLSHIKLSHYINLWKTRVCIPWISHLTTPCFEFTKEH 670

445 EKLTYLD-----ISYTNKIDF--DGIPLGTSLNTLTMAQN----- 479

671 ERTISRYITVDSQSLTSPGNLSLSPANKKVDISIEGAEENLSLKLIDLSNPPYTSWS 730

480 --SEKID--NTLSNV-FANT-----TNLTFLD 500

731 PTAFRLDLSHSSISINMANTGLFSMPKFSHRSIQSLNISCNKIYELSEKDLAPLTKVVALD 790

501 LSKQLEQISMGVDDTLHRQLQMLSMNNLLFLDSSHYNOYSL----- 544

791 ISHNKLQISSMAEPILHKLQMLVNSANPITHLTNEHIOQLYKLYNIPDNARPYQISIL 850

Qy 545 -----STLDCSFNRIFTSKGILOHFPKSLAFENLTNNSVACICEHCKFLQ 569

Db 851 SNLPLHTTYVIDIKESALDRQFTYADTR--LRLHL--VAGRNLTIEVGAFATIRGF-- 904

Qy 590 WKEOKQPLVNVBQMTCAPEVMNTSLVLDENNSTCYMTKTIISVSVSYIVV----- 642

Db 905 -----RVRIEIHNSIEBFPSR--IFDTLTGISILSLSDNKLTYTF 944

Qy 643 ----STVA 646

Db 945 NPROSTVA 952

RESULT 10

A29944 chaptin precursor - fruit fly (*Drosophila melanogaster*)

N:Alternate names: photoreceptor cell-specific membrane protein

C:Species: *Drosophila melanogaster*

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004

C:Accession: A29944; A21123

R:Retinke, R.; Krantz, D.B.; Yen, D.; Zipursky, S.L.

Cell 52, 291-301, 1988

A:Title: Chaptin, a cell surface glycoprotein required for *Drosophila* photoreceptor cell

A:Reference number: A29944; PMID:88135762; PMID:3124963

A:Accession: A29944

A:Molecule type: DNA

A:Residues: 1-1134 <REI>

A:Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M1901

R:Zipursky, S.L.; Venkatesh, T.R.; Teplov, D.B.; Benzer, S.

Cell 36, 15-26, 1984

A:Title: Neuronal development in the *Drosophila* retina: monoclonal antibodies as molecu

A:Reference number: A21123; PMID:84106810; PMID:6420071

A:Accession: A21123

A:Molecule type: protein

A:Residues: 31-43; 'HX', 46-49; 'H' <ZIP>

C:Genetics:

A:Gene: FlyBase:chp

A:Cross-references: FlyBase:FBgn0000313

A:introns: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2

C:Superfamily: Chaptin; leucine-rich alpha-2-glycoprotein repeat homology

C:Keywords: cell adhesion; glycoprotein; membrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-1134/Product: chaptin #status predicted <MUT>

F:80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR2>

F:103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>

F:128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>

F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>

F:177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>

F:201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>

F:226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>

F:250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>

F:279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>

F:303-325/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>

F:326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>

F:351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>

F:375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>

F:401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>

F:428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>

F:453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>

F:477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>

F:502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

F:527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>

F:551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>

F:577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>

F:601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>

F:625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>

F:649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>

F:673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>

F:708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>

F:733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>

F:757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>

F:781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>

F:805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
 F:828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
 F:854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
 F:879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
 F:903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
 F:928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR35>
 F:949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
 F:973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
 F:996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
 F:1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
 F:1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Query Match 7.0%; Score 303.5; DB 1; Length 1134;
 Best Local Similarity 20.8%; Pred. No. 8.6e-11;

Matches 169; Conservative 122; Mismatches 275; Indels 247; Gaps 31;

44 LSKVDD-----IPST-----KNIDSFNPLTKISYFSN 75
 114 LTEIDDAFTGLERLMEILRPNDLVEIPSKSLHLOKRLHLDGYHITHITQIHDSPFG 173
 76 FSE-LQWLDLSCIEIETEDKAMHGLHLSNLIITGNPIQSPSPF-SGLTSLNLYAV 133
 174 LEDSLQTLIRNENCISQLMHSFSGLLIETDLSGNMLFEIDPNVVFVGMRLRLILT 233
 134 ETKLASLSPFGIOLITLKLNVANRPHSCLPAYF---SNLNLVHVDLSYNYITQT 189
 234 DNLSEIPYDALGPKSLKTTLDISHNVWSLSGNETYEIKASTKLDNLHLEYNHIEVL 293
 190 TVNDIQFLRENPOVNLSDMSINPIDIQDAFOGKIKHETLR-----GNF 236
 294 PPNSSKRYF---DTVVRTF-PDGNPIHTLRBEDAFKARIREIMRQGLTNISPVAFSLV 349
 237 NSSNIMKTCLONLAGLHAYHRLI-----LGEFKERNLEIPEPSIMEGLCVTIDEPL 289
 350 NSLIQLDLSGNLTLKHL-HKLFNPFVLRVISMRDNK-IKIQPTEFNAHYTL-LKL 405
 290 TYTNFSDDIYKHECLAVASAM-SLAGVISIKLEBV---PKPKF---WQSLSTIRCOL 340
 406 DLGG-RNDPTNLQTLRMTNRMRNRSLSISRLGSSVGPEDPKPGVELELDQITRASL 464
 341 KQPLTDLPLKSL-----TLTNWKSISFKVALP----- 371
 465 SGIOHAKRYRGLKRLDPSENGISSINDAFHEIGHSLISLMSHGYSGLAPRLRH 524
 372 --SLSYDLSSNALSFSGCCSYSDI-----GT-----NSLRHLDLS 405
 525 LTSIQELDFSNNHITSSMDTSFHFKNLRLLEHNDRIEYVLKGFQGDHSHKLEISLR 584
 406 ENGALIMAN-----FMGLEBELQHLDPQHSITLKVTERPSA 440
 585 FNHLTSSIQHTFFEDLEALRKLHLDNKKIDKIERAFNNIDLELEYLSLRGNKINNLD-ES 643
 441 FLSEKL----- 447
 644 FQNLPELEIDMAFNQLEPNFEDYDQVGTLSNLNANVSHNOIRQMLMTNSSKGENEIG 703
 448 LY-----LDISYNTKIDFDGIFL-GLTSLNTLTKMANSFKDNTLSNVFANTNLTELD 500
 704 MYHSNIKILDLSSHNNISIIHPGYFRPAISLTLHLGNSLM-NTTRVFGMPLHQLWD 762
 501 LSKQLEBISGVPDLRLQLLMSHNNLFLDSSHNNQLYSLTDLCSFR----- 552
 763 LSYNMIHLDPAFNKTKQLQVFGHNYLSDIPDIPKPYQGRIVDFVSHHLLRGLDN 822
 553 -----RIETSKGIIQHPFKS-----LAFNLTNNSVACICE---HOKF-LQW 590
 823 LFNNGMEKLDVSHNMKIPSSSLSLAALTLCGLHLSNNPISITISHMDLSNKRSLRY 882
 591 VKEQKQFLVNEQMTCAFPVEMNTSLVLDPNNS 623
 883 LDISYNYLLRIDDAVFAT---MPKLAVALDLSHN 912

RESULT 11

A41915

insulin-like growth factor-binding complex acid-labile chain precursor - human

N/Alternate names: Acid-labile Subunit (ALS)

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: A41915

R/leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.

Mol. Endocrinol. 6, 870-876, 1992

A/Title: Structure and functional expression of the acid-labile subunit of the insulin-1

A/Reference number: A41915; MUID:9257025; PMID:1379671

A/Accession: A41915

A/Status: preliminary

A/Molecule type: mRNA; protein

A/Residues: 1-605 <LEO>

A/Cross-references: UNIPROT:p35858; GB:M86826; NID:g184807; PIDN:AAA36047.1; PID:g184808

A/Note: sequence extracted from NCBI backbone (NCBI:110171)

F:75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>

F:99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>

F:123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>

F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>

F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>

F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>

F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>

F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>

F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>

F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>

F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>

F:339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>

F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>

F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>

F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>

F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>

F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>

F:483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>

F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

Query Match 6.7%; Score 291.5; DB 2; Length 605;
 Best Local Similarity 22.0%; Pred. No. 2e-10;

Matches 147; Conservative 86; Mismatches 233; Indels 201; Gaps 17;

39 CMDQKSKVPPDIPSTKNIDLSFNPLTKISYFSNSELQWLDLSRCIEIETEDKAMH 98
 60 CSSNLTRLPDGVGCGTQALWLDGNLSSVPPAFQNLSSIGFNLQGGQGLSEPOLLL 119
 99 GHLHLSNLIITGNPIQSPSPSGSLTSLNLYAVETGLALESFPIQLITLKLNVAN 158
 120 GLENLCHLERNQRLSLATGTFATPALASLGSNRLSRLDEGLFEGLSLMDNLGW 179
 159 NFIIH-----SKRPAYFSNLTNLVHVDLSYNYITQITVNDLQ 195
 180 NSLAVLPDAFRGGLSRELYLAGNRLAYIOPALFSGLAELRELDLSNALRAIYAN--V 237
 196 FLRENPOVNLSDMSINPIDIQDAFOGIR-LHELTLRGNPNSSNIMKTCLQNLGAV 254
 238 FVQPLRQKQIYLDRLN--IAVAPGAFGLKALRWLDSH--RVAAGLEDFPGLGLRV 294
 255 HRLIGFKERNLEIPEPSIMEGLCVTIDEFLTYTNFSDDIYKHECLAVASAMSLA 314
 295 LRL-----SHNIA 303
 315 GVSFKYLEVDKFKRMQSLSTIRCOLKQFPTLDLPKLSLTLTNWKSISFKVALPSSL 374
 304 SLR-----PRTRK-----DLHFLBEL----- 319
 375 YLDSRNALSFSGCCSYSDIGTNSLRHLS-SFNCAIIMSANFMGLBELQHLDPQHSITLKR 434
 320 -----QLGHNRIROL-----AERSFEGIGQLEVLTLDHNOQOE 352
 435 VTERSAFLSEKLYLDISYNTKIDPDGIFLGITSLNTLTKMANS----- 480
 353 V-KAGAPFLGTLNVAVMNLGNCNLRLNPQVFRGLGKLHSLHLEGSCLGRIAPHTFTGLSG 411

Qy 481 -----FKONTLSNVFANT-----TNLTFDLISCKQLEQISWGVDPDLRLQLLNNSHNLL 531
Dy 412 LRLFLKDNGLVGEBOISWGLABELLDELDTLSNQTLPHRLFGDLGKLEVLILSRRLA 471
Qy 532 FLDSHYNQVLSLTLDSCFNRIETSKGILQHPFKSLAFNULTNSVACICEHOKFQ-- 589
Dy 472 ELFPADALGPIQRAFWLIDVSHNRLEALPNSLAPLGRRLYLSLRNNSLRTFTTQPPGLERL 531
Qy 590 WVEKQKQFLVNVQMTCAATPE-----NMNTSLVDENNSTC-----YMYKTIIIS 633
Dy 532 WLEG-----NPMDCGCPILKALRDPALQNPASVPRFVQALCEGDDCQPPATYNNITC 583
Qy 634 VSQSVVI 640
Dy 584 ASPEEV 590

RESULT 12
T42218
alt-1 protein homolog - rat
N:Alternate names: MEGF4 protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T42218
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomic 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T42218
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1531 <NNK>
A:Cross-references: UNIPROT:088279; EMBL:AB011530; NID:G3449289; PIDN:BAA32460.1; PID:G3
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF4
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Query Match 6.6%; Score 287.5; DB 2; Length 1531;
Best Local Similarity 21.0%; Pred. No. 1.3e-09;
Matches 161; Conservative 99; Mismatches 266; Indels 239; Gaps 26;
Qy 5 WLAATLIMALFFSCITPGLN-----PCIEV 31
Dy 229 WLRQRTI-GLFTQCGSPASLGLNVAEYKSEFSCSGGGAQVPACTLSSGSCPMCS 287
Qy 32 VPIITVQCMQKLSKVPDDIPSTKNIDLSFNPPLKILKYSFSPSELQMLDLSREIEIT 91
Dy 288 CSNGIVDCRGKGLTALPAMLPETMEIRLELNGIKSIIPGAFSPYKLRIDLSNNQIAE 347
Qy 92 IEDKAWHGHLSNLITGNPIQSFSPGSGLTSLNVAVETKLASLESPFIQOLITL 151
Dy 348 IAPDAQGLSLNSLVYXGKIIDLRGVYGGIYTIQQL-----LMA 390
Qy 152 KKLVAHNPFLHSCKLPAVFSNLTNLVHVDLSYNYIQTITVNDLOFLRENPQVNLSDMSL 211
Dy 391 NKIN-----CIRPDAFQDLQNLISLSDYDNKIOSLAKGFTSIR-----AIOQLHMQ 438
Qy 212 NPIDFIODAFQGIKHELTLRGNFNSNMKT-----CL--QNLAGLHYHRLILGEFKDE 265
Dy 439 NP--FTCD-----CNLKMADFLKTNPIETTGARCAFPRLANKRIQOISKFKRCS 488
Qy 266 RNLEIFPESIMEGLCDVTIDFRLTYNDPSDDIVKPH-CLAVVSAMSLAGVI-KYLED 333
Dy 489 AKQOYFPG-----TEDYHL--NSECTSVACHKRCRASVVEGSGKLKSKIPER 537
Qy 324 VPKHFKWQSLIIRCOQKQPPITDLPLKSLITLTMNGSISPKKVALPSLYDLSNKL 383
Dy 538 IP-----QSTTELRLNNNEISILEATGL-----FKK--LSHKIKINLSNKKV 577
Qy 384 S-----PSGCCSYSD--LGTNSLRHLDLSFGALIMSANFMGLEELQHDLPQSTLTKRV 435

Dy 578 SEIEDGPFEGATSVSEHLHTANQLES-----VRSQMFRLDGLRTLMNRNRISCI 628
Qy 436 TEPFASLEKLYLDISTYNTKIDDPGIFLGLTSLNTLMAGNSPKDN----- 484
Dy 629 HN-DSFGLRNVALISLYDNHITTTISPGADFTLOALSTMLANPNCQOLAMLDMLR 687
Qy 485 -----TL 486
Dy 688 KRKITVGNPRCONPDFLRQIPLQDVAFPPDRCEGGEVGCPRPQCPQACADTVVRC 747
Qy 487 SN-----VPANTNLTFDLISCKQLEQISWGVDPDLRLQLLNNSHNLLFLDSH 537
Dy 748 SNKHQALPKGIPKQVTEL-YLDGNOFTLV-----GQLSTFKYIQVLDLSNNKISSLSNSS 803
Qy 538 YNQLISLTDCSNRLETSEKGIQHPFKSLAFNULTNSVA----- 579
Dy 804 FTNMSQULTLILSYNALQCCIPPLAFQGLRSRLSLSLGNDVSTLQEGIPADVTSLSHAI 863
Qy 580 -----CICEHOKFLQWKEQKQFLVNVQMTCAATPEANNTSLVL 618
Dy 864 GANPLYCDCHLRMLSSWVKGYK---EPGIARCAQPEPMGSKILL 905

RESULT 13
T10504
disease resistance protein Cf-2.1 - currant tomato
C:Species: Lycopersicon pimpinellifolium (currant tomato)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10504; T10515
R:Dixon, M.S.; Jones, D.A.; Keddie, J.S.; Thomas, C.M.; Harrison, K.; Jones, J.D.
Cell 84, 451-459, 1996
A:Title: The tomato Cf-2 disease resistance locus comprises two functional genes encoding
A:Reference number: Z17062; MUID:96190812; PMID:8608599
A:Accession: T10504
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1112 <DX>
A:Cross-references: UNIPROT:041397; EMBL:U42444; NID:g1184074; PIDN:AAC15779.1; PID:g118
A:Experimental source: cultivar Cf 2
A:Gene: Cf-2
C:Superfamily: Cf-2

Query Match 6.5%; Score 283.5; DB 2; Length 1112;
Best Local Similarity 22.6%; Pred. No. 1.4e-09;
Matches 182; Conservative 109; Mismatches 285; Indels 231; Gaps 32;
Qy 11 LIMALFPGCTPGSLNPCIENVNIT--YQCMQDKLSKVPDDIP--SSTKNIDLSFNPYLK 66
Dy 385 LEMLYLYNNQLSGSPASIGNLNNLSRLLYNNQLSGSPETIGYLSLTITVDLSNNSIN 444
Qy 67 ILKYSFNSFSELDWLSRCEIETEDKAWHGHLSNLITGNPIQSFSPGSGGLTS 126
Dy 445 GRIPLASFQMSLAFLELYENQLASSVPEIGYLSLVLDLSNALNSIPASFGNLAN 504
Qy 127 LENLVAETKLASLSFPFIQOLITLKLVAHNPFLHSCKLPAVFSNLTNLVHVDLSYNYI 186
Dy 505 LSRNLNLYNNQLSGSPETIGYLSLVLDLSNALNG-SIPASFGNLANLSRLNLYNNQ 563
Qy 187 QITTVNDLOFLRENPQVNS-----LDM----- 209
Dy 564 SGSIPEIGYLSLNDLGLSENALNSIPASIGNLNNLSMLLYNNQLSGSPETIGYLS 623
Qy 210 -----SLN---PIDFIODAFQGIKHELTLRGNFNS-----NTM 242
Dy 624 SLTYLSLGNNSLNGLIPAFGNRNQALINDNNLIGEIPSVCNLTSLLEVLYMPRNML 683
Qy 243 K-----TCLQNLAGLHYHRLILGEFKDERNLETFEPIIMGCLCDVTIDFRLTYNDPSDD 288
Dy 684 KGKVPQCLGNISNLYQLSMSNSNFSGEL-----PSSISNLTSLQIIDFG---RNNLEGA 734

QY 299 IYKPHICLANVSMSL-----AGVISIKYL-----EDVKKH-----K 329
 Db 735 IYKPHICLANVSMSL-----AGVISIKYL-----EDVKKH-----K 329
 QY 330 MOSLSIINCOQKQ--PPTL--DLPFLKSLITLTKMK--GSI--SPKVALPSLYLDSRA 382
 Db 793 LQVLDLGNQNLDTTPMMLGTLPRLVRLKLTNSKLGPRSSRAIMFEDLRIIDLSRA 852
 QY 363 LSPSCGCSYDGLSTSLRHLDLISFNGALIMSANFMGLLEQLDFOHSTLKAETESAPL 442
 Db 853 FS-----QDLPTSLFHL-----KGM-----TVDKTMEPSVE 881
 QY 443 SLEKLLYDIDYNTYKIDPDGIFLGITSLNTLKKMGNSFKONTLSNVANTNLTFELDS 502
 Db 882 S-----YDDSVVVVTK-----GLEIVIRILSL-----YVIDLS 912
 QY 503 KQLEQISWGVFDTLHRQLQNLMSHNNLLFLDSHYNOQLSLSTIDCSFNRLETSGILQ 562
 Db 913 SNKEGHIPSVLDGLIARILANVSHNALQGYIPSSLSGLSLESIDLSFNQLS-----G 966
 QY 563 HFPKSLA-----FNLTNNSV-ACICEHOKFLQW-----V 591
 Db 967 EIPQALSLTLEFLANTLHNTYQGTPOGPOPTRESNSYEGNDLRCGYPPVSKGCKDPV 1026
 QY 592 KEQKQFLVNEQMTCAPEVEMNTSLVLDENNSTCYMTKTIISVSVV-IVST-----V 645
 Db 1027 SEKNTVALRDO-----ESNBEFNDPFWKALMGSGLCIGSMYIILISTONLML 1080
 QY 646 AFLIYHFFHILLAGCKKYSRGESIT 672
 Db 1081 ARILEKLEKIMOR--RKKQRCGRNY 1105

RESULT 14

B3665

slit protein 2 precursor - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002

C/Accession: B3665

R/Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.

Genes Dev. 4, 2169-2187, 1990

A/Title: slit: an extracellular protein necessary for development of midline glia and co

A/Reference number: A3665; MUID:91099665; PMID:217636

A/Accession: B3665

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-146 <ROT>

A/Cross-references: GB:X53959

C/Genetics:

A/Genes: FlyBase:slit

A/Cross-references: FlyBase:FBgn0003425

C/Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

F/66-91/Domain: proteoglycan amino-terminal homology <PAH1>

F/101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F/125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F/149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F/173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F/197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F/228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>

F/288-313/Domain: proteoglycan amino-terminal homology <PAH2>

F/323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F/371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F/419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

F/450-494/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>

F/512-537/Domain: proteoglycan amino-terminal homology <PAH3>

F/547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>

F/596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>

F/620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>

F/651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>

F/708-733/Domain: proteoglycan amino-terminal homology <PAH4>
 F/743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
 F/767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
 F/846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
 F/1028-1061/Domain: EGF homology <EGF>
 F/1068-1099/Domain: EGF homology <EGF2>
 F/1115-1148/Domain: EGF homology <EGF1>

Query Match 6.3%; Score 273; DB 2; Length 1469;
 Best Local Similarity 21.6%; Pred. No. 9.4e-09;
 Matches 150; Conservative 86; Mismatches 241; Indels 218; Gaps 23;

QY 39 CMDQKSLKVPDDIPSSSTKNIDLSFNPDLKLSYFSNFSSELOMDLSRCEITIEDKAWH 98
 Db 308 CREKSLTSVPVTLPTDITDVLQGVNFIETLPKPSFSRRLRRIDLSNNNISRILAHDLIS 367
 QY 99 GLHLSNLILGNPILQSFSGFSGLTLENUVAVETKLASLESPIGQLITLKKLVANAH 158
 Db 368 GLKQLTTLVLYGNKIKDIPSGVFPGKLSRLILLANAEI----- 406
 QY 159 NFHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPOVNLSDMSINPIDFIO 218
 Db 407 -----SCIRKDAFRDLHSLSLSLYDNNIQLANGTFDAMKSMKTVAL-----AKNP--FIC 456
 QY 219 DOAFQGIK--LHELTIRGNFNSSNIMKTCLONLAGLHYHRLILGEFKDERMLEIPEPSIM 276
 Db 457 DQNRMLADYLHKNPIETSGARCESPK-----RHRRRISLR----- 496
 QY 277 EGLCDVTIDBERLYTYNDPSDIYKFLCLANVAMSILAGVSIKYLEDPK--HFKWQSL 334
 Db 497 -----KFKCSWELMKKLSG--ECRMDSDCPAMCHCGTVD 531
 QY 335 IIRCOLKQPTLDPFLKSLTLTKMK--GSIISFKV--ALPSLYLDSHNLSPSGCC 389
 Db 532 CTGRKLRKIPR-DLP-LHTTELLANDNEIGRISDGLFGRPLVLYLTKRNL----- 583
 QY 390 SYSDLGTNSLRLHDLISFNGALIMSANFMGLLEQLDFOHSTLKRVEFSAPLSLEKLY 449
 Db 584 --TGIEPVA-----FEGASHIQELQGEKKIKELISN--KNFGLGHQK 623
 QY 450 LDISTYNTKIDPDGIFLGITSLNTLKKMGNSFKONTLSNVAN----- 492
 Db 624 LNYLDNOISCVMPGSPFHLNLSLTSLNLSNPNFCNCHLWPAECVRKKSILNGARCAP 683
 QY 493 -----TNNLFLDLKSLQLOISGV--- 513
 Db 684 SKVADVOIKDLPHEBPKCSSENSGCCGADGCPSPCTGTGVACSRNQLKEIPRGIPAE 743
 QY 514 -----FDTLH-----RLQLNMSHNNLLFLDSHYNOQLYSLTIDCSFNRIR 555
 Db 744 TSELYLSNEIEQHYERIRHRLRSLTLDLSNNQITLISNTFANLTGLSLIISYNTLQ 803
 QY 556 -----TSKGI-----LQHP-----KSLAFNLTNNSVACICEHOKFLQW 591
 Db 804 CLQRLALSGNLNLRVSLHGNRISMLPEGSFEDLKSLTHIALGSPNYCDGLKWFSDWI 863
 QY 592 KEQKQFLVNEQ--MTCATPEVEMNTSLVLDENNST 624
 Db 864 K-----LDYVEPGIARCAEPQMDKILITPSSS 893

RESULT 15

A3665

slit protein 1 precursor - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002

C/Accession: A3665; A31640; S13523

R/Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.

Genes Dev. 4, 2169-2187, 1990

A/Title: slit: an extracellular protein necessary for development of midline glia and co

A/Reference number: A3665; MUID:91099665; PMID:217636

A/Accession: A3665

A/Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-1480 <ROT>
 A:Cross-references: GB:X53959; NID:98614; PIDN:CAA37910.1; PID:98615
 R:Rothenberg, U.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
 Cell 55, 1047-1059, 1988
 A:Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
 A:Reference number: A31640; MUID:98077533; PMID:3144436
 A:Accession: A31640
 A:Molecule type: DNA
 A:Residues: 881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YHA', <RO2>
 A:Cross-references: GB:M23543; NID:g340939; PID:g514357
 C:Genetics:
 A:Gene: FlyBase:slit
 A:Cross-references: FlyBase:FBgn0003425
 A:Locations: 1351/3
 C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
 C:Keywords: alternative splicing; growth factor
 F:66-91/Domain: proteoglycan amino-terminal homology <PAH1>
 F:101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:135-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:228-232/Domain: proteoglycan carboxyl-terminal homology <PCS1>
 F:288-313/Domain: proteoglycan amino-terminal homology <PAH2>
 F:323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
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 F:371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
 F:450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
 F:512-537/Domain: proteoglycan amino-terminal homology <PAH3>
 F:547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
 F:572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
 F:596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
 F:620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
 F:651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
 F:708-733/Domain: proteoglycan amino-terminal homology <PAH4>
 F:743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
 F:767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
 F:791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
 F:815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
 F:846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
 F:1028-1061/Domain: EGF homology <EGF>
 F:1068-1099/Domain: EGF homology <EGF2>
 F:1115-1148/Domain: EGF homology <EGF1>

Query Match 6.3%; Score 273; DB 2; Length 1480;

Best Local Similarity 21.6%; Pred. No. 9.5e-09;

Matches 150; Conservative 86; Mismatches 241; Indels 218; Gaps 23;

QY 39 CNDQKSKYVDDPSSTKNIIDSFNPKILKSYFSNFSFELQWLDLSRCEIETIEDKAWH 98
 DB 308 CEKSKLSYVPTLDDTTDVRLQNFITELPPKSFSPRLRRIDLSNNNISRIADALS 367
 QY 99 GLTHLSNLITGNPIQSFSGSGSLTSDENLVAVETKLASLESPIGQILITKULNVAH 158
 DB 368 GLKQLTTLVLVGNKKIDLPBGVFKGLGSLRLILLANNEI----- 406
 QY 159 NFTHSCKLPAYFSNLTNLVAVDLSYVIQITIVNDLQFLRNPQVNLSDMSLNPIDFIQ 218
 DB 407 -----SCIRKDAFRLDLSLSLYDNNTOSLANGTFDAMKSMKTVHL---AKNP--FTC 456
 QY 219 DQAFQGIK--LHELTLRGNFNSNIMKTCQNLGLVHRLILGEFDEERLEIFEPSIM 276
 DB 457 DCNLRWLIADYLNKPIETSGARCESPK-----RMHRRRIEELREE----- 496
 QY 277 EGLCDVTITDFRLTYTNSFSDDIKFKCLANVSAMSLAGVSIKYLEDPK--HFKWQSL 334
 DB 497 -----KFKCSWGLRMKLSG--ECRWDSDCPAMCHCEGTIVD 531
 QY 335 IIRQLKQFPFLDLPLKSLTLTMNK--GSISFKY--ALPGLSYLDLSRNALSFSGCC 389

DB 532 CTGRRLKEIPR-DIP-LHTTEILLNDNELGRISDGLFGRLPLVLYKLEIKRNL----- 583
 QY 390 SYDDLTGNSLRHLDLSFNGLIIMSANFMGLBELOHLDFOHSTLKRYTEFSAPLSLEKLY 449
 DB 584 --TGIEPNA-----FEGASHIQEIQLOENKIKEISN-KMFLGHLQVLT 623
 QY 450 LDISYNTKIDPDGIFLAGTSINTLTMAGNSFKDNTLSNVFAN----- 492
 DB 624 LNIYDNGISVMPGSEHNSLTSNLASNPFCNCHLWFAECVAKKSINGAARCGAP 683
 QY 493 -----TNUITFLDLSKCOLEOISWGV--- 513
 DB 684 SKYRDVQIKDLPHSEFKCSSENEGCLGDGCPSPCTGTGTVACSRNQLKEIPRGIPAE 743
 QY 514 -----FDTLH-----RLQLNNSHNNLLFLDSHYNOYLSLTLDSPNRIE 555
 DB 744 TSELYESNEIEQIHYERINHLRSLTRLDLSNNQITLSYTTANLTKSTLIISVTKQ 803
 QY 556 -----TSKGI-----LOHFP-----KSLAFNLTNNSVACTCEHOKFLQWV 591
 DB 804 CLQRHALSGIANNLRVYSLHGNRISMLPEGSFEDUKSLTHIALGSNPLCYDCGLKWFSDWI 863
 QY 592 KEOKQFLVNYEQ--MTCATVEKNTSLVDPNNST 624
 DB 864 K-----LDYVEPGIARCAEPQWMDKLIISTPSS 893

Search completed: March 12, 2005, 19:57:16
 Job time : 27.5445 secs